



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 96137**

**TO: Lorraine Spector**  
**Location: cm1/10b11/10b19** ✓  
**Art Unit: 1647**  
**Monday, June 16, 2003**

**Case Serial Number: 877804**

**From: Susan Hanley**  
**Location: Biotech-Chem Library**  
**CM1-6B05**  
**Phone: 305-4053**

**susan.hanley@uspto.gov**

### **Search Notes**



# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor  
308-4258, CM1-1E01

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 – Circ. Desk



QY	1	AGGAGCTGGGGAACTGTGGAACTTTTCGCGCTGATGCAGAAAGAACTCGGTGAATGG	60
Db	1 <th>AGGAGCTGGGGAACTGTGGAACTTTTCGCGCTGATGCAGAAAGAACTCGGTGAATGG</th> <th>60</th>	AGGAGCTGGGGAACTGTGGAACTTTTCGCGCTGATGCAGAAAGAACTCGGTGAATGG	60
QY	61 <th>ATAAATAAGAGTGGCGTTGCTCTGGTGTCCTTTGCTGGCAATCTTGGGCAGCGAATCTGG</th> <th>120</th>	ATAAATAAGAGTGGCGTTGCTCTGGTGTCCTTTGCTGGCAATCTTGGGCAGCGAATCTGG	120
Db	61 <th>ATAAATAAGAGTGGCGTTGCTCTGGTGTCCTTTGCTGGCAATCTTGGGCAGCGAATCTGG</th> <th>120</th>	ATAAATAAGAGTGGCGTTGCTCTGGTGTCCTTTGCTGGCAATCTTGGGCAGCGAATCTGG	120
QY	121 <th>ATGTCATCACTGGCTGTGTCATTTGCTCTAAATAGGGTCTTTTCTGCGCAAGACAGACAGGT</th> <th>180</th>	ATGTCATCACTGGCTGTGTCATTTGCTCTAAATAGGGTCTTTTCTGCGCAAGACAGACAGGT	180
Db	121 <th>ATGTCATCACTGGCTGTGTCATTTGCTCTAAATAGGGTCTTTTCTGCGCAAGACAGACAGGT</th> <th>180</th>	ATGTCATCACTGGCTGTGTCATTTGCTCTAAATAGGGTCTTTTCTGCGCAAGACAGACAGGT	180

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Qy	572	CTGAGTCTTTGAAAGTGTGATTTTTATGCGTCGAGTAAGAATGGGATTCGAAGAAATACACAAC	631
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Qy	812	TCAACATACGGCTTGAAAAGCTCCCTAATCTGGACAAGTTGTCTACCCCTCATGGAGGCC	871
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RESULT 3  
US-09-804-626-3  
; Sequence 3, Application US/09804626  
; Patent No. US20020128190A1  
; GENERAL INFORMATION:  
; APPLICANT: Lobel, Leslie  
; APPLICANT: Lustbader, Joyce  
; TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF

US-09-804-626-3  
 ; Sequence 3, Application US/09804626  
 ; Patent No. US20020128190A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lobel, Leslie  
 ; APPLICANT: Lustbader, Joyce  
 ; TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF  
 ; TITLE OF INVENTION: GONADOTROPIN RECEPTOR  
 ; FILE REFERENCE: 0575/62259/JPW/SHS  
 ; CURRENT APPLICATION NUMBER: US/09/804,626  
 ; CURRENT FILING DATE: 2001-03-09  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1551  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; US-09-804-626-3

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RESULT 4
US-09-804-626-5
; Sequence 5; Application US/09804626
; Patent No. US20020128190A1
; GENERAL INFORMATION:
; APPLICANT: Lobel, Leslie
; APPLICANT: Lustbader, Joyce
; TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR T
; FILE REFERENCE: GONADOTROPIN RECEPTOR
; CURRENT APPLICATION NUMBER: US/09/804,626
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-804-626-5

Query Match      28.0%; Score 663; DB 10; Length 2100;
Best Local Similarity 61.8%; Pred. No. 3.3e+200;
Matches 1116; Conservative 0; Mismatches 670; Indels 21; Gaps 3;

Qy      247 AGTCATCCCGAAAGGATCATCTTGCTGGATTGGAGACCCTGGAGAAAAATAGAGATCTCTCA 306
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Db      186 AGTGAATCCCATCTCAAGCITTCAGAGACTTAATGAGTGCTATAAAAATTTGAATCTCTCA 245

Qy      307 GAATGATGCTCTTGGAGTAATAGAGGCCAGATGTGTTCTCCAACCTTACCAAAGTTGCATGA 366
          ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db      246 GATTGATTCCTTGGAAAGATAGAAGCTAATGCCTTTGACAACCTCCTCAATTTGTCTGA 305
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Db 1488 ANTCTATGTTGGCCCTTGTGGGTGTCAGCAATGATGAGGTGAGTATTTGCTTCCC 1547  
Oy 1624 CATTGATGACGAGCGCTTGTGACAGCTGATGTTTGGCCCTGCTGCTGCTCATGT 1683  
Db 1548 CATTGATGACGAGCGCTTGTGACAGCTGATGTTTGGCCCTGCTGCTGCTCATGT 1607  
Oy 1684 CTTGGCTCTTTGGTCTATCTGCTGCTGCTATACCCATCTACCTCAGAGTGAATCC 1743  
Db 1608 GTGGGCTCTCTCATATTTGCTGCTGCTATTAATTTTGGCAGTTCGAACCC 1667  
Oy 1744 TACCATTTGCTGCTCATCAAGCCACCAAGATTTGCCAAGCGCATGGCCACATCTCT 1803  
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Oy 1804 CACAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1863  
Db 1728 CACCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1787  
Oy 1864 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1923  
Db 1788 ACTCTATCAGATGACCACTGCTAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1847  
Oy 1924 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1983  
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Oy 1984 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2043  
Db 1908 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2003  
Oy 2044 ATCCGCT 2050  
Db 1968 TTCAGCT 1974

1444 ATTGACGCTCACCCTAGAAAGATGGCATACCATCAGATCTGATGCACTGGAATG 1503  
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1428 AAAGTGTGGAATTAAGACATGGCCATCTGATTTGCTTGGAGGATGGCTTTCTTCT 1487  
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1744 TACCATTTGCTGCTCATCAAGCCACCAAGATTTGCCAAGCGCATGGCCACATCTCT 1803  
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1728 CACCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1787  
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2044 ATCCGCT 2050  
1968 TTCAGCT 1974

RESULT 5  
US-09-877-804-1  
; Sequence 1. Application US/09877804  
; Patent No. US20020061557A1  
; GENERAL INFORMATION:  
; APPLICANT: Nikolic, Karoly  
; APPLICANT: McFarland, Keith C.  
; APPLICANT: Segalo, Deborah L.  
; APPLICANT: Seeburg, Peter H.  
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules  
; FILE REFERENCE: P057691C2  
; CURRENT APPLICATION NUMBER: US/09/877,804  
; PRIOR APPLICATION NUMBER: US/08/207,814  
; PRIOR FILING DATE: 1994-03-07  
; PRIOR FILING DATE: 1991-10-31  
; PRIOR FILING DATE: 1989-05-05  
; NUMBER OF SEQ ID NOS: 22  
; SEQ ID NO 1  
; LENGTH: 2902  
; TYPE: DNA  
; ORGANISM: Rattus  
US-09-877-804-1

Query Match 27.1%; Score 640.8; DB 10; Length 2902;  
Best Local Similarity 61.4%; Pred. No. 5.1e-193;

Matches 1108; Conservative 0; Mismatches 677; Indels 21; Gaps 4;

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QY 241 AGTAATTCATCAACAGCTTTACAGGAGCTTAATGAGGTCGTAAATAATGAAATCTCTCA 300
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QY 307 GAATGATGCTTGGAAAGTAATAGAGGACAGATGTTCTCCAACTACCCCAAGTTGCATGA 366
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 GAGTGATTCCTGGAAGGATAGAAGCTAATGCTTTGACAACCTCCTCAATTTGCTGA 360
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 367 AATTAGATTGAAGGCCAACAAATCTTCTGTACATCAACCCGGAGCCCTTCAGAAATCT 426
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QY 361 ACTACTGATCCAGAACACCAAAACCTGCTATACATTGAACCTGGTCTTTACAAACCT 420
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 427 CCCAGCTCTCAGATATCTGTTAATATCCACACAGGCATTAAGCACTTGGCCAGCTGTCA 486
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QY 487 CAAGATCCAGTCTCTCCAA---AAGGTTCTACTAGACATTCAGATATAACATAAACATCCA 543
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 GAAGATCTCCTCTCTGAAATTAATTTCAATCTGGAATCTGTGATACTTACACATAAC 540
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QY 544 CATCGTTGCCAGCAACTCCTTCAATGGGACTGAGTTTGAAGTGTGATTTTATGGCTGAG 603
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QY 601 TGAATGGAATTTGAAGAGTCAAAAGCCATGATTTCAATGAGGAGCACTTAATCTCGCT 660
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QY 664 GAATCTAAGCGATPACAAATTAATTTGAAGAAATGSCCTAATGAGCTTTCCAGGGAGCCTC 723
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QY 721 GGGGCCAGCATCCTGGATATTTCTTCCACCAATTTGCAGGCTGCTCCGAGGCCACGGCT 780
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QY 844 GGACAAATTTGTCACCTCATGGAGGCCAGCCCTCACTACCCAGCACTGCTGTGCTTT 903
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QY 841 AGAAAAATTCACGAGCTCTGCTGCGCAGCTGACCTACCCAGCACTGCTGCGCCTT 900
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 904 TGCAAACTTGAACGGGCAATCTCTGAACCTTCATCAATTTGCAACAAAGTCTATTTAAG 963
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 -----CAGGAATTTGCCGAAGAAAGAACAGAAATTTTTCATTTTCCATTTTGTG 947
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 964 GCAAGATATTGATGATGACTCAATTTGGGATCAGAGTCTCTCTGATAGATGA 1023
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 948 AAACTTCTCCAACAAATCGGAAGCAGAGTTAGAAGCAGATAGAACAGACCTTTAT 1007
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QY 1024 ACCAGTTATGGAAGGATCTGACATGATGTACAATGATTTGATTTATGACTTATGATA 1083
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1008 CCGCCATCTTTGAGGAGAA--TGAACCTCAGTGGCTGGATATGATTTATGCTGCTG--- 1062
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QY 1084 TGAAGTTGTTGATGTGACCTGCTCACCAGCCAGCATGATTAATTCATGTGAAGATAT 1143
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QY 1063 TTCAACCAAGACACTCCAATGTGCTCCAGAACAGATGCTTTCAACCCCTGTGAAGATAT 1122
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QY 1123 TATGGCTATGCCCTCTCTAGGCTGCTGATTTGGCTGATTAATATAGTACGCCCTTTGG 1182
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1204 GAACACCAAGTCTGGTGGTCTGACCAAGCCCAATACAACTAACTGTGCCCGGTT 1263
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1183 CAACCTGACAGTCTCTTTGTTCTCTGACCACTGCTTATAAATCAAGTGGCCGCTT 1242
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1264 TCTTATGTGTAACCTGCGCTCTGCTGATCTCTGCTAGGCACTTACTTGTCTATTAGC 1323
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1243 CCTCATGTGTAATCTCTCTCTTTCAGACTTTTTCATGGGGCTCTACCTGCTGCTATTCG 1302
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

## RESULT 6

US-10-045-624B-1

; Sequence 1, Application US/10045624B

; Publication No. US20030009778A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Keith D.

; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING THYROID

; FILE REFERENCE: R-666

; CURRENT APPLICATION NUMBER: US/10/045, 624B

; PRIOR FILING DATE: 2002-08-19

; PRIOR FILING DATE: 2001-10-26

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2512

; TYPE: DNA

; ORGANISM: Mus musculus

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QY 1324 ATCAGTTGACATCCATACCAAGACCCAGTACCACAACTATGCCATTGACATGGCAACAGG 1383
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1303 CTCGGTGAGCTCCCAACAAAGGCCAGTACTATAACACAGCCATAGACTGGCAGACAGG 1362
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1384 AGCAGGCTGTGATGCTGCTGCTGCTTTTCACTGCTTTTCCAGTGAAGTGTCACTCTACAC 1443
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1363 GAGTGGCTGGGTGACAGCTGGCTTCTTTACTGTGTTTCCAGTGAAGTCTCTGTCTACAC 1422
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1444 ATTCACAGCCATCACCCCTAGAAAAGTGGCATACCATCACATGCTATGCAACTGGAATG 1503
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1423 CCTGACGGTTATCACCTGGAAGGTGGCACACCATCACCCTATGCTGTACAGCTAGACCA 1482
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1504 CAAGGTGACATCCGGCATGCTGCCAGGCTCATGCTGATTTGGGTGGACTTTTGGCTTTCG 1563
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1483 AAAGCTAAAGACTGAGGCATGCCATCCCAATTTATGCTCGGAGGATGGCTCTTTCTACGCT 1542
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1564 AGCTGCTCTCTCCCATCTTTGGCATCAGTACATGAAAGTGAAGCATCTGCCCTGCC 1623
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1543 GATCGCACAGATGCCCTTGTGGGTATCAGCAATTTACATGAAGTCAAGCATCTGCCCTCCC 1602
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1624 CATGGATATCGACAGCCCTTTGTACAGCTGTATGTTATGGCCCTCTCTTGTCTCAATGT 1683
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1603 CATGGATGTGAATCCACTCTGTCCCAAGTCTACATATTTATCCATCTTATCTCAAGCT 1662
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1684 CTTGGCTTTGTGGTCATCTGTGGTCTATATCCACATCTACCTCACAGTGAAGATCC 1743
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1663 GGTGGCTTTGCTGCTCATCTGTGCTTGTCTACATTTAGGATCTACTTTGCAGTTCAAAATCC 1722
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1744 TACCATTGTCTCTCATCAAGCGCACCAAGATTTGCCAAGCGCATGCCACACTCATCTT 1803
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1723 AGAGCTGACAGCTCTTAAAGAGCACAAAATTTGCTAAGAGTGGCCATCTCTCATCTT 1782
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1804 CACAGACTTTCTCTGATGSCCCCATTTTCATTTCTTGGCATTTTGGCTCTCCCTCAAGGT 1863
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1783 CACAGACTTTCAGCTGATGSCGCCCATCTCTTCTTTGGCATCTCGGCTGCTCAAGT 1842
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1864 GCGCTCATCATCTGTGTCAGGCGCAAGATTTCTCTAGTTCTGTCTTACCCCATCAATTC 1923
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1843 GCGCTTATCATCTGTCCCAACTCGAAATCTTACTGGTCTCTTTTATCTCTGTCATTC 1902
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1924 TTGTGCAATCTCTCTCTACGCCATTTTCACCAAGAACTTCCGGAGGACTTCTTCTCAT 1983
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1903 TTGTGCAATCTCAATTTCTGTATCGGATCTTCAGAGGCGCTTTCAGAGAGATTTCTTCT 1962
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1984 CTFGCTGAGCAAGTTTGGCTGTTTATGAAATGCAAGCCCGAGATTTACAGGACAGAAACCTC 2043
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1963 GCTGCTGAGCGGATTCGGCTGTGTAACGCCGGCGGAGCTTTACAGAGGAGGAAT 2022
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2044 ATCCGC 2049
DB ||| |||
QY 2023 TTCTGC 2028
DB ||| |||
```

## RESULT 6

US-10-045-624B-1

; Sequence 1, Application US/10045624B

; Publication No. US20030009778A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Keith D.

; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING THYROID

; FILE REFERENCE: R-666

; CURRENT APPLICATION NUMBER: US/10/045, 624B

; PRIOR FILING DATE: 2002-08-19

; PRIOR FILING DATE: 2001-10-26

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2512

; TYPE: DNA

; ORGANISM: Mus musculus



## RESULT 8

US-09-804-551B-19

; Sequence 19, Application US/09804551B

; Patent No. US20020056151A1

; GENERAL INFORMATION:

; APPLICANT: Bayer Aktiengesellschaft

; TITLE OF INVENTION: Receptors for peptides from insects

; FILE REFERENCE: Le A 34 394

; CURRENT APPLICATION NUMBER: US/09/804,551B

; CURRENT FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: DE 100 13 618.4

; NUMBER OF SEQ ID NOS: 92

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 2586

; TYPE: DNA

; ORGANISM: Drosophila melanogaster

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2583)

; US-09-804-551B-19

## Query Match

Best Local Similarity 8.2%; Score 193.6; DB 10; Length 2586;

Matches 471; Conservative 0; Mismatches 419; Indels 6; Gaps 2;

QY	1084	TGAAGTTGTGATGTGACCTGCTCACCAGCCAGATGATGATTAATCCATGTGAAGATAT	1143
DB	693	TCAACCGGGTTCGGTGCAGTGCCTGCCAATGCCAGGACCTTTTCTACCTGCGCCCATCT	752
QY	1144	CATGGGGTCAACATCTCTAGGCTCTGTATATGTTTATTAGCATCCTGGCCATTAAGTG	1203
DB	753	CTTCGATTGGTGACTCTGCGCTGCGGAGTGTGGGGTGTCTGTCTCTCTCTGGG	812
QY	1204	GAACACACAGTCTGTGTGCTCTGACCAACCCCAATACAACTAACTGCGCCCGGT	1263
DB	813	CAACGNAAGTGTGTGTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	872
QY	1264	TCTTATGTGTAACCTCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1323
DB	873	TCTAGTCTGTAATCTGCGCGCGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	932
QY	1324	ATCAGTTGATCATCCATACCAAGAGCCAGTACCAACATATGCCATTTGACTGGCAACAGG	1383
DB	933	CATTGTGGATGCGCGGCGAGTGGGCGAATTTTCGCATGTTTGGCCATTCCTTGGCAGATGC	992
QY	1384	AGCAGGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1443
DB	993	CGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1052
QY	1444	ATTGACAGCCATCACCTAGAGATGGCATACCATACCATGCTATGCTGCTGCTGCTGCTGCTGCT	1503
DB	1053	GTTGGCTGTGATCATCTTTGGAGCGCAATACGCCATCATCTGCTGCTGCTGCTGCTGCTGCTGCT	1112
QY	1504	CAAGGTGCAGCTCGGCGATCTGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1563
DB	1113	GAGGCTCTCTGAGGAGCGCGGATATATTAATGAGTGTAGGATGGGTTTTCCTCCCTGAT	1172
QY	1564	AGCTGCTCTCTTCCCATCTTTTGGCATCTAGTACATCAAGTGAAGCATCTGCTGCTGCTGCTGCT	1623
DB	1173	CATGGCTTTGATGCTTTGTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1232
QY	1624	CATGGATATCGACA---GCCCTTTGTACAGCTGTATGTTATGGCCCTCTCTGCTGCTGCTGCTGCT	1680
DB	1233	ATTCGAGACCAACCATGAGCCGCGAGTTTGAACCTATGTAATCTCACTGATGTTCACTCA	1292
QY	1681	TGCTCTGGCTTTGTGCTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1740
DB	1293	CGGATGCGCATTTCTCACTCTGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1350

## RESULT 9

US-09-864-761-4143

; Sequence 4143, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aeonica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1

; SEQ ID NO 4143

; LENGTH: 407

; TYPE: DNA

; ORGANISM: Homo sapiens



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; SEQ ID NO 263
; LENGTH: 2724
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-251-385-263

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Query Match: 3.4%; Score 80.4; DB 9; Length 2724;  
Best Local Similarity 43.8%; Pred. No: 4.2e-14;  
Matches 397; Conservative 0; Mismatches 506; Indels 3

Qy	1082	AATGAAGTTGTTGATGTGACCTTGCTGCTCACCAGGACGATGCAATTTAATCCATGTGAAGAT	1144
Db	1600	AAAGCCCTTCATTTCAGTGCAGTGTTCACCTTCCCGACGGCCCTTCAAACCCCTGTGAACAC	1659
Qy	1142	ATCATGGGGTACAACATCCTCAGGGTCTTGATATGTTTATTAGCATCTCGGCCATTACT	1201
Db	1660	CTGCTGTATGGCTGGCTGATCAGAAATGGAGTGTGGACCATAGCAGTCTTCGGCATTACT	1719
Qy	1202	GGGAACACCCACAGTGTGTGGTGGTCTGACCACAGGCAATPACAACTTAACGTGTGCCCGG	1261
Db	1720	TGTAATGCTTTGTGACTTCAACAGTTTTTCAGATCCCTCTGTACATTTCCCCCATTAATA	1779
Qy	1262	TTTCTTATGTGAACCTCGCCTTGCTGCTGATCTCTGATAGGCAATCTACTTGTACTATA	1321
Db	1780	CTGTTAATTTGGGGTCATCGCAGCAGTGAACATGCTCAGGGAGTCTCCAGTGGCGTGTG	1839
Qy	1322	GCATCAGTTGCACATCCATACCAAGAGCCAGTACCACACATATGCCATTGACTGGCAACA	1381
Db	1840	GCYGGTGTGATGCGTTTCATTTTGGCAGCTTTTGACGAGCATGGTGGCTGGTGGGAGAAT	1899
Qy	1382	GGAGCAGGCTGTGATGTGCTGGCTTTTTCACCTGTCTTTGCCAGTGAACCTGTCAGTCTAC	1441
Db	1900	GGGGTTGGTTGCCATGTCAATGTCTTTTGTCTCATTTTGCTTCAGAACTACTGTGTTTC	1959
Qy	1442	ACATTTGACAGCCCATACCCTAGAAGATGGCATACCATCACATGCTATGCAACTGGAA	1501
Db	1960	CTGCTTACTCTGGCAGCCCTGGAGCGTGGGGTCTCTCTGTAATATTCTGCAAAATTTGAA	2019
Qy	1502	TGCAAGGTGCAGCTCCGGCATGCTGCCAGCGTCATGGTATTTGGGCTGGACTTTTGCCCTC	1561
Db	2020	ACGAAGCTCCATTTCTAGCCCTGAAGTAATCATTTTGTCTCTGTGGCCCTGCTGGCCCTG	2079
Qy	1562	GCAGCTGCTCTCTTTCCCATCTTTTGGCATCAGTAGCTACATGAAAGTGAGCATCTGCCTG	1621
Db	2080	ACCATGSCCGCAGTTCCCTTGCTGGGTGGCAGCAAGTATGGCGCCTCCCTCTCTGCCTG	2139
Qy	1622	CCCATGGAATATGACAGCCCTTTGTGCAGCTGTATGTTATAGGCCCTCTCTTGTCTCAAT	1681
Db	2140	CCTTTGCTTTTGGGAGCCAGCACCATGGGCTACATGGTCTGCTCTCATCTTGTCTCAAT	2199
Qy	1682	GTCTGSCCTTTTGGTGCATCTGGCGTGTATACCCACATCTACCTCAGATGAGGAAT	1741
Db	2200	TCCCTTGTCTTCCATGATGACATTTGCCCTACACCAAGCTCTACTGCAATTTTGGACAAG	2259
Qy	1742	CCTACCAATTTGTCTCATCAAGCGACACCAAGATTGCCAAGGCGATGGCCACACATCATC	1801
Db	2260	GGAGACCTGGAGAATATTT--GGGACTGCTCTATGTAACAACATTTGCCCTGTGTGCTC	2316
Qy	1802	TTACAGACATTTCTGTCATGGCCCCCATTTTCATCTTTTGGCCATTTCTGCCCTCCCTCAAG	1861
Db	2317	TTCAACCACTGCATCTCTAAAGTGGCTGTGGCTTTCTGTGCTCTCTCTCTTTTAATAAAC	2376
Qy	1862	GTGCGCTCATCACTGTGTCCAGGCCAAGATCTCCTAGTCTTCTGTCTACCCCATCAAT	1921
Db	2377	CTTACATTTATCAGTCTCGAAGTAATTAAGTTATTCCTCTGTGGTGTAGTCCCACTTCCT	2436
Qy	1922	TCTTGTGCCAATCCTTTTCTCTACGGCCATTTTCAACCAAGAACTTCCGACGGGACTCTTC	1981
Db	2437	GCATGTCTCAATCCCTTCTCTACATCTTCTTCAATCCCTCACATTTAAGGAGGATCTGGTG	2496
Qy	1982	ATCCGTG	1987
Db	2497	AGCCTG	2502

RESULT 12

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US-10-251-385-277
; Sequence 277, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 277
; LENGTH: 2724
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-251-385-277

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Query Match 3.3%: Score 78.8: DB 9: Length 2724.

QY	1082	AATGAAGTGTTCATGTGACCTGCTCACCAAGCCAGATGCATTTAATCCATCTGAAGAT	1141
Db	1600 <td>AAAGCCCTTCATTCAGTGCAGTGTTCACCTTCCCAGGCCCTTCAACCCCTGTGAACAC</td> <td>1659</td>	AAAGCCCTTCATTCAGTGCAGTGTTCACCTTCCCAGGCCCTTCAACCCCTGTGAACAC	1659
QY	1142 <td>ATCATGGGGPACAAACATCCCTCAGGGCTTTGATATGGTTATTAGCATCTCGGCCCATTTACT</td> <td>1201</td>	ATCATGGGGPACAAACATCCCTCAGGGCTTTGATATGGTTATTAGCATCTCGGCCCATTTACT	1201
Db	1660 <td>CTGCTTGATGGCTGGCTGATCAGAAATGGAGTGTGGACCATACGAGTCTCTGGCACCTTACT</td> <td>1719</td>	CTGCTTGATGGCTGGCTGATCAGAAATGGAGTGTGGACCATACGAGTCTCTGGCACCTTACT	1719
QY	1202 <td>GGGAACACCACAGTGTGGTGGCTTGACCCACAGCCAAATACAACTAAGTGTGCCCGG</td> <td>1261</td>	GGGAACACCACAGTGTGGTGGCTTGACCCACAGCCAAATACAACTAAGTGTGCCCGG	1261
Db	1720 <td>TGTAATGCTTTGTGTGACTTCAACAGTTTTTCAGATCCCCCTCTGTACATTTTCCCCCATTTAA</td> <td>1779</td>	TGTAATGCTTTGTGTGACTTCAACAGTTTTTCAGATCCCCCTCTGTACATTTTCCCCCATTTAA	1779
QY	1262 <td>TTTCTTATGTGAACCTCGCCTTCGTGTGATCTCTGCATAGGCATCTACTTGGTACTTTATA</td> <td>1321</td>	TTTCTTATGTGAACCTCGCCTTCGTGTGATCTCTGCATAGGCATCTACTTGGTACTTTATA	1321
Db	1780 <td>CTGTTAATGGGGTCATCGCAGCAGTGAACATGCTCACGGAGTCTCCAGTGGCGTGCCTG</td> <td>1839</td>	CTGTTAATGGGGTCATCGCAGCAGTGAACATGCTCACGGAGTCTCCAGTGGCGTGCCTG	1839
QY	1322 <td>GCATCAGTTGACATCCATACCAAGAGCCAGTACCCAACTATGCCATTTGACTGGCAACA</td> <td>1381</td>	GCATCAGTTGACATCCATACCAAGAGCCAGTACCCAACTATGCCATTTGACTGGCAACA	1381
Db	1840 <td>GC'TGGTGTGGATCGCTTCACTTTTGGCAGCTTTTGCAGACATGGTGCCTGGTGGGAGAAT</td> <td>1899</td>	GC'TGGTGTGGATCGCTTCACTTTTGGCAGCTTTTGCAGACATGGTGCCTGGTGGGAGAAT	1899
QY	1382 <td>GGAGCAGGCTGATGCTGCTGGCTTTTTCACATGCTTTGGCCAGTGAACCTGTGAGTCTAC</td> <td>1441</td>	GGAGCAGGCTGATGCTGCTGGCTTTTTCACATGCTTTGGCCAGTGAACCTGTGAGTCTAC	1441
Db	1900 <td>GGGGTTGGTTGCCATGTGATGGTTTTTGTGTCATTTTTCAGAAATCATCTGTTTTC</td> <td>1959</td>	GGGGTTGGTTGCCATGTGATGGTTTTTGTGTCATTTTTCAGAAATCATCTGTTTTC	1959
QY	1442 <td>ACATTGACAGCCATCACCTTAGAAGATGGCATACCATCACACATGCTATGCAACTGGAA</td> <td>1501</td>	ACATTGACAGCCATCACCTTAGAAGATGGCATACCATCACACATGCTATGCAACTGGAA	1501
Db	1960 <td>CTGCTTACTCTGGCAGCCCTGGAGCGTGGGTCTCTGTGAAATATTCGCAAAATTTGAA</td> <td>2019</td>	CTGCTTACTCTGGCAGCCCTGGAGCGTGGGTCTCTGTGAAATATTCGCAAAATTTGAA	2019
QY	1502 <td>TGCAAGGTGAGCTCCGGCATGCTGCCAGGGTCATGGTATPVGCGCTGGACTTTTGCCCTC</td> <td>1561</td>	TGCAAGGTGAGCTCCGGCATGCTGCCAGGGTCATGGTATPVGCGCTGGACTTTTGCCCTC	1561
Db	2020 <td>ACGAAAGCTCCATTTCTAGCCCTGAAAGTAATCATTTTGTCTGTGCCCCCTGCTGGCCCTG</td> <td>2079</td>	ACGAAAGCTCCATTTCTAGCCCTGAAAGTAATCATTTTGTCTGTGCCCCCTGCTGGCCCTG	2079
QY	1562 <td>GCAGCTGCTCTCTTTCCCCATCTTTGGCATCAGTAGCTACATGAAGTGAAGTCTGCCTG</td> <td>1621</td>	GCAGCTGCTCTCTTTCCCCATCTTTGGCATCAGTAGCTACATGAAGTGAAGTCTGCCTG	1621
Db	2080 <td>ACCATGGCCGAGTCTCCCTTGTGGTGGCAGCAAGTATGGCGCCCTCCCTCTCTGCCTG</td> <td>2139</td>	ACCATGGCCGAGTCTCCCTTGTGGTGGCAGCAAGTATGGCGCCCTCCCTCTCTGCCTG	2139
QY	1622 <td>CCCATGGATATCAGACAGCCCTTTGTGCACAGCTGTATGTTATGGCCCTCTCTTGTCTCAAT</td> <td>1681</td>	CCCATGGATATCAGACAGCCCTTTGTGCACAGCTGTATGTTATGGCCCTCTCTTGTCTCAAT	1681
Db	2140 <td>CCTTTGCTTTTGGGGGCCACGACCATGGGCTACATGGTGCCTCTCATCTTGTCTCAAT</td> <td>2199</td>	CCTTTGCTTTTGGGGGCCACGACCATGGGCTACATGGTGCCTCTCATCTTGTCTCAAT	2199
QY	1682 <td>GTCCCTGGCCTTTGTGGTCACTCTGTGGTGGCTATACCCACATCACTCAAGTGAGGAAT</td> <td>1741</td>	GTCCCTGGCCTTTGTGGTCACTCTGTGGTGGCTATACCCACATCACTCAAGTGAGGAAT	1741
Db	2200 <td>TCCTCTGTCTCTCATGATGACCATTTGCCCTACACCAAGCTCTACTGTCAATTTTGGACAAG</td> <td>2259</td>	TCCTCTGTCTCTCATGATGACCATTTGCCCTACACCAAGCTCTACTGTCAATTTTGGACAAG	2259



Qy	1742	CCTACCAATTGTTGCTCATCAAGGAGCACCAAGATTGCCAAGGGCATGGCCACNACTCATC	1801
Db	2260	GGAGACTCGGAGAAATTT---GGGACTGCTCTGTAANAANACATTTGCCCTGTTGCTC	2316
Qy	1802	TTCAACAGACTTTCTGCAATGGGCCCCCAATTTCTATCTTCCCATTTCTGGCTCTCCCTCAAG	1861
Db	2317	TTCAACAACTGCATCTGAATGCCCTGGGCTTTCTTGTCTCTCTCTTTTAATAAAC	2376
Qy	1862	GTGCGGCTCATCACTGTGTCCAGGCGCAAGATTTCTCTAGTTCTTGTCTACCCCATCAAT	1921
Db	2377	CTTACATTTATCAAGTCTCTGAAGTAAATTAAGTTTATCTCTGGTGGTAGTCCCACTTCTC	2436
Qy	1922	TTCTGGCCAACTCTTCTCTAGGCCAATTTTCCCAAGAACTTTCCGCAAGGACTCTTCTC	1981
Db	2437	GCATCTCTAACTCCCTCTCTACATCTTGTCTGTCTCATTCCTCACTTTTAAGGAGGAGTCTGGTG	2496
Qy	1982	ATCCTG	1987
Db	2497	AGCCTG	2502

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RESULT 13
US-09-822-846-124
US-09-822-846-124 Application US/09822846
PUBLICATION NO. 2001-03-29
GENERAL INFORMATION:
APPLICANT: Jacoby, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LeValley, Edward R.
APPLICANT: Collins-Bacie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hillary
APPLICANT: Fechtel, Kim
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulkota, Kamalakhar
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT PILING DATE: 2001-03-29
PUBLICATION DATE: 2001-03-29
PRIOR PILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 829
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 124
LENGTH: 3429
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-846-124

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DB	376	TGTACACCTTCACAGAGTGCTTTTACGCCCTGTGAATTTTCTGGGAAGCTGGATGATT	435		
QY	1163	AGGGCTGTGATGATTTAGATCTTGGCCATTTACTGGGACACAGCTGCTGGTG	1222		
DB	436	CGTCTTACTGCTGGTCTTCTTCTGGTCTGGTCTTCTTCTGCTGATCTGATTA	495		
QY	1233	GTCTGACCAAGCCAACTACCTGACCAACTACTGTGCCCGGGTTTCTATGTGTGACACTCGCC	1282		

[illegible]

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1  RESULT 14
2  US-09-862-767A-1
3  : Sequence 1, Application US/09862767A
4  : Patent No. US20020034786A1
5  : GENERAL INFORMATION:
6  : APPLICANT: Pan, Yang
7  : TITLE OF INVENTION: TANGO-72 AND TANGO-77 NUCLEIC ACID MOLECULES AND POLYPEPTIDES
8  : FILE REFERENCE: MBIO1997-008P1RCP1CN1(M)
9  : CURRENT APPLICATION NUMBER: US/09/862.767A
10 : CURRENT FILING DATE: 2001-03-21
11 : PRIOR APPLICATION NUMBER: US 09/127,856
12 : PRIOR FILING DATE: 1998-08-03
13 : PRIOR APPLICATION NUMBER: US 60/054,646
14 : PRIOR FILING DATE: 1997-08-04
15 : NUMBER OF SEQ ID NOS: 9
16 : SOFTWARE: FastSeq for Windows Version 3.0
17 : SEQ ID NO: 1
18 : LENGTH: 3688
19 : TYPE: DNA
20 : ORGANISM: Homo sapiens
21 : FEATURE:

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NAME/KEY: CDS  
LOCATION: (2)...(1894)  
US-09-862-767A-1

Query Match 2.9%; Score 67.8; DB 10; Length 3688;

Best Local Similarity 43.2%; Pred. No. 5.6e-10;

Matches 373; Conservative 0; Mismatches 487; Indels 3; Gaps 1;

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QY 1163 AGGCTCTTATAGCTTTTATAGCATCTGCGCCATTTACTGGGAACACACATGCTGGTG 1222  
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DB 785 GTGCTAATTTATCTGGAATCTTATGTCATCTTCTGTCATCTTCTGTCGCTGCTGCT 844  
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RESULT 15

US-09-864-761-8142

Sequence 8142, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
FILE REFERENCE: Aecmca-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
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PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
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PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117,  
SEQ ID NO 8142  
LENGTH: 580  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.9  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.7  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7  
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.1  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.9  
US-09-864-761-8142

Query Match 2.3%; Score 53.8; DB 10; Length 580;

Best Local Similarity 56.5%; Pred. No. 4.1e-06;

Matches 100; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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QY 800 CTGAGGGCCAGGTCAACATACCCCTTGAAAGAGTCCCTTAATCTGGACAAAGTTTGTACC 859

Db 84 CTGATGACGAGAACACCTGGAGCTCTTAGGAACTTCCACTTTCCTTGAGTTTCTTCAC 143  
Oy 860 CTCATGGAGGCGCCTCAGCTACCGCCAGCCACTGCTGCTTTTCCAACTTGAG 916  
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Job time : 331 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 05:17:26 ; Search time 5925 Seconds  
(without alignments)  
11621.475 Million cell updates/sec

Title: US-09-877-804-5  
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Scoring table: IDENTITY\_MATRIX  
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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1	2366	100.0	2366	10	RATFSHTRA L02842 Rattus sp.
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3	1699.6	71.8	2393	9	HUMFSHRE M55085 Human foll
4	1681	71.0	2222	6	A76125 Sequence 1
5	1680	71.0	2186	9	HUMFSHRE M5489 H. sapiens f
6	1677.6	70.9	2179	6	AR003719 Sequence
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16	1564.6	66.1	2089	4	PIGFORE L31966 Sus scrofa
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18	1522.2	64.3	2428	4	SHPFTR L36115 Ovis aries
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20	1220.6	51.6	187310	2	AC101870 Mus muscu
21	1129.4	47.7	3115	5	D87871 U51097 Gallus gall
22	1125.2	47.6	2468	5	GGU51097 AC007189 Homo sapi
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ALIGNMENTS

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DEFINITION	Complete cds.					
ACCESSION	L02842.1	GI-204183				
VERSION	L02842.1	GI-204183				
KEYWORDS	follicle stimulating hormone (FSH) receptor.					
SOURCE	Rattus sp.					
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
REFERENCE	1 (bases 1 to 2366)					
AUTHORS	Sprenkel,R., Braun,T., Nikolic,K., Segaloff,D.L. and Seeburg,P.H.					

TITLE The testicular receptor for follicle stimulating hormone: structure and functional expression of cloned cDNA  
JOURNAL Mol. Endocrinol. 4 (4), 525-530 (1990)  
MEDLINE 91125358  
PUBMED 2126341

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BASE COUNT 642 a 608 c 486 g 630 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 AGGAGCTGGGAATCTGTGAAGTTTTCGGCTGATGCAGAAAGTCGGTGAATGG 60  
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2041	CTCATCGCTACCCACAACTTCCATCGCCGCAAGAGCCACTGCTCTCAGTCTCCAGAGT	2100
2101	CACCAATGATTTAGTCTGTGGTCTCTTAATCATTTTCATCGCCAGAGCTAAATAATCATGTG	2160
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2161	AAATATGATCTCTACCTCTGAAGACAAATATGACTCTTCTCGAGCAGGCCATCGACT	2220
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2221	AAATGGCAATCTCTATGACATCTCATCTAAATTAATCTCTCTGGGTCTCTGCATGGCAGT	2280
2221	AAATGGCAATCTCTATGACATCTCATCTAAATTAATCTCTCTGGGTCTCTGCATGGCAGT	2280
2281	ACTATCAGGAGCACTTAATATCAGCCTTTTGGCTCTCTGCACACTTAAATAATGTTAAGC	2340
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2341	CAATATGAGCACTTCAAAACCGCAC	2366
2341	CAATATGAGCACTTCAAAACCGCAC	2366
RESULT 2		
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LOCUS	Mus musculus follicle stimulating hormone receptor (Fehr) mRNA,	AF095642.1
DEFINITION	complete cds.	GI:3789955
ACCESSION	AF095642	
VERSION	AF095642	
KEYWORDS	Mus musculus.	
SOURCE	Mus musculus.	
ORGANISM	Mus musculus.	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE	Tena-Sempere,M., Manna,P.R. and Huhtaniemi,I. Molecular cloning of the mouse follicle-stimulating hormone receptor complementary deoxyribonucleic acid: functional expression of alternatively spliced variants and receptor inactivation by a	

JOURNAL	C56GT transition in exon 7 of the coding sequence
MEDLINE	Biol. Reprod. 60 (6), 1515-1527 (1999)
PUBMED	99262223
REFERENCE	2 (bases 1 to 2079)
AUTHORS	Tena-Sempere,M., Menna,P.R. and Huhtaniemi,I.
TITLE	Direct Submission
JOURNAL	Submitted (29-SEP-1998) Physiology, Biomedicine, Kluomeylinlinkatu 10, Turku 20200, Finland
FEATURES	Location/Qualifiers
source	1. genome="Mus musculus" 2. strain="129/Sv"
gene	/db_xref="taxon:10090"
CD5	/Locus_type="testis" 1..2079 /gene="Fshr" 1..2079 /note="FSHR" /product="follicle stimulating hormone receptor" /protein_id="AACG359.1" /db_xref="GI:378955"
BASE COUNT	534 a 552 c 429 g 564 t
ORIGIN	
Query Match	79.1% Score 1872.6; DB 10; Length 2079;
Best Local Similarity	91.8%; Prid. No. 0;
Matches 1950; Conservative	Mismatches 129; Indels 0; Gaps 0;
QY	71 ATGGCCCTTCCTCGTCTCCTTCCTCGTGCGCATCTTTGGGCACGGATCTGGATGTCATCAC 130
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QY	131 TGGCTGTGTCATGCTCTTAATAGGGTCTTTCTCTGCCAGACGAAGGTGACAGAGATT 190
DB	61 TGGCTGTGTCATGCTCTTAACAGGTTCTCTCTCCAGATACCAAGGTGACCAAGGT 120
QY	191 CCGACGACCTCCCGCGAAGCCCATTCGAATGAGTTTGCTCTACCAAGCTTCGAGTC 250
DB	121 CCGCCGACCTCCCGCGAAGCCCATTCGAATGAGTTTGCTCTACCAAGCTTCGAGTC 180
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DB	181 ATTCCAAAAGGATCATTTTCTGGAATTTGGGAGACTCGGAAAAATAGAGATCTCTCAGAAT 240
QY	311 GATGTCTTGGAAAGTAATAGAGCGCAGATGTGTTCTCCAACTACCAGATTCGATGAATT 370
DB	241 GATGTCTTGGAGATTAATAGAGCGCAGATGTGTTCTCCAACTACCAGATTCGATGAATT 300
QY	371 AGAGTCAAAAGCCCAAGCATCTTGTGTCATACTCCAGCGGAGCGGCTTCGAGATCTCCG 430
DB	301 AGGATCAAAAGGCTAACATCTGCTGTACATCAACCTCGAGGCTTCCNGAGATCTTCCC 360
QY	431 AGTCTCAGATATCTGTTTAATATCCACACAGGCATTAAGCACTTGCAGCTTGTCTCAAG 490
DB	361 AGTCTCCGATATCTGTTTAATATCCACACAGGCATTAACACATCTGCCAGCTTCTCAAG 420
QY	491 ATCCAGTCTCTCCAAAAGGTTCTACTAGACATTCGAATTAACATAATACATCCACATCGTT 550







QY 1924 TTGTGCCAATCCTTCTCTACGCCATTTTACCAAGAACTTCCGCGAGGACTTCTTCAT 1983  
 Db 1923 CTGTGCCAACCCCTTCTCTATGCCATCTTTACCAAAAACCTTTCGACAGATTCTTCAT 1982  
 QY 1984 CTGTCTGAGCAAGTTTGGCTGTATGAATGAAGCCAGATTTTACAGGACAGAAACCTC 2043  
 Db 1983 TCTGTGAGCAAGTTGCTGTATGAATGAAGCCAGATTTTATAGGACAGAAACTTC 2042  
 QY 2044 ATCCCGTACCCCAACTTCCATCCGCGGAAAGGACCTGCTCTCAGCTCCAGAGTCA 2103  
 Db 2043 ATCCCACTGTCCCAACACCCATCCAAAGGAATGGCCACTGCTCTCAGCTCCAGAGTCA 2102  
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 QY 2158 GTGAATAGGATCCACCTTGAAGACAAATATGAC--TCCTTCTGAGAGCAGGCCAT 2215  
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 QY 2216 GGACTAAATGGCAATCCTACTGCACATCTCATTAATTAATCTCTGCGTCTCTGCAT 2275  
 Db 2222 CAAGAGCTGACAGCTCTACATTTTCACTAATTTAATTAATTTCCCTGGCATCTTTA 2281  
 QY 2276 GGCAGACTGATCAGGACCAATTAATCACCCTTTGGCTCTCTCACACTTAATAATAGT 2335  
 Db 2282 AGGTAATTTGGTCAGCAACTATTAAATTCATGATACATTTAGGAAGCTGAATATTAGT 2341  
 QY 2336 ACACGCAATTAACCAACCAACCAACCGCAC 2365  
 Db 2342 AACACAATTAATTAAGATGAATAC 2371

## RESULT 4

A76125 2222 bp DNA linear PAT 19-OCT-1999  
 LOCUS  
 DEFINITION  
 A76125 Sequence 1 from Patent WO9320199.  
 A76125  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 DiJkema, R. and De L.R.  
 HUMAN GONADOTROPIN RECEPTOR (FSH RECEPTOR)  
 Patent: WO 9320199-A 1 14-OCT-1993;  
 AK20 NV (NL); DIJKEMA REIN (NL)  
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 ERNSFVGLSFVILWLNKNGLOELHNCAFNCTOLDENLSDNNLELPLNDVDFGAS  
 GPVILDISTRHSLPSGLENLKLRSTRYNLKLPLTEKLVALMEASLYTPSHCC  
 AFANRRQISELHPICDFAFPCEIDYNTQTGRQSSLAEDNESSYRGFTMTYFEF  
 YDLCEVDVDTSPKDFNCEIDYNTQTGRQSSLAEDNESSYRGFTMTYFEF  
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 DTRIAKRNALJTFELCMAPISFPAISNLSKVLPLTVSKAKILLVLPINSCNPF  
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 BASE COUNT 598 a 565 c 453 g 606 t

## ORIGIN

Query Match 71.0%; Score 1681; DB 6; Length 2222;  
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 QY 7 CTGGGAATCTGTGGAAGCTTTTCGGGCTGTAGTCAGAAAGAGTTCGGTGAATGGTAAT 56  
 Db 21 CTGAGATCTGTGGAGGTTTTTCTCTGCAAAATGCGAGAAAGAAATCAGGTGGATGGAT 80  
 QY 67 AAGGATGCCCTTGTCTCTCTGCTGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 126  
 Db 81 AATATATGCCCTGCTCTCTCTGCTGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 140  
 QY 127 TCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186  
 Db 141 TCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 200  
 QY 187 GATTCGCGACGACCTCCCGGACGACCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 246  
 Db 201 GATTCCTTCTGACCTCCCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 260  
 QY 247 AGTCATCCGAAAGGATCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306  
 Db 261 AGTCATCCAAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 320  
 QY 307 GAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366  
 Db 321 GAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 380  
 QY 367 AATAGGATTTGAAAGGCGCAACAATCTTCTGATCATCAACCGGAGGCTTCCAGAGCT 426  
 Db 381 AATAGGATTTGAAAGGCGCAACAATCTTCTGATCATCAACCGGAGGCTTCCAGAGCT 440  
 QY 427 CCCCAGTCTCAGATCTGTTAATATCAACACAGGCTTAAAGCACTTTGCCAGCTGTTCA 486  
 Db 441 TCCCAACCTTCAATATCTGTTAATATCAACACAGGCTTAAAGCACTTTGCCAGCTGTTCA 500  
 QY 487 CAAGATCAGCTCTCCAAAGGCTTCTACTAGACATTCAGACATTAACATAACATCCACAT 546  
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 QY 547 CTTTCCCGAGGAACTCTTTCATGGGCTGAGTTTTCAGAGTGATTTATGCTGCTGAGTAA 606  
 Db 561 AATTCAGAGAAATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620  
 QY 607 GAATGGATTTGAAGAAATACAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666  
 Db 621 GAATGGATTTGAAGAAATACAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680  
 QY 667 TCTAAGCAGTAAACATAATTTTGAAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726  
 Db 681 TCTAAGCAGTAAACATAATTTTGAAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740  
 QY 727 GCGAGTCTTTAGATATCTCAAGGACAAAGGCTTCCCTTACCAACCTGCTGCTGCTGCTGCTGCTGCT 786  
 Db 741 ACCAGTCTTTAGATATTTCAAGAACAGGATTCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800  
 QY 787 AATCTGAAGAGCTGAGGCGCAGGCTCAACATACCTGCTTGAAGAAAGCTTCCCTTAACTGCTGCTGCTGCTGCT 846  
 Db 801 AATCTGAAGAGCTGAGGCGCAGGCTCAACATACCTGCTTGAAGAAAGCTTCCCTTAACTGCTGCTGCTGCTGCT 860  
 QY 847 CAAGTTTGTACCCCTCAGGAGGCGCAGGCTCACTTACCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906  
 Db 861 AAGCTTGTGCGCTCATGGAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920  
 QY 907 AACTTTGAAGCGGCAAACTCTCTGAACTTCATCAATTTGCAACAAGCTTCTATTTTAAAGCA 966  
 Db 921 AACTTTGAAGCGGCAAACTCTCTGAACTTCATCAATTTGCAACAAGCTTCTATTTTAAAGCA 980  
 QY 967 AGATATTGATGATGACTCAAAATTTGGGCTGAGAGTCTCTCTGATAGATG---ATGA 1023  
 Db 981 ACAAGTTGATGATGACTCAAAATTTGGGCTGAGAGTCTCTCTGAGGACAGACATGA 1040

[illegible]

Oy	127	TCACTGGCTGTGTCATTTGCTCTAATAAGGGTCTTTCTCTGCCAAGACAGCAAGGTGACAGA	186
Db			
Db	132	TCATCGGATGTGTCACGTGCTTAACAGGGTTTTTCTCTGCCAAGAGAGCAAGGTGACAGA	191
Oy	187	GATTCCACCAGCCTCCCCGGAGCCATTGAACCTGAGGTTTGCTGCCTCACCAAGCTTCG	246
Db			
Db	192	GATTCTTCTGACTCCGAGGAATGCCATTGAACCTGAGGTTTTGTCTCTCACCAGGCTTCG	251
Oy	247	AGTCATCCCAGAAAGGATCATTTGCTGGATTGGAGACCTGGAGAAAATAGAGATCTCTCA	306
Db			
Db	252	AGTCATCCAAAAGGTGCTATTTTCAGGATTGGGGACCTGGAGAAAATAGAGATCTCTCA	311
Oy	307	GAATGATGCTTGGAGTAATAGAGGAGAGATGTGTTCTCCAACCTACCCAAAGTTGCATGA	366
Db			
Db	312	GAATGATGCTTGGAGGTGATAGAGGCAGATGTGTTCTCCAACCTTCCCAAATTAGCATGA	371
Oy	367	AATTAGGATTGAAAAGGCCAACCAATCTTCGTACATCAACCCGAGSCCTTCCAGAACTCT	426
Db			
Db	372	AATTAGGAATTGAAAAGGCCAACCACTGCTCTACATCAACCTTGAGCCCTTCCAGAACCT	431
Oy	427	CCCCAGCTCTCAGATATCTGTTAATATCCAAACACAGGCATTAAAGCACTTGCCAGCTGTCA	486
Db			
Db	432	TCCCAACCTTCAATATCTGTTAATATCCAACACAGGTATTAAAGCACCTTCCAGATGTCA	491
Oy	487	CAAGATCCAGTCTCTCCAAAAGTTCTACTAGACATTCAGAGATAACAATAAACATCCACAT	546
Db			
Db	492	CAAGATTCTCTCTCCAAAAGTTTACTTGACATTCAGAGATAACAATAAACATCCACAC	551
Oy	547	CGTTGCCAGGAACCTCTCATGGSACTGAGTTTTGAAAGTGTGATTTATATGGCTGAGTAA	606
Db			
Db	552	AATTGAAGAAATTTCTTTCGTGGGGCTGAGCTTTGAAAGTGTGATTTATGGCTGAATAA	611
Oy	607	GAATGGGATTGAAGAAATACACAACCTGTCATTCACGGAACTCAGCTAGATGAACCTGAA	666
Db			
Db	612	GAATGGGATTCAAGAAATACACAACCTGTCATTCAAATGGAACCCCACTAGATGAGCTGAA	671
Oy	667	TCTAAGCGATAACAATAATTTGGNAGAAATGTCCTAATGACGTTTTCCAGGGAGCCTCTGG	726
Db			
Db	672	TCTAAGCGATAAATAATTTAGAAGAAATGTCCTAATGATGTTTTCCACGGAGCCTCTGG	731
Oy	727	GCCAGTCATTTTGTATATCTCAAGGACAAAGGTCATTCCTTACCAAAACCATGGCTTAGA	786
Db			
Db	732	ACCAGTCATCTAGATATTTCAAGAACAGGATCCATTCCTGCCTAGCTATGGCTTAGA	791
Oy	787	AAATCTGAAGAGCTGAGGGCCAGGTCAACATACCGCTTGAAAAGCTCCCTAATCTGGA	846
Db			
Db	792	AAATCTTGAAGAGCTGAGGGCCAGGTGAGCTTACAACCTTAAAAAGCTGCTACTCTGGA	851
Oy	847	CAAGTTTGTCACTCATGAGGGCCAGCTCACCTACCCAGGCACCTGCTGCTCTTTTCG	906
Db			
Db	852	AAAGCTGTGCCCCCTCATGGNAGCCAGCTCACCTATCCCAGCCATTCGTGTCCTTTTCG	911
Oy	907	AAACTTGAAGCGGCAATCTCTGAACTTCATCCAAATTTGCAACAAGTCTATTTTAAAGCCA	966
Db			
Db	912	AAACTGGAGACGCAATCTCTGAGCTTCATCCAAATTTGCAACAATACTATTTTAAAGCCA	971
Oy	967	AGATATTGATGATATGACTCAAAATTTGGGGATCAGAGAGTCTCTCTGATAGATG---ATGA	1023
Db			
Db	972	AGNAGTTGATTTATGACTTCAGACTAGGGGTACAGAGATCTCTCTGTCGACAGACAATGA	1031
Oy	1024	ACCAGTTATGGAAGGATCTGACATGATGTACAATGAATTTGATTTATGACTTATGCTAA	1083
Db			
Db	1032	GTCCAGCTACAGCAGAGGATTTGACATGACGTACACTGAGTTTGACTTATGACTTATGCAA	1091
Oy	1084	TGAAGTTGTTGATGTGACCTGCTCACCANAAGCCAGATGCATTTTAAATCCATGTGAAGATAT	1143
Db			
Db	1092	TGAAGTGGTTGACGTGACCTGCTCCCTCAAGCCAGATGCATTCACACCCATGTGAAGATAT	1151
Oy	1144	CATGGGGTACAACATCTCTCAGGGTCTTGATATGGTTTATTAGCATCTCGCCATTTACTCG	1203
Db			
Db	1152	CATGGGGTACAACATCTCTCAGAGTCTGATATGGTTTATCAGCATCTCGCCATCACTGG	1211

Qy	1204	GACACACAGTGGTGCTGACCAAGCCAAATACAACACTAAGTGTGCCCGGTT	1266
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Qy	1264	TCTATTGTGAACCTGCCTTCGCTGATCTCTGCATAGGCAATCACTTGCCTACTATTAGC	1323
Db	1272	CCTTATGTGAACCTGCCTTCGCTGATCTCTGCATGGAAATCTACTGCTGCTCAATGC	1331
Qy	1324	ATCAGTTTGACATCCATACCAGAAGCCAGTAGTACCACAACATATGCCATTGACTTGGCAAACAGG	1383
Db	1332	ATCAGTTTGATATCCATACCAGAAGCCAAATATACAACATATGCCATTGACTTGGCAAACAGG	1391
Qy	1384	AGCAGGCTGTATGCTGCTGGCTTTTTCAGTCTGCTTTGGCAGTGAAGTGTCACTGTACAC	1443
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Qy	1624	CATGGATATCGACAGCCCTTTGTGCAGCTGTATGTTATGGCCCTCTCTGCTCAATGT	1683
Db	1632	CATGGATATTCAGACAGCCCTTTGTGCAGCTGTATGTCATGCTCCTCTGCTCAATGT	1691
Qy	1684	CCTGGCCTTTGTGTCATCTGTGCTGTATPACCCACATCACTCACAGTGAAGAAC	1743
Db	1692	CCTGGCCTTTGTGTCATCTGTGCTGTATATCCACATCTACTCTACAGTGGGAACCC	1751
Qy	1744	TACCATTGTGTCPCATCAAGACGACCAAGANTGCCAAGCGCATGCCACACTCATCTT	1803
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Qy	1864	CGCCCTCATCACTGTGTCGAAGCCAGATCTCCTAGTTCTGTTCTACCCCATCAATTC	1923
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Qy	1924	TTGTTGCCAATCCTTTCTCTACGCAATTTTCACCAAGAACTTCGCGAGGACATTTCTTCAT	1983
Db	1932	CTGTGCCAACCCCTTCTCTATGTCATCTTTACCAAAACTTTTGGCAGAGATTTCTTCAT	1991
Qy	1984	CCTGCTGAGCAAGTTTGGCTGTATGAATGCAAGCCAGATTTACAGGACAGAAACCTC	2043
Db	1992	TCTGCTGAGCAAGTTGCTGCTATGAATGCAAGCCAAATTTATAGGACAGAAATTC	2051
Qy	2044	ATCCGCTACCCACAACTTCCATGCGCCGNAAGAGCCACTGCTCTCAGCTCCCAGAGTCAC	2103
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Qy	2104	CAAT-----AGTTTACGTGCTTGTGCTCTTAATCATTTCCAGAACTTAAAAATCAAT	2157
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Db	2172	GTGAANAATGTATC	2184

RESULT 6  
AR003719  
LOCUS  
DEFINITION

AR003719 2179 bp DNA linear PAT 04-DEC-1998

[illegible]







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Db 491 CAAGATTCATTTCTCCAAAAGTTTTACTTGACATTCAGATTAACATTAACATCCACAT 550  
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Db 851 AAGCTTGTGCGCTCTCATGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 910  
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Oy 1024 ACCAGTTATGGAAGGATCTGACATGATGTACATGATGATGATGATGATGATGATGATGAT 1083  
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Db 1211 GACATCATAGTCTAGTGTGATCTTACTTACCGCATATTAACATCAAGTCCCGAGGTT 1270  
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RESULT 10  
BOVESHR  
LOCUS  
DEFINITION

2375 bp mRNA linear MAM 13-OCT-1994  
Bovine follicle stimulating hormone receptor (FSHR) mRNA, complete cds.



L22319  
 VERSION L22319.1 GI:404671  
 KEYWORDS follicle stimulating hormone (FSH) receptor.  
 SOURCE Bos taurus (strain Holstein) cDNA to mRNA.  
 ORGANISM Bos taurus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 2375)  
 AUTHORS Houde, A., Lambert, A., Saumande, J., Silversides, D.W. and  
 Lussier, J.G.  
 TITLE Structure of the bovine follicle-stimulating hormone receptor  
 complementary DNA and expression in bovine tissues  
 JOURNAL Mol. Reprod. Dev. 39 (2), 127-135 (1994)  
 MEDLINE 95127199  
 PUBMED 7826612  
 REFERENCE 2 (bases 1 to 2375)  
 Lussier, J.G.  
 DIRECT SUBMISSION  
 TITLE Submitted (30-SEP-1993) Jacques G. Lussier, CRRA, Faculty of  
 Veterinary Medicine, University of Montreal, P.O. Box 5,000, 3,200  
 Sicotte, St-Hyacinthe, Quebec, J2S 7C6, Canada  
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Search completed: June 16, 2003, 10:45:35  
Job time : 5938 secs





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RESULT 2
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XX
AC AAQ50013;
XX
Df 05-MAY-1994 (first entry)
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Xc FSH receptor.
XX
KW FSH; receptor; follicle stimulating hormone; GST;
KW glutathione-S-transferase; primer; PCR; amplification;
KW polymerase chain reaction; probe; antibody; overstimulation; ds.
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XX
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XX
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XX WPI; 1993-336907/42.
XX
XX P-PSDB; AAR42082.
XX
XX New follicle stimulating hormone receptor - and derived
XX antibodies, anti-idiotypic antibodies, and transfected cells,
XX useful e.g. in diagnosis and as antidote for FSH overstimulation
XX
XX Disclosure; Page 20-23; 42pp; English.
XX
XX The primers given in AAQ50029-34 were used in the cloning of GST-FSH-
XX R1, GST-FSH-R2 and GST-FSH-R3 fusion protein constructs.
XX Screening of the human testis cDNA library with a FSH-R specific
XX probe resulted in five recombinant phages positive in hybridisation.
XX Sequence analysis was performed of the 2222 bp fragment of pGEM32c1
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DB 1401 GGCAGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1460  
OY 1444 ATTGACAGCCTATCCCTAGAAAGATGGCATACCATCAGCATGCTATGCAACTGGAATG 1503  
DB 1461 TCTGACAGCTATCACTTTGAAAGATGGCATACCATCAGCATGCTGCTGCTGCTGCTGCT 1520  
OY 1504 CAAGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1563  
DB 1521 CAAGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1580  
OY 1564 AGCTGCTCTCTTCCCTTCTTGGCATCAGTAGTACATGAAAGTGAAGTGAAGTGAAGTGAAG 1623  
DB 1581 AGCTGCTCTCTTCCCTTCTTGGCATCAGTAGTACATGAAAGTGAAGTGAAGTGAAGTGAAG 1640  
OY 1624 CATGGATATCGACAGCCCTTTGTCACAGCTGTATGTTATGSCCTCTCTGCTCTCAATGT 1683

DB 1641 CATGGATATGACAGCCCTTTGTCACAGCTGTATGTCATGCTCCCTCTCTGTCCTCAATGT 1700  
OY 1684 CCTGGCCTTTTGTGCTCATCTGTGCTGCTATATACCCACATCTACCTACAGTGTGAGGAATCC 1743  
DB 1701 CCTGGCCTTTTGTGCTCATCTGTGCTGCTATATACCAATCTACCTACAGTGTGAGGAATCC 1760  
OY 1744 TACCATTTGTGCTCTCATCAAGCGACACCAAGATTTGCCAAGCGCATGGCCACATCATCTT 1803  
DB 1761 CAACATGCTGCTCTCTCTAGTGACACAGGATGCCAAGCGCATGGCCACATCATCTT 1820  
OY 1804 CACAGACTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1863  
DB 1821 CACTGACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1880  
OY 1864 GCCCTCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1923  
DB 1881 GCCCTCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1940  
OY 1924 TTGTGCCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1983  
DB 1941 CTGTGCCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2000  
OY 1984 CCTGCTGAGCAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2043  
DB 2001 TCTGCTGAGCAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2060  
OY 2044 ATCCGCTACCCACAACTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2103  
DB 2061 ATCCGCT 2120  
OY 2104 CAAT-----AGTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2157  
DB 2121 CAATGCT 2180  
OY 2158 GTGAAATGATGCT 2187  
DB 2181 GTGAAATGATGCT 2210

RESULT 3  
AAT63181  
ID AAT63181 standard; DNA; 2179 BP.  
XX AAT63181;  
AC AAT63181;  
XX AAT63181;  
DT 20-JUN-1997 (first entry)  
XX FSH receptor gene wild-type allele.  
DE Follicle stimulating hormone receptor; FSH receptor;  
KW ovarian dysgenesis; hypergonadotropic hypogonadism; diagnosis; ss.  
XX Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 75..2159  
FT mutation /\*tag= a  
FT 640  
FT /\*tag= b  
FT /note= "a C to T mutation in codon 189 correlates with ovarian dysgenesis"  
FT exon 70..227  
FT /\*tag= c  
FT /note= "nucleotides 70-227 correspond to nucleotides 1-158 of fshr exon 1"  
FT exon 228..298  
FT /\*tag= c  
FT /note= "nucleotides 228-298 correspond to nucleotides 7-77 of fshr exon 2"  
FT exon 299..373  
FT /\*tag= c  
FT /note= "nucleotides 299-373 correspond to"



QY 1204 GAACACCAAGTCTGGTGGTCTGACACCAAGCCAACTACAACTAACTGTGCCCGGTT 1263  
DB 1211 GAACATCATAGTGTAGTGTCTTACCTACAGCCCAATATAAATCAAGTCCCGAGTT 1270  
QY 1264 TCTTATGTAACTCGCTGGCTGTCTGTGATAGGCACTACTTGTCTACTTATAGC 1323  
DB 1271 CCTTATGTCAACCTGGCTTGTCTGTCTGTGATGGAATCTACCTGCTCTATTGC 1330  
QY 1324 ATCAGTTGATCATCCATACCAAGAGCAGTACCAACAACTATGCCATTGACTGCAACAGG 1383  
DB 1331 ATCAGTTGATCATCCATACCAAGAGCAGTACCAACAACTATGCCATTGACTGCAACAGG 1390  
QY 1384 AGCAGCTGTGATGTCTGGCTTTTTCACCTGTCTTTGGCAGTGAACCTGAGTCTACAC 1443  
DB 1391 GCGAGCTGTGATGTCTGGCTTTTTCACCTGTCTTTGGCAGTGAACCTGAGTCTACAC 1450  
QY 1444 ATTGACAGCCATCACCTTGAAGAAGTGGCATACCATCACATGCTATGCAACTGGAATG 1503  
DB 1451 TCTGACAGCTATCACCTTGAAGAAGTGGCATACCATCACATGCTATGCAACTGGAATG 1510  
QY 1504 CAAGTGGCAGCTCCGCGATGCTGCCAGCGTCTATGTTGGCTGGACTTTTGCCTTCCG 1563  
DB 1511 CAAGTGGCAGCTCCGCGATGCTGCCAGCGTCTATGTTGGCTGGACTTTTGCCTTCCG 1570  
QY 1564 AGCTGCTCTCTTCCCGATCTTTGGCATCAGTACATGAAAGTGAAGTGAAGTGAAGTGAAG 1623  
DB 1571 AGCTGCTCTCTTCCCGATCTTTGGCATCAGTACATGAAAGTGAAGTGAAGTGAAGTGAAG 1630  
QY 1624 CATGATATGACAGCCCTTTGTCACAGCTGTATGTTATGGCCCTCTTGTCTCAATGT 1683  
DB 1631 CATGATATGACAGCCCTTTGTCACAGCTGTATGTTATGGCCCTCTTGTCTCAATGT 1690  
QY 1684 CTGGCTTGTGGTCTATGCTGGCTGTATACCCACATCTACCTCAGAGTGAAGTCC 1743  
DB 1691 CTGGCTTGTGGTCTATGCTGGCTGTATACCCACATCTACCTCAGAGTGAAGTCC 1750  
QY 1744 TACCATTTGTCTCATCAAGGACACCAAGATTTGCCAAGCGATGGCCACATCTCATCTT 1803  
DB 1751 CAACATCGTCTCTCTCTAGTGACACCAAGATTTGCCAAGCGATGGCCACATCTCATCTT 1810  
QY 1804 CACAGACTTCTCTGATGGCCCGCCCATTTTCATTTCTTGGCATTTTCTGCTCCCTCAAGT 1863  
DB 1811 CACTGACTTCTCTGATGGCCCGCCCATTTTCATTTCTTGGCATTTTCTGCTCCCTCAAGT 1870  
QY 1864 GCGGCTCATCAGTCTGCAAGGCAAGATTTCTCTAGTCTTCTTACCCCATCAATTC 1923  
DB 1871 GCGGCTCATCAGTCTGCAAGGCAAGATTTCTCTAGTCTTCTTACCCCATCAATTC 1930  
QY 1924 TTGTGCAATCTCTCTTACCGCCATTTTCACCAAGAACTTCCGCGAGGACTTCTTCTAT 1983  
DB 1931 CTGTGCAACCCCTCTCTATGCCATTTTACCAAAACTTTTCGAGAGATTTCTTCTAT 1990  
QY 1984 CTTGCTGAGCAAGTGTGGCTGTATGAATGCAAGCCAGATTTACAGGACAGAAACCTC 2043  
DB 1991 TCTGCTGAGCAAGTGTGGCTGTATGAATGCAAGCCAGATTTTATAGGACAGAACTTC 2050  
QY 2044 ATCCGCTTACCAACTTCCATCCGGAAGCAAGTCTGCTCTCAGCTCCAGAGTCCAC 2103  
DB 2051 ATCCATGCTCCACACACCCATCCAGGAATGGCCACTGCTCTTACGCTCCCAAGTCCAC 2110  
QY 2104 CAAT-----AGTTAGCTGCTTGTCTCTTAACTATTCATCCAGAACTTAAATCAAT 2157  
DB 2111 CAATGGTTCCATTTACATACTTGTCCCTCTTAAGTCACTTTAGCCCAAACTTAAACACAAT 2170  
QY 2158 GTGAAAT 2165  
DB 2171 GTGAAAT 2178

RESULT 4

AAQ29377

ID AAQ29377 standard; DNA; 2180 BP.

XX AAQ29377;  
XX AC  
XX DT 04-MAR-1993 (first entry)  
XX FSHR DNA.  
XX DE  
XX KW Human: follicle stimulating hormone receptor; maturation;  
XX KW spermatogenesis; birth control; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 75..2159  
XX FT /\*tag= a  
XX FT sig\_peptide 75..126  
XX FT /\*tag= b  
XX FT mat\_peptide 127..2159  
XX FT /\*tag= c  
XX PN W09216620-A.  
XX XX  
XX PD 01-OCT-1992.  
XX PF 02-JAN-1992: 92WO-US00122.  
XX PR 15-MAR-1991: 91US-0670085.  
XX PA (ISTF ) ARS APPL RES SYST HOLDING NV.  
XX PI Cheng SVY, Kelton CA, Nugent NP, Schweickhardt RL;  
XX WPI: 1992-349206/42.  
XX P-PSDB; AAR29377.  
XX PT Pure human FSH receptor, fragments and mutants - for preventing  
XX PT follicle growth, maturation and spermatogenesis, also for use of  
XX PS appropriate cell lines for bio-assays of FSH  
XX PS Claim 7; Page 25; 48pp; English.  
XX CC The DNA sequence encoding human follicle stimulating hormone  
XX CC receptor (FSHR) was obt'd. by screening a lambda gt11 cDNA library  
XX CC constructed from RNA extracted from human testis and amplified, with  
XX CC a rat FSHR cDNA clone as a probe. Positive colonies were used for  
XX CC a secondary screen which isolated five putative human FSHR clones.  
XX CC None of the clones contained the complete hFSHR coding region but  
XX CC could be overlapped using GCG to give the complete sequence. hFSHR  
XX CC binds to FSH to reduce endogenous FSH bioactivity, in females to  
XX CC prevent follicle growth and maturation and in males to prevent  
XX CC spermatogenesis, i.e. as a birth control agent.  
SQ Sequence 2180 BP; 577 A; 560 C; 444 G; 599 T; 0 other;

Query Match 70.7%; Score 1673.4; DB 13; Length 2180;  
Best Local Similarity 86.6%; Pred. No. 0;  
Matches 1869; Conservative 0; Mismatches 280; Indels 9; Gaps 2;

QY 18 GTGGAAGTTTTCGGCTGATGTCAGAAAGATCGGTGAATGAATAAATAGGATGCGCT 77  
DB 23 GAGGTTTTCCTCTGCAAAATGCAAGGAAGAAATCAGGTGGATGATCAATATATGCCC 82  
QY 78 TGCTCCTGGTCTCTTCTGCTGGCATTCTTGGCAGGATCTGGAATGTCATCAGTGGCTGT 137  
DB 83 TGCTCCTGGTCTCTTCTGCTGGCATTCTGAGCTTGGCTCAGGATGTCATCAGGATCT 142  
QY 138 GTCATTTGCTTAATAGGGTCTTTTCTTGCACAGACAGCAAGGTGACAGATTCGACCG 197  
DB 143 GTCACCTGCTTAACAGGGTTTTTCTCTGCAAGAGAGAGCAAGGTGACAGATTCCTTCTG 202  
QY 198 ACCTCCCGGAGAGCGCCATTGAACTGAGTTTGTGCTCACCAGCTTCGAGTCAATCCGA 257  
DB 203 ACCTCCCGGAGAGCGCCATTGAACTGAGTTTGTGCTCACCAGCTTCGAGTCAATCCGA 262





FH Key Location/Qualifiers  
 FT Intron 1..102  
 FT exon /\*tag= a  
 FT 103..1450  
 FT /\*tag= b  
 FT /\*number= "10"  
 FT CDS 103..1336  
 FT /\*tag= c  
 FT /codon\_start= 104  
 FT /partial  
 FT primer\_bind complement (53..72)  
 FT /\*tag= d  
 FT /note= "primer A1"  
 FT primer\_bind complement (225..244)  
 FT /\*tag= e  
 FT /note= "primer B1"  
 FT primer\_bind 254..273  
 FT /\*tag= f  
 FT /note= "primer A2"  
 FT primer\_bind complement (468..487)  
 FT /\*tag= g  
 FT /note= "primer C1"  
 FT primer\_bind 493..512  
 FT /\*tag= h  
 FT /note= "primer B2"  
 FT primer\_bind complement (675..694)  
 FT /\*tag= i  
 FT /note= "primer D1"  
 FT primer\_bind 713..732  
 FT /\*tag= j  
 FT /note= "primer C2"  
 FT primer\_bind complement (850..869)  
 FT /\*tag= k  
 FT /note= "primer E1"  
 FT primer\_bind 904..923  
 FT /\*tag= l  
 FT /note= "primer D2"  
 FT primer\_bind complement (1023..1041)  
 FT /\*tag= m  
 FT /note= "primer F1"  
 FT primer\_bind 1049..1088  
 FT /\*tag= n  
 FT /note= "primer E2"  
 FT primer\_bind complement (1171..1190)  
 FT /\*tag= o  
 FT /note= "primer G1"  
 FT primer\_bind 1230..1249  
 FT /\*tag= p  
 FT /note= "primer F2"  
 FT primer\_bind 1409..1423  
 FT /\*tag= q  
 FT /note= "primer G2"  
 XX WO200144502-A2.  
 XX 21-JUN-2001.  
 XX 18-DEC-2000; 2000WO-EP12886.  
 XX 16-DEC-1999; 99EP-0125148.  
 XX 29-FEB-2000; 2000US-0185670.  
 XX (GROM/) GROMOLL J.  
 XX Gromoll J, Simoni M, Nieschlag E, Behre MH, Perez M;  
 XX WPI; 2001-398165/42.  
 XX P-PSDB; AAB82468.  
 XX Determining dosage of follicle-stimulating hormone (FSH) for the  
 XX treatment of infertility of women, comprises determining a FSH receptor  
 XX variant of a woman to be treated, by restriction fragment length  
 XX polymorphism

XX Disclosure; Fig 6; 27pp; English.  
 XX The present sequence is that of the exon 10 region of the human  
 CC follicle stimulating hormone (FSH) receptor gene on chromosome 2p21.  
 CC This region of the gene encodes the transmembrane and intracellular  
 CC domain (see AAB82468) of the FSH receptor. A claimed method for  
 CC determining the dosage of FSH required in the treatment of  
 CC infertility of a woman comprises determination of the FSH receptor  
 CC variant by isolating genomic DNA from a blood sample of the woman  
 CC and determining whether the isolated DNA codes for the FSH receptor  
 CC variant Ala307/Ser680 or Thr307/Asn680. This is achieved by  
 CC partial amplification of the FSH receptor DNA by using a pair  
 CC of primers that flank the DNA coding for amino acids 307 and/or 680  
 CC of the FSH receptor protein. The amplified DNA is then digested,  
 CC preferably using BsrI, and the FSH receptor variant is determined  
 CC by restriction fragment length polymorphism. Suitable primers are  
 CC given in AAF90530-43. Women bearing the homozygous FSH receptor  
 CC variant Ala307/Ser680 may be given a high dosage of FSH. Women  
 CC bearing the homozygous FSH receptor variant Thr307/Asn680 may be  
 CC given a low dosage of FSH, while women with a heterozygous state  
 CC may be given an intermediate dosage of FSH.  
 XX

SQ Sequence 1450 BP; 356 A; 387 C; 283 G; 424 T; 0 other;  
 Query Match 41.2%; Score 975.6; DB 22; Length 1450;  
 Best Local Similarity 86.4%; Pred. No. 1.3e-293;  
 Matches 1103; Conservative 0; Mismatches 164; Indels 9; Gaps 2;  
 QY 923 ATCTCTGAACCTTCATCCAAATTTGCAACAAGTCTATTATTAAGCAACATATTTGATGATG 982  
 DB 101 AGCTCTGAGCTTCATCCAAATTTGCAACAATCTATTATTAAGCAAGTGTATTATATG 160  
 QY 983 ACTCAAAATTTGGGATCAGAGAGTCTCTCTGATAGATG---ATGAACCCAGTATGGAAGA 1039  
 DB 161 ACTCAGACTAGGGGTGAGAGATCCTCTCTGGCAGAGACAATGAGTCCAGCTACACGAGA 220  
 QY 1040 GGATCTGACATGATGTACAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1099  
 DB 221 GGATTTGACATGACGTACACTGAGTTTGTGATTTGATTTGATTTGATTTGATTTGATTTG 280  
 QY 1100 ACCTGCTCACCAGGAGCAGATGATTAATCCATGTGAAGATATCATGGGTGACAACATC 1159  
 DB 281 ACCTGCTCCCTTACGACAGATGATTCACCCATGTGAAGATATCATGGGTGACAACATC 340  
 QY 1160 CTCAGGGTCTTGATATGGTTTATTAGCATCTCTGGCCATTTACTGGGAACACACAGAGCTG 1219  
 DB 341 CTCAGAGTCTGATATGGTTTATTAGCATCTCTGGCCATTTACTGGGAACATCATAGTGCTA 400  
 QY 1220 GTGGTCTGACCAAGCCAATACAACTAACTGTCGCCCGGTTTCTTATGTGTACCTC 1279  
 DB 401 GTGATCCTTAACCTACCAAGCCAATATAAATCACTGAGTCCCGAGGTTCCTTATGTGCAAC 460  
 QY 1280 GCCTTCGCTGATCTCTGATAGGATCTACTTCTACTTATAGCATCAGTTGACATCCAT 1339  
 DB 461 GCCTTTGCTGATCTCTGATAGGATCTACTTCTACTTATAGCATCAGTTGATATCCAT 520  
 QY 1340 ACCAAGAGCAGTACCAACTATGCAATGATGCAACAGAGAGAGAGCTGTGATGCT 1399  
 DB 521 ACCAAGAGCAGTACCAACTATGCAATGATGCAACAGAGAGAGAGCTGTGATGCT 580  
 QY 1400 GCTGGGCTTTTTCAGTGTCTTTGGCAGTGAAGTGTGATCTACACATTTGACAGCCATCACC 1459  
 DB 581 GCTGGGCTTTTTCAGTGTCTTTGGCAGTGAAGTGTGATCTACACATTTGACAGCCATCACC 640  
 QY 1460 CTAGAAAGATGGCATACCATGCTATGCAACTGGAATGCAAGTGCAGCTCCCG 1519  
 DB 641 TTGGAAGATGGCATACCATGCTATGCAACTGGAATGCAAGTGCAGCTCCCG 700  
 QY 1520 CATGCTGCCAGCGTCAATGGTATTTGGCTGGAGCTTTTTCCTTTCGAGCTCTCTCTTCC 1579  
 DB 701 CATGCTGCCAGTGTCAATGGTATTTGGCTGGAGCTTTTTCCTTTCGAGCTCTCTCTTCC 760

WPI: 2001-398165/42.

Determining dosage of follicle-stimulating hormone (FSH) for the treatment of infertility of women, comprises determining a FSH receptor polymorphism.

Disclosure: Flg 5: 27pp: English.

The present sequence is that of the exon 10 region of the human follicle stimulating hormone (FSH) receptor gene on chromosome 2p21. This region of the gene encodes the transmembrane and intracellular domain of the FSH receptor. A claimed method for determining the dosage of FSH required in the treatment of infertility of a woman comprises determining a polymorphism in the FSH receptor gene of a genomic DNA from a blood sample of the woman and determining whether the isolated DNA codes for the FSH receptor variant Ala307/Ser680 or Thr307/Asn680. This is achieved by partial amplification of the FSH receptor DNA by using a pair of primers that flank the DNA coding for amino acids 307 and/or 680 of the FSH receptor protein. The amplified DNA is then digested, preferably using BspI, and the FSH receptor variant is determined by restriction fragment length polymorphism. Suitable primers are variant AA990530-43. Women bearing the homozygous FSH receptor variant Ala307/Ser680 may be given a high dosage of FSH. Women bearing the homozygous FSH receptor variant Thr307/Asn680 may be given a low dosage of FSH. Women bearing a heterozygous state may be given an intermediate dosage of FSH.

Sequence 1243 BP; 297 A; 354 C; 247 G; 345 T; 0 other;

Query Match 39.9%; Score 943.2; DB 22; Length 1243;  
Best Local Similarity 86.8%; Pred. No. 1.6e-283;  
Matches 1075; Conservative 0; Mismatches 153; Indels 10; Gaps 3;

923 ATCTCTGAGCTTCATCCAACTTTGCAACAGTCTATTTTAAGSCAAGATATTGATGATGTC 982  
Db 4 AGCTCTGAGCTTCATCCAACTTTGCAACAAATCTATTTTAAGSCAAGATTTGATTTATG 63  
Oy 983 ACTCAATTTGGGATCAGAGATCTCTCTGATAGTGTG---ATGACCCAGTTATGGAAA 1039  
Db 64 ACTCAATAGGGGTCAGAGATCTCTCTGCGAGATGACATCTGCGCTACAGACGAA 123  
Oy 1040 GCATCTGCATGATGACATGAATGATTTGATTTGATGACTTTATGATGATGTTGATGTCG 1099  
Db 124 GCATTTGCATGATGACGTTACATCTGACTTTGACTATGACTTTATGCAATGAAGTGTTCAGCTG 183  
Oy 1100 ACCTGCTGCACAAAGCCAGATGCATTTAATCCATGTGAGATATCATGGGTGCACATC 1159  
Db 184 ACCTGCTGCCCTTAAGCCAGATGCATTTAACCATATGAGATATCATGGGTGCACATC 243  
Oy 1160 CTGAGGCTCTGATATGGTTATATGATATCTCTGGCCATCTATCGGGAAACACCACTGCTG 1219  
Db 244 CTGAGATGCTGATATGTTTATNCAGCTCTCTGGCATCTATCGGGAAACATCATGTCGTA 303  
Oy 1220 GTGCTGCTTGACACAGSCAATCAACAATCACTGTGGCCGGTCTTCTATGCTGAACCTC 1279  
Db 304 GTGATCTCTACTACCAAGCCATATAAATCTACAGATGCCCAAGTCTGCTTATGTCGAACCTG 363  
Oy 1280 GCCTTGCGTGTATCTCTCATAGGATCTACTTCTGCTACTATATAGCATCACTTGACATCCAT 1339  
Db 364 GCCTTTGTGTATCTCTCATATGGAATCTTACCTGCTGCTCATTTGATGATGATATCCAT 423  
Oy 1340 ACCAAGACGCCATGACCAACTATATGCTTGCATTCGCAACAGGACAGGCTGTGATGCT 1399  
Db 424 ACCAAGAGCCATATACACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483  
Oy 1400 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1459  
Db 484 GCTGGCTTTTCTACTGCTTTTGGCAGTGAGCTCTGATGCTACATCTCGACAGCTATCACC 543  
Oy 1460 CTAGAAGATGGCATACATCATCATCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1519

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Db 544 TTGAAAGATGGCATACCATCAGCATGCCATGCGAGCTGCAAGGTGCAGCTCCGC 603
Qy 1520 CATGCTGCCAGCTCATGGTATTTGGGCTGACATTTTGGCTTCGACGTGCTCTCTCCCC 1579
Db 604 CATGCTGCCAGTGTCAATGGTATTTGGGCTGAGTATTTGCTTTTCAGCTGCCCTCTTCC 663
Qy 1580 ATCTTTGGCATCAGTACATACATGAAAGTGAAGTGCCTGCTGCCATGATGATGCAGAGC 1639
Db 664 ATCTTTGGCATCAGCAGCTACATGAGGTGAGCATCTGCTGCCATGATGATGAGAGC 723
Qy 1640 CTTTGTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1699
Db 724 CTTTGTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 783
Qy 1700 ATCTGTGGCTGCTATACCCACATCTACCTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1759
Db 784 ATCTGTGGCTGCTATACCCACATCTACCTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 843
Qy 1760 TCAAGGCACACCAAGATTTGCCAAGCGCATGCCACACTCATCTTTCACAGACTTTCTCTGC 1819
Db 844 TCTAGTGCACACC-AGGTGCGCAGAGCGATGCGCATCTCATCTTCTAGTCTCTCTGC 902
Qy 1820 ATGGCCCCATTCATTTCTTTGCTGATTTCTGCTTCCCTCAAGGTGCGCTCATCACTGTG 1879
Db 903 ATGGCACCCATTTCTTTGCTGATTTCTGCTTCCCTCAAGGTGCGCTCATCACTGTG 962
Qy 1880 TCCAGGCCAAGATTTCTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939
Db 963 TCCAGGCCAAGATTTCTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
Qy 1940 CTCTAGCCCATTTTCCACCAAGATTTCCGCGAGGACTTCTTTCATCTGCTGCTGCTGCTGCT 1999
Db 1023 CTCTAGCCCATTTTCCACCAAGATTTCCGCGAGGACTTCTTTCATCTGCTGCTGCTGCTGCT 1082
Qy 2000 GGCTGTTATGAATGCAAGCCCAAGATTTACAGGACAGAAACCTCATCCGCTACCCACAAC 2059
Db 1083 GGCTGTTATGAATGCAAGCCCAAGATTTATAGGACAGAAACCTCATCCACTGTCCACAAC 1142
Qy 2060 TTCCATGCCGGAAGAGCAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2113
Db 1143 ACCATCCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1202
Qy 2114 GTCTGTGCTCTTATCATTCATCCAGCAATAAA 2151
Db 1203 ATACTTGCTCTCACTGATTTAGCCCAAACTAAA 1240

RESULT 7
AAT45148
ID .AAT45148 standard; cdna; 1316 BP.
XX AC AAT45148;
XX 09-MAR-1997 (first entry)
XX DE Gonadotropin receptor hFSHR-EC CDNA.
XX KW Gonadotropin receptor; follicle stimulating hormone receptor; FSHR;
XX KW baculovirus; AcNPV; Spodoptera frugiperda; insect; Sf9;
XX KW contraceptive; mimetic; antagonist; ss.
XX OS Chimeric Homo sapiens;
XX OS Chimeric Autographa californica nuclear polyhedrosis virus.
XX PH Key Location/Qualifiers
FT promoter 1..996
FT FT /*tag- a
FT FT /*note- "AcNPV polyhedrin promoter"
FT FT misc_RNA 97..137
FT FT /*tag- b
FT FT /*note- "AcNPV flanking polyhedrin region"
FT FT 138..1310
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FT FT /*tag- c
FT FT /product- gp67-hFSHR-EC
FT FT 138..251
FT FT /*tag- d
FT FT /*note- "AcNPV gp67 signal peptide replaces native
FT FT FSHR signal peptide to promote correct
FT FT folding and secretion in insect host cells"
FT FT mat_peptide 252..1307
FT FT /*tag- e
FT FT /*note- "mature FSHR extracellular domain (amino
FT FT acid residues 1-349) and N-terminal
FT FT tripeptide linker"
FT FT primer_bind complement (255..280)
FT FT /*tag- f
FT FT /*note- "5' primer binding site"
FT FT primer_bind 1289..1316
FT FT /*tag- g
FT FT /*note- "3' primer binding site"
XX W09638575-A1.
XX 05-DEC-1996.
XX 03-JUN-1996; 96WO-1B00709.
XX 02-JUN-1995; 95US-0460576.
XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX Buckler DR, Cheng SV, Prentice HL, Sisk WP;
XX WPI; 1997-034385/03.
XX P-PSDB; AAW06532.
XX Baculovirus transfer vector expresses gonadotropin receptor
XX extracellular domain - can be linked to affinity column to extract
XX hormone mimetic(s) or antagonists
XX Example 2; Fig 3; 66pp; English.
XX A CDNA construct (AAT45148) codes for human follicle stimulating
XX hormone receptor extracellular domain (hFSHR-EC) in which the
XX native signal peptide is replaced by the gp67 signal peptide of
XX a baculovirus (AcNPV). It is obtd. by PCR amplification (see also
XX AAT45149-50) of hFSHR cDNA and ligation into baculovirus transfer
XX vector pACGP67-A. The construct allows prodn. of soluble hFSHR-EC
XX in insect host cells. The hFSHR-EC can be used as an affinity
XX ligand to extract hormone mimetics or antagonists, and to purify
XX gonadotropins, or can be used to modulate hormone action in vivo,
XX e.g. as a contraceptive.
XX SQ Sequence 1316 BP; 405 A; 291 C; 268 G; 352 T; 0 other;
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Query Match 34.6%; Score 818.8; DB 18; Length 1316;
Best Local Similarity 87.1%; Pred. No. 13e-244;
Matches 911; Conservative 0; Mismatches 132; Indels 3; Gaps 1;
Qy 122 TGTCTATCATGCTGTGCTCATCTCTAATAGGCTCTTTCTCTCCCAAGACAGAGTG 181
Db 261 TGTCTATCATGCTGTGCTCATCTCTAATAGGCTCTTTCTCTCCCAAGACAGAGTG 320
Qy 182 ACAGAGATCCGACCGACCTCCCGGACCGATTCGCTGAGTGTGCTGCTCACCAG 241
Db 321 ACAGAGATCCCTTCTGACCTCCCGGAGGATTCGCTGAGTGTGCTGCTCACCAG 380
Qy 242 CTTCTGAGTCATCCGAAAGGATCATTTGCTGGATTTGGAGACCTGGAGAAATAGAGATC 301
Db 381 CTTCTGAGTCATCCAAAAGGTCATTTTTCAGGATTTGGGACCTGGAGAAATAGAGATC 440
Qy 302 TCTCAGAATGATCTCTTGGAGTAAATAGAGGAGATGTGTTCTCCAACTACCCAAAGTTG 361
Db 441 TCTCAGAATGATCTCTTGGAGTAAATAGAGGAGATGTGTTCTCCAACTACCCAAATTA 500
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Oy	362	CATGAATATAGGATGGAAGGGCCAGCAATCTCTGTACATATGACCGGAGGCGCTTCGAG	421
Db	501	CATGAATATAGGATGGAAGGGCCAGCAACCTGCTCTACATCAACCTCGAGGCGCTTCGAG	560
Oy	432	AATCTGCCCGGAGCTGCAGATATCTGTTATATCCACACAGCGGATTAAGCACTTCCGCACT	481
Db	561	AACCTGCCCAACCTTCATATCTGTTATATCCACACAGGATTAAGCACTTCCAGAT	620
Oy	492	GTTCCAAAGATCCAGTCTCTCCMAAAGGTTCTACTAGACATTCAGATTAACATAAACATCT	541
Db	621	GTTCCAAAGATTCATCTCTCCMAAAGGTTTACTTGACATTCAGATTAACATAAACATCT	680
Oy	542	CACATCTGCCCGAAGATCTCTCTCAGGAGCTAGGTTTGGAAAGTGTGATTTATATGGCTG	601
Db	691	CACATCTCCAGAAATCTCTCTCGGGGCTGAGCTTGGAAAGTGTGATTTATATGGCTG	740
Oy	602	AGTAGAATGGGATGGAAGAAATACACATCTGTGATTCATCAAGCAAGCTCAGCTAGATGAA	661
Db	741	AATAAGAAATGGGATTCGAAGAAATACACACTGTGCAATTCATCAAGTGAACCCCACTAGATGAG	800
Oy	662	CTGAATCTAAGCGGATACAAATATTTGGAAAGATTCGCTTAATGACGTTTTTCCAGGGAGCC	721
Db	801	CTGAATCTAAGCGGATATATATATTTAGAAAGATTCGCTTAATGATGTTTTTCCAGGGAGCC	860
Oy	722	CTCGGGCGAGTCATTTAGATATCTCAGGACAAAGGTCGATTCCTTACCAACCAATGCGC	781
Db	861	CTCGGCGAGTCATTTAGATATCTCAGGACAAAGGTCGATTCCTTACCAACCAATGCGC	920
Oy	782	TTAGAAAATCTGAAGAGCTGAGGGCCAGGTCACATACCGCTTCGAAAAGCTCCCTTAAT	841
Db	921	TTAGAAAATCTTGAAGAGCTGAGGGCCAGTGCACCTTACACATTTAAAAGCTGCCTACT	980
Oy	842	CTGGCAAGTTTGTCAACCTCATGAGGCGCAGCTCAGCTACCCGAGCCAGCTGTGTGCT	901
Db	981	CTGGCAAGTTTGTGGGCTCATGAGGCGCAGCTCAGCTATCCGAGCCATTTGTGTGGCC	1040
Oy	902	TTTGCAAAATGAGCGCGCAATCTGGAATCTATCCAAATTTGCAACAAAGTCTATTTTA	961
Db	1041	TTTGCAAAATGAGCGCGCAATCTGGAATCTATCCAAATTTGCAACAAAGTCTATTTTA	1100
Oy	962	AGGCAAGATATGATGATGATCTCAATTTGGGAGTCAGAGCTCTGTGATAGTGC	1019
Db	1101	AGGCAAGATTTGATTATATGACTCAGACTAGAGGGTCAGAGATCTCTCTGGCAGAGAC	1160
Oy	1020	-ATGAAACCAAGTTATGCAAAAGGATCTGACATGATCTACATCAATTTGATATGACCTTA	1078
Db	1161	AATGAGTCCAGCTACAGCAGAGGATTTGACATGACGTACTCAGTTTGACTATGACCTTA	1220
Oy	1079	TGTATGAAGTGTGTGATGTGACCTGCTCACCMAAGCCAGATGCATTTAATCATGTGAA	1138
Db	1221	TGCMAATGAAGTGTGTGAGTGTGACCTGCTCCCTTAGCCAGATGCATTCACCCCATGTGAA	1280
Oy	1139	GATATCATGGGGTCACACATCTCCAG	1164
Db	1281	GATATCATGGGGTCACACATCTCCAG	1306
RESULT 8			
AAV33371			
ID	AAV33371 standard; DNA; 1300 BP.		
AC	AAV33371;		
XX	21-DEC-1998 (first entry)		
DE	PROLAC FLAG-connect-sense/connect-antisense-JTHRR/JFHSR 1.		
XX	Prolectin leader sequence-FLAG; G protein-coupled receptor; GPCR;		
KW	inhibition; Agonist; antagonist; human; chromatin receptor; THRR;		
KX	follicle stimulating hormone receptor; FSHR; ds.		
OS	Synthetic.		

FH	Key	Location/Qualifiers
FT	CUS	10..1236
FT	FT	/tag= a
FT	FT	/product= "PROLAC FLAG-connect-sense/connect-antisense
FT	FT	hTHRR/hFSHR"
FT	misc_feature	138..164
FT	FT	/tag= b
FT	FT	/note= "Insert within the PflMI restriction site"
FT	misc_feature	145..147
FT	FT	/tag= c
FT	FT	/note= "encodes stop codon in protein"
FT	misc_feature	149..151
FT	FT	/tag= d
FT	FT	/note= "encodes stop codon in protein"
FT	misc_feature	153..155
FT	FT	/tag= e
FT	FT	/note= "encodes stop codon in protein"
FT	FT	
PN	WO9834948-A1.	
PD	13-AUG-1998.	
PD	XX	
PP	05-FEB-1998:	98WO-US02377.
PP	XX	
PR	06-FEB-1997:	97US-0795876.
PR	XX	
PA	(CORR ) CORNELL RES FOUND INC.	
PA	XX	
PI	Geras-Raaka E, Gershengorn MC, Nussenzveig DR;	
PI	XX	
XX	WPI: 1998-447165/38.	
DR	P-FSDB: AAW0392.	
XX	XX	
PT	Identifying peptide agonists and antagonists of G protein-coupled	
PT	receptors - using new construct that encodes library of peptide(s)	
PT	tethered to the receptor for transforming cells, used to identify	
PT	potential drugs and natural ligands for orphan receptors	
XX	XX	
XX	Example 1: Pages 33-35; 101pp: English.	
XX	XX	
CC	This is the nucleotide sequence of a PROLAC	
CC	FLAG-connect-sense/connect-antisense-hTHRR/hFSHR (human thrombin	
CC	receptor/human follicle stimulating hormone receptor), used in the	
CC	method of the invention involving the use of G protein-coupled	
CC	receptor (GPCR). Any small peptide that can activate GPCR, or	
CC	inhibit constitutively active GPCR, can be identified in a	
CC	combinatorial library. Agonists and antagonists are potentially	
CC	used as diagnostic and therapeutic agents, and can also be used	
CC	to identify novel drugs, or determine the physiological	
CC	function, of orphan receptors.	
XX	XX	
SO	Sequence 1300 BP; 304 A; 374 C; 274 G; 348 T; 0 other;	
XX	XX	
XX	Query Match	33.8%; Score 799.8; DB 19; Length 1300;
XX	Best Local Similarity	87.4%; Pred. No. 1.1e-238;
XX	Matches 889; Conservative	0; Mismatches 122; Indels 6; Gaps 1;
OY	1139	GATATCATCGGGTCAACAATCCATCGGGTCTTGATATGGTTATTATGACATCTCTGGCCATT 1198
DB	282	GTTTACCTCGGGGTCAACAATCCATCGAGTCTCATATGGTTTATGACATCTCTGGCCATC 341
OY	1199	ACTGGGAACACACATGCTGGTGGTCTTGACACACAGCCATACACAACTACTGTGCCC 1258
DB	342	ACTGGGACATCATATGCTGATGCTTCTTACTACGCCCATATGACTACTGTGACTCT 1318
OY	1259	CGGTTCTTATGTTACTGTCGGCTGGCTGCTGCTGACATGAGCATCTACTGTGACTCT 401
DB	402	AGGTCCTTATGTGCAACCTCGGCTTTGCTGATCTCTGCATCTGGAATCTACTCTGCTC 461
OY	1319	ATAGACTCAGTTGACATCCATACACAGAGCCAGTACCACAACTATGACCTATGACTGGCAA 1378
DB	462	ATTGCATCAGTTGATTCATCAATACACAGAGCCCAATATGACAACTATGCGATCGCACTGGCAA 521



Db 582 TACACTCTGACAGCTATACCTTGGAAAGATGGCATACCATCAGCATGCGAGTG 641  
Oy 1499 GAATGCAAGGTGACCTCCGGATGCTGCGAGCTCATGTATTTGGCTGACATTTGCC 1558  
Db 642 GACTGCAAGGTGACCTCCGGATGCTGCGAGCTCATGTATTTGGCTGACATTTGCC 701  
Oy 1559 TTGCGAGCTGCTCTCTGCGGATCTTTGGCATGCTAGCTACATGAAGTGAAGCATCTGC 1618  
Db 702 TTGCGAGCTGCTCTCTGCGGATCTTTGGCATGCTAGCTACATGAAGTGAAGCATCTGC 761  
Oy 1619 CTGCGCATGATATGACAGCGCTTTGTCACAGCTGATGTATATGGCCCTCTTGTCTCTC 1678  
Db 762 CTGCGCATGATATGACAGCGCTTTGTCACAGCTGATGTATATGGCCCTCTTGTCTCTC 821  
Oy 1679 ATGCTCTGCGCTTTGCTGCTATCTGCTATACCCACATCTACCTCAAGTGGG 881  
Db 822 ATGCTCTGCGCTTTGCTGCTATCTGCTATACCCACATCTACCTCAAGTGGG 881  
Oy 1739 ATGCTCTGCGCTTTGCTGCTATCTGCTATACCCACATCTACCTCAAGTGGG 1798  
Db 882 AACCCCAACATCTGCTCTCTAGTACACAGGATGCGCAAGCGCATGCGCATGCTCTC 941  
Oy 1799 ATGCTCTGCGCTTTGCTGCTATCTGCTATACCCACATCTACCTCAAGTGGG 1858  
Db 942 ATGCTCTGCGCTTTGCTGCTATCTGCTATACCCACATCTACCTCAAGTGGG 1901  
Oy 1859 AGTGTGCGCTCTCATCTGCTGCTGCGAGCGGAGATCTCTGCTGCTGCTGCTGCTGCT 1918  
Db 1002 AGTGTGCGCTCTCATCTGCTGCTGCGAGCGGAGATCTCTGCTGCTGCTGCTGCTGCT 1961  
Oy 1919 ATGCTCTGCGCTTTGCTGCTATCTGCTATACCCACATCTACCTCAAGTGGG 1978  
Db 1062 AACTCTGCTGCGCAAGCTCTCTGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1121  
Oy 1979 ATGCTCTGCGCTTTGCTGCTATCTGCTATACCCACATCTACCTCAAGTGGG 2038  
Db 1122 ATGCTCTGCGCTTTGCTGCTATCTGCTATACCCACATCTACCTCAAGTGGG 1181  
Oy 2039 ACTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2098  
Db 1182 ACTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1241  
Oy 2099 CTCACCAAT-----AGTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2149  
Db 1242 CTCACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1298

RESULT 10

AAO22937  
ID AAO22937 standard; cDNA; 2987 BP.  
AC AAO22937;  
XX  
XX 24-JUL-1992 (first entry)  
XX  
DE Sequence encoding luteinizing hormone (LH)-human chorionic  
DE gonadotropin (hCG) receptor protein.  
XX  
XX Contraceptive; diagnosis; ovarian disease; oligospermia;  
XX testicular disease; ss.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
PH CDS 1..2100  
FT /\*tag= a  
XX  
XX EP475292-A.  
XX  
XX 18-MAR-1992.  
XX  
XX 06-SEP-1991; 91EP-0115088.

XX 20-OCT-1990; 90JP-0280583.  
PR 10-SEP-1990; 90JP-0236994.  
XX (TAKE ) TAKEDA CHEMICAL IND KK.  
XX  
XX Igarashi M, Minegishi T, Nakamura K;  
PI WPI: 1992-089955/12.  
DR P-PSDB: AAR22187.  
XX  
XX Human LH-LCG receptor protein - uses cDNA to encode it, for  
XX recombinant prodn. of human luteinizing hormone human chorionic  
XX gonadotropin  
XX  
XX Claim 5; Page 10-15; 24pp; English.  
XX  
XX The inventors claim a protein with the 50 in AAR22187 or a protein  
XX lacking AAs 227-289, and DNA (AAO22937) encoding it. Transformants  
XX carrying the DNA are also claimed, specifically transformants E.  
XX coli JM109/pUC (FERM BP-3127), E. coli DH1/pLHR (UBX2) (FERM BP-  
XX 3545) and E. coli JM109/pLHR (GEX-3X) (FERM BP-3544).  
XX  
XX Sequence 2987 BP; 861 A; 672 C; 950 G; 904 T; 0 other;  
XX  
XX Query Match 28.0%; Score 661.4; DB 13; Length 2987;  
XX Best Local Similarity 61.7%; Pred. No. 3.4e-195;  
XX Matches 1115; Conservative 0; Mismatches 671; Indels 21; Gaps 3;  
XX  
Oy 247 AGTCATCCGGAAGGATCATTTGCTGGATTTGGAGACCTGGAGAAATAGAGTCTCTCA 306  
Db 186 AGTCATCCCATCTCAAGCTTTCCAGAGCTTAATGAGCTATAAAATGAAATCTCTCA 245  
Oy 307 GAATGATGCTGGAGTATAGAGAGAGATGTTCTCCAGCTACCCAGTGGCATGA 366  
Db 246 GATTGATCTCGGAAGGATAGAGTAATGCTTTGCAACCTCTCATTTGCTCTGA 305  
Oy 367 AATTAGGATGAAAAGGCCAACATCTCTGTACATCAACCCGGAGGCTTCCAGAACT 426  
Db 306 AATACTGATCCAGAACACCAAAATCTGAGATACATTGAGCCGGAGCATTTATAACT 365  
Oy 427 CCCAGCTCTCAGATATCTGTTAATATCCACAGAGCATTAAGCACTTCCAGCTGTTC 486  
Db 366 TCCCGGATTAATAATCTTGAAGCTCTGTAACACAGCATCAAGATTTCCAGATGTAC 425  
Oy 487 CAG---ATCCAGCTCTCCCAAGGTTCTACTAGACATTCAGATTAACATAACATCA 543  
Db 426 GAAGTCTCTCTCTGATCAATTCATCTGGAAATTTGTAATCTTACATACATAC 485  
Oy 544 CATGCTGCCAGGACCTCTCTCCAGCTGAGTCTTGAAGTGTGATTTATGCTGAG 603  
Db 486 CACCATACAGGAATGCTTTTCAAGGGATGAATATGATCTGTACACTCAACTATA 545  
Oy 604 TAAGAATGGATTAAGAAATACAACTGTGCAATTCACGGAATCAGCTAGATGACT 663  
Db 546 TGGAAATGGATTTGAAGAGTACAAAGTCAATGATGCAATGAGGCTTCCGTTGGG 605  
Oy 664 GAATCTAAGCCATAAATAATTTGGAGAAATGSCCTAATGAGCTTTCCAGGGAGCTC 723  
Db 606 GGAGCTAAGGAAACCTTGGATATTTCTCCACCAATTTGCGAGCTTCCGTTGGG 665  
Oy 724 TGGCCAGTCAATTTAGATATCTCAGGAGCAAGGTCATTTCTTACCAACCATGGCT 783  
Db 666 AGGCCGAAACCTTGGATATTTCTCCACCAATTTGCGAGCTTCCGTTGGG 725  
Oy 784 AGAAATCTGAGAGCTGAGGCGGAGGTCACATACCGCTTGAANAAGCTCCCTAATCT 843  
Db 726 AGAGTCAATTCAGAGCTTAATGCGCAGCTCATCTATTCTCTAANAANAATGCCATCA 785  
Oy 844 GCACAAGTTGTCACCTCATGAGGCGGAGCTTCCATCTACCCAGCAGCTGCTGCTTT 903  
Db 786 AGAAACATTTGCTCAATCTCTCGAGGCCAGCTTGAATACCCAGCAGCTGCTGCTTT 845









OY 1798 CATCTTCACAGACTTTCTCGCATGGGCCCCCATTCATCTTTGGCATTTTCGCTCCCT 1857  
DB 1771 CATCTTCACAGACTTTCTCGCATGGGCCCCCATTCATCTTTGGCATTTTCGCTCCCT 1830  
OY 1858 CAAGTGGCGCTCATCTGCTCGCAAGGCAAGATCTCTAGTCTGCTGCTACGCCAT 1917  
DB 1831 CAAGTACCTCTTATCAGATAGCAACACTCTAAGTTTACTGGTCTTTTATCCCAT 1890  
OY 1918 CATTCTCTGCTGCCATCTCTTCTCTACGCCCATTTTCAACCAAGAACTTCCGACGGACTT 1977  
DB 1891 CATTCTCTGCTGCCATCTCTTCTCTACGCCCATTTTCAACCAAGAACTTCCGACGGACTT 1950  
OY 1978 CTTATCTCTGCTGAGCAAGTTTGGCTCTTATGAATGCAAGC 2019  
DB 1951 CTTTCTTTTCTGAGCAAGTTTGGCTCTGCTGAACGCTGGGC 1992

RESULT 13

AACT71467  
ID AACT71467 standard; DNA: 642 BP.  
AC AACT71467;  
DT 09-FEB-2001 (first entry)  
DE Single nucleotide polymorphism containing sequence #432.  
KW Single nucleotide polymorphism; SNP; human; genetic disease;  
KW disease susceptibility; cardiovascular system; endocrine system;  
KW neurological system; forensic testing; paternity testing; ds.  
XX Homo sapiens.  
XX WO200059519-A2.  
XX 05-OCT-2000.  
XX 30-MAR-2000; 2000WO-US08440.  
XX 31-MAR-1999; 99US-0127248.  
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
XX (AFFY-) AFFYMETRIX INC.  
XX Althuler D, Cargill M, Daley GO, Ireland JS, Lander ES;  
XX Lipshutz RJ, Patil N, Sklar P;  
XX WPI, 2000-611722/58.

XX Nucleic acid selected from one of 106 genes comprising single  
XX nucleotide polymorphisms, allele-specific oligonucleotides to  
XX are useful for phenotypic correlations, forensics, paternity testing,  
XX medicine and genetic analysis .  
XX Claim 1; Fig 5; 214pp; English.  
XX The present invention is concerned with a number of human single  
XX nucleotide polymorphisms (SNPs) which the inventors identified in human  
XX genes. These SNPs can be used in disease diagnosis and prediction of an  
XX individual's susceptibility to disease, in forensic and paternity testing  
XX and in genetic mapping. In particular, the SNPs of the invention can be  
XX used to diagnose susceptibility to diseases of the cardiovascular,  
XX endocrine and neurological systems, such as coronary artery disease,  
XX Alzheimer's, cancer, autoimmune diseases, Alzheimer's and Parkinson's  
XX disease.  
XX Note: The degenerate codon within the sequence represents the position  
XX of an SNP, for example the letter S represents a polymorphism where the  
XX nucleotide may be C or G.

SQ Sequence 642 BP; 138 A; 201 G; 116 C; 186 T; 1 other:  
Query Watch . 21.0%; Score 496; DB 21; Length 642;  
XX

Best Local Similarity 87.0%; Pred. No. 6e-144;  
Matches 557; Conservative 1; Mismatches 76; Indels 6; Gaps 1;  
OY 1518 GCATCTGCGCCAGCTCATGGTATGGGTGGGACTTTTGGCTTCGCGAGCTGCTCTCC 1577  
DB 1 CCCATCTGCGCCAGCTCATGGTATGGGTGGGACTTTTGGCTTCGCGAGCTGCTCTCC 60  
OY 1578 CCATCTTTGGCATCAGCATAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1637  
DB 61 CCATCTTTGGCATCAGCATAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120  
OY 1538 GCGCTTTGTGACAGCTGTATGTATGGCTCTCTGCTCAATCTGCTGGCCTTTTGGG 1697  
DB 121 GCGCTTTGTGACAGCTGTATGTATGGCTCTCTGCTCAATCTGCTGGCCTTTTGGG 180  
OY 1698 TCATCTGTGGCTCTATACCCATCTACCTACAGTGAAGTGAAGTGAAGTGAAGTGAAG 1757  
DB 181 TCATCTGTGGCTCTATATCCATCTACCTACAGTGAAGTGAAGTGAAGTGAAGTGAAG 240  
OY 1758 CATCAAGCGACAGCAAGATTTGCCAAGGCGATGGCCACACTCATCTTCCAGAGCTTTCT 1817  
DB 241 CCTCTAGTGAACAGAGATCGCCAGCGCATGGCCATGCTCATCTCATGACTTCTCT 300  
OY 1818 GCATGGCCGCCATTTCTATCTTTGGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1877  
DB 301 GCATGGCCGCCATTTCTATCTTTGGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
OY 1878 TGTCGAAGGCAAGATTTCTCTAGTCTGCTTACCCCATCATCTTCTTGGCAATCTT 1937  
DB 361 TGTCGAAGGCAAGATTTCTCTAGTCTGCTTACCCCATCATCTTCTTGGCAATCTT 420  
OY 1938 TCCTCTAGCGCATTTTCCCAAGAACTTCCGAGGAGCTTCTTCACTGCTGAGCAAGT 1997  
DB 421 TCCTCTATGCGCATCTTTTACCAAAACTTTTGGCAGAGATTTCTTCAATCTGCTGAGCAAGT 480  
OY 1998 TTGCTGTTATGAATGAAGCCAGATTTACAGGACAGAACTCATCGCTACCCACA 2057  
DB 481 GTGCTGCTTATGAATGAAGCCAGATTTACAGGACAGAACTCATCGCTACCCACA 540  
OY 2058 ACTTCCAGTCCGCAAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2111  
DB 541 ACACCCATCCAGGAATGGCCACTGCTCTTCAGCTCCGAGAGTCCACAGTCCACAGTGGTCCACTT 600  
OY 2112 AGCTGCTGCTGCTCTTAAATCATTCATCCGAGAACTAAAA 2151  
DB 601 ACATACTGCTGCTCTTAAGTCAATTTAGCCCAAACTAAAA 640

RESULT 14

AACT71470  
ID AACT71470 standard; DNA: 642 BP.  
AC AACT71470;  
DT 09-FEB-2001 (first entry)  
DE Single nucleotide polymorphism containing sequence #433.  
KW Single nucleotide polymorphism; SNP; human; genetic disease;  
KW disease susceptibility; cardiovascular system; endocrine system;  
KW neurological system; forensic testing; paternity testing; ds.  
XX Homo sapiens.  
XX WO200059519-A2.  
XX 05-OCT-2000.  
XX 30-MAR-2000; 2000WO-US08440.  
XX 31-MAR-1999; 99US-0127248.  
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
XX



Db 122 ATTTGACATGACCTACACTGCTTTGACTATGACATTATGCAATGAAGTGGTTGACGTGAC 181  
Oy 1102 CTGCTACCCAAAGCCAGATGCAATTTATCCATGTGGAAGATATCATCTGGGGTGACACATCCT 1161  
Db 182 CTGCTCCCTAAGCCAGATGCAATTCACCCATGTGAAGATATCTGGGGTGACACATCCT 241  
Oy 1162 CAGGGCTTGTATGCTTTATTAAGCATCTGGGCATTAAGTGGACACACAGCTGCTGT 1221  
Db 242 CAGAGTCTGTATGCTTTATCAGCATCTGGCCATCACTGGGACATCATATGCTGCTAGT 301  
Oy 1222 GGTCTGACCAAGCCAAATACAAACTAATCTGGCCCGGTTTCTTATGTGTAACCTGCG 1281  
Db 302 GATCCTAATACCAAGCCAAATATAAATCAACAGTCCCGAGTTCTTATGTGCAACTGCG 361  
Oy 1282 CTTGCTGATCTCTCATAGGCATCTACTTCTACTTATAGCATCAGTTCACATCCATAC 1341  
Db 362 CTTTGTGATCTGCAATGGAATTAATCTGCTGCTCATTTGCAATCAGTTCATATCATAC 421  
Oy 1342 CAGAGCCAGTTCACACACTATGCAATTAATCTGCAACAGAGCAGCTGTGATGCTGC 1401  
Db 422 CAGAGCCAAATACACACTATGCAATTAATCTGCAACAGAGCTGTGATGCTGC 481  
Oy 1402 TGGCTTTTCACTGCTTTTGGCAGTGAATGTCAGTCTACACATTCAGCCATCAGCT 1461  
Db 482 TGGCTTTTCACTGCTTTTGGCAGTGAATGTCAGTCTACACATTCAGCTATCACCT 541  
Oy 1462 AGAAGATGGCATACATCACACTGCTATGCAATGGAATGCAAGGTGCACTCCGCCA 1521  
Db 542 GGAAGATGGCATACATCACACTGCTATGCAATGGAATGCAAGGTGCACTCCGCCA 601  
Oy 1522 TCTGCGCCATCATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1557  
Db 602 TCTGCGCCATCATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 637

Search completed: June 16, 2003, 09:06:28  
Job time : 531 secs



```

: LIBRARY: 19t11 cDNA library, Clontech #HL1010b
: CLONE: pFEShr11-11, pFEShr15-6
: FEATURE:
: NAME/KEY: protein coding region
: LOCATION: 75 to 2159
: US-08-487-886-1

```

Query Match 70.9%; Score 1677.6; DB 1; Length 2179;

Best Local Similarity 86.5%; Pred. NO. 0;  
Matches 1876; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

[illegible]

911	AAACTGGAGACGGCAAACTCTGAGCTTCATCCAATTTGCAACAAATCTATTTTAAGGCA	970
967	AGATATTGATGATATGACTCAAAATTTGGGATCAGAGAGTCTCTCTGATAGATG- -ATGA	1023
971	AGAAAGTTGATTATGACTCAGACTAGGGGTGAGAGATCTCTCTGGCAGACACAATGA	1030
1024	ACCCAGTTATGGAAAAGGATCTGACATGATGTACAATGAATTTGATTTATGACTTTATGTAA	1083
1031	GTCCAGCTACAGCAGAGGATTTGACATGACGTACACTGAGTTTGACTATGACTTATGCAA	1090
1084	TGAAGTTGTTGATGTGACCTGCTCACCAGCCAGATGCATTTAATCCATGTGAAGATAT	1143
1091	TGAAGTGGTTTGAGCTGACCTGCTCCCTTAAGCCAGATGCATTCAGCCCATGTGAAGATAT	1150
1144	CATGGGTACAACATCCTCAGGGTCTTGATATAGTTTATTAGCATCTCGGCCAATTACTGG	1203
1151	CATGGGTACAACATCCTCAGAGTCTGTGATATGGTTTATCAGCATCTGGCCATCAGCTGG	1210
1204	GAACACACAGTCTGGTGGTCTGTGACCAACAGCCCAATACAAAATACTGTGCCCGGTT	1263
1211	GAACATCATAGTGTAGTGATCTTACTACCGCAATATAAACTCACAGTCCCAAGTT	1270
1264	TCYTATGTGTAACTCGCCTTCGTGATCTCTGCATAGGCATCTCTGCTACTTATAGC	1323
1271	CCYTATGTGAACTCGCCTTCGTGATCTCTGCATTTGGAATACGCTGCTCATTTGC	1330
1324	ATCAGTTGACATCCATACCAAGACGACAGTACCACAATATGCCATTTGACTGGCAACAGG	1383
1331	ATCAGTTGATATCCATACCAAGAGCCATATCACACTATGCCATTTGCTGGCAAACTGG	1390
1384	AGCAGGTGTGATGCTGCTGGCTTTTTCATCTGTCTTTGCCAGTGAATGTGCTAGCTACAC	1443
1391	GGCAGGTGTGATGCTGCTGGCTTTTTCATCTGTCTTTGCCAGTGAGCTGTGCTAGCTACAC	1450
1444	ATTGACAGCCATCACCTAGAAAGATGGCATACCATCACACATGCTATGCAACTGGATG	1503
1451	TC TGACAGCTATCACCTTGGAAAGATGGCATACCATCACAGTGCATGCGAGCTGGAC	1510
1504	CAAGGTGCAGCTCCGGCATCTGCCAGCTGATGGTATTGGCTGGACTTTTGCTTTCGC	1563
1511	CAAGGTGCAGCTCCGGCATCTGCCAGTGTGATGGTGGATGGCTGGATTTTGGCTTTGC	1570
1564	AGCTGCTCTCTCCCATCTTTGGCATGCTAGCTACATGAAAGTGAAGTATGCTGCTGCC	1623
1571	AGCTGCCCTCTTTCCCATCTTTGGCATGCTAGCTAGCTACATGCAAGTGAAGTATGCTGCTGCC	1630
1624	CATGGATATCGACAGCCCTTTGTCACAGCTGTATGTTATGGCCCTCTCTGCTCAATGT	1683
1631	CATGGATATTGACAGCCCTTTGTCACAGCTGTATGTCATGCTGCTCTCTGCTCAATGT	1690
1684	CTTGGCTTTTGGTGCATCTGGCTGCTATACCCACATCTACCTCACAGTGAAGGATCC	1743
1691	CCTGGCTTTTGGTGCATCTGGCTGCTATATCCACATCTACCTCACAGTGGGAACCC	1750
1744	TACCATTTGCTCTCATCAAGGACACCAAGATTTGCCAAGCGCATGGCCACATCTCATCTT	1803
1751	CAACATCGTGTCTCTCTAGTGACACACAGGATCGCCAAGCGCATGGCCATGCTCATCTT	1810
1804	CACAGACTTCTCTGCATGGCCCCCATTTTCATTTGTCATTTCTGCTGCCCTCAAGGT	1863
1811	CATGACTTCTCTGCATGGACCCCATTTCTTTCTTTTGGCCATTTCTGCTGCCCTCAAGGT	1870
1864	GCCGCTCATCTGTGTGCAAGGCCAAGATTTCTCTAGTTCTGCTTACCCCATCAATTC	1923
1871	GCCCTCATCTGTGTCCAAAGCAAGATTTCTGCTGGTTCTGTTTACCCCATCAACTC	1930
1924	TTGTGCCAATTCCTTCTCTACGCCATTTTCAACAAAGAACTTCCGCAAGGACTTCTTCAT	1983
1931	CTGTGCCAACCCCTTCTCTATGCCATCTTTACCAAAAACCTTTCGACAGAGATTTCTCAT	1990
1984	CTGCTGAGCAAGTTTGGCTGTTATGAATGCAAGCCCCAGATTTTACAGGACAGAACTTC	2043
1991	TC TGCTGAGCAAGTGTGGTGTATGAATGCAAGCCCCAAATTTATAGCAGCAAACTTC	2050

Qy 2044 ATCCGCTACCCACACACCTTCATGCGCCGAAGAGCCACTGCTCTCAGCTCCAGAGTCAC 2103  
Db 2051 ATCCAGCTCTCCACACACACCTTCATGCGCCGAAGAGCCACTGCTCTCAGCTCCAGAGTCAC 2110  
Qy 2104 CAAT-----ACTACGCTGCTGCTCTCTTAATCATCTCCAGAGCTAAATAT 2157  
Db 2111 CAATGCTTCCAGCTTACATCTGCTCTCTTAATCATCTCCAGAGCTAAATAT 2170  
Qy 2158 GTGAAATG 2166  
Db 2171 GTGAAATG 2179

RESULT 2  
US-08-531-070A-1  
Sequence 1, Application US/08531070A  
GenBank Information:  
APPLICANT: Albert, Albert  
APPLICANT: Altomski, Kristina  
APPLICANT: Huhtanen, Ilpo  
TITLE OF INVENTION: Method For Diagnosis Of Ovarian Dysgenesis  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SEQUENCE CHARACTERISTICS:  
CURRENT APPLICATION NUMBER: US/08531070A  
FILING DATE: 20-SEP-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28113/32879  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3836  
INFORMATION CONTAINED ON NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2179 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-531-070A-1

Query Match 70.9%; Score 1677.6; DB 2; Length 2179;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 1876; Conservative 0; Mismatches 284; Indels 9; Caps 2;

Qy 7 CTGGGAATCTGTGGAAAGTTTTCGCGCTGATGCGAAGAAAGTCGGTGAATGGATTAAT 66  
Db 11 CTGAGATCTGTGGAGTTTTCGCGCTGATGCGAAGAAAGTCGGTGAATGGATTAAT 70  
Qy 67 AAGAGTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126  
Db 71 AATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 130  
Qy 127 TCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186  
Db 131 TCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190

Qy 187 GATTCGAGCCGACCTCCCGAAGCGCCATTGACCTGAGGTTTGTGCTCACCAGCTTCG 246  
Db 191 GATTCCTTCTGACCTCCCGAAGCGCCATTGACCTGAGGTTTGTGCTCACCAGCTTCG 250  
Qy 247 AGTCATCCGGAAGAGATCATCTGCTGGATTGAGAGCTGGAGAAATAGAGATCTCTCA 306  
Db 251 AGTCATCCGGAAGAGATCATCTGCTGGATTGAGAGCTGGAGAAATAGAGATCTCTCA 310  
Qy 307 GATTCATCTGGAAGATTAATGAGGAGATGCTGCTGAGCTGAGAGTGGATGCTGATG 366  
Db 311 GATTCATCTGGAAGATTAATGAGGAGATGCTGCTGAGCTGAGAGTGGATGCTGATG 370  
Qy 367 AATTAGGATTAAGAGGCGCAACAATCTCTCTGATCATCAACCGGAGGCTTCCAGATCT 426  
Db 371 AATTAGGATTAAGAGGCGCAACAATCTCTCTGATCATCAACCGGAGGCTTCCAGATCT 430  
Qy 427 CCCAGCTCAGATATCTGTTAATATCCCAACAGGCTTAAGCACTTGGCAGCTGTTC 486  
Db 431 TCCAGCTTCAATATCTGTTAATATCCCAACAGGCTTAAGCACTTGGCAGCTGTTC 490  
Qy 487 CAGATCTAGCTCTCCAAAGGCTTACTAGACATTCAGATTAACATAAACATCCACAT 546  
Db 491 CAGATCTAGCTCTCCAAAGGCTTACTAGACATTCAGATTAACATAAACATCCACAT 550  
Qy 547 CTTCCCGAGGAGCTCTCTCATGGAGCTGAGCTTTCGAAGTGTGATTTATGCTGCTGAT 606  
Db 551 AATTCAAGAAATCTCTTCTGGGCTGAGCTTTCGAAGTGTGATTTATGCTGCTGAT 610  
Qy 607 GAATGGATTAAGAAATATACACACTGTGCTTCAAGGAGCTCAGCTAGATGACTGAA 666  
Db 611 GAATGGATTAAGAAATATACACACTGTGCTTCAAGGAGCTCAGCTAGATGACTGAA 670  
Qy 667 TCTAAGGATTAAGAAATATGAGGAGCTTTCGAAGTGTGATTTTCAGGAGGCTCTGG 726  
Db 671 TCTAAGGATTAAGAAATATGAGGAGCTTTCGAAGTGTGATTTTCAGGAGGCTCTGG 730  
Qy 727 GCACTCATTTAGATATCTCAAGGAGGCTTTCGAAGTGTGATTTTCAGGAGGCTCTGG 786  
Db 731 AACTCTGAGAGCTGAGGAGGCTTTCGAAGTGTGATTTTCAGGAGGCTCTGG 846  
Qy 787 AACTCTGAGAGCTGAGGAGGCTTTCGAAGTGTGATTTTCAGGAGGCTCTGG 850  
Db 791 AACTCTGAGAGCTGAGGAGGCTTTCGAAGTGTGATTTTCAGGAGGCTCTGG 850  
Qy 847 CAAGTTTGTGAGGCTTTCGAAGTGTGATTTTCAGGAGGCTTTCGAAGTGTGATTTTC 906  
Db 851 AAGGTTTGTGAGGCTTTCGAAGTGTGATTTTCAGGAGGCTTTCGAAGTGTGATTTTC 910  
Qy 907 AACTGAGGCGGCAATCTCTGAGCTTTCGAAGTGTGATTTTCAGGAGGCTTTCGAAGGCA 966  
Db 911 AACTGAGGCGGCAATCTCTGAGCTTTCGAAGTGTGATTTTCAGGAGGCTTTCGAAGGCA 970  
Qy 967 AGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1023  
Db 971 AGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1030  
Qy 1024 ACCAGTTTGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083  
Db 1031 GTCCAGCTACAGCAGAGGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1090  
Qy 1084 TGAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143  
Db 1091 TGAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1150  
Qy 1144 CATGGGTTACACATCTCTGAGGCTTTCGATGATGATGATGATGATGATGATGATGATGAT 1203  
Db 1151 CATGGGTTACACATCTCTGAGGCTTTCGATGATGATGATGATGATGATGATGATGATGAT 1210  
Qy 1204 GAGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263  
Db 1211 GAGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1270  
Qy 1264 TCTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323

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1271 CCTATGCAACCTGCGCTTTGCTGATCTCTGCAATGGAATCTACCTGCTGCTCATTC 1330
1324 ATCAGTTGACATCCATACCAAGAGCCAGTACCAACATATGCAATGCTGCGCAACAGG 1383
1331 ATCAGTTGATATCCATACCAAGAGCCAAATATCAACATATGCAATGCTGCGCAACAGG 1390
1384 AGCAGGCTGTGATGCTGCTGCTTTTCTGCTGCTTTTCTGCTGCTGCTGCTGCTGCTG 1443
1391 GGCAGGCTGTGATGCTGCTGCTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1450
1444 ATTGACAGCATCACCCCTAGAAAGATGGCATACCATACATGCTATGCAATGGAATG 1503
1451 TCTGACAGCTATCACCTTGGAAAGATGGCATACCATACATGCTATGCAATGGAATG 1510
1504 CAAGGTGACCTGCGGATGCTGCGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1563
1511 CAAGGTGACCTGCGGATGCTGCGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1570
1564 AGCTGCTCTCTTCCCATCTTTTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1623
1571 AGCTGCTCTCTTCCCATCTTTTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1630
1624 CATGGATATCACAGCCCTTTGTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1683
1631 CATGGATATGACAGCCCTTTGTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1690
1684 CTTGGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1743
1691 CTTGGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1750
1744 TACCATGCTGCTCTATCAAGGACACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1803
1751 CAACATGCTGCTCTCTATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1810
1804 CACAGACTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1863
1811 CACTGACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1870
1864 GCGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1923
1871 GCGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1930
1924 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1983
1931 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1990
1984 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2043
1991 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2050
2044 ATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2103
2051 ATCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2110
2104 CAAT-----AGTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2157
2111 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2170
2158 GTGAAATG 2166
2171 GTGAAATG 2179

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RESULT 3  
 US-08-482-855-1  
 : Sequence 1, Application US/08482855  
 : Patent No. 6121016  
 : GENERAL INFORMATION:  
 : APPLICANT: Kelton, Christie Ann  
 : APPLICANT: Schweickhardt, Rene Lynn  
 : APPLICANT: Cheng, Shirley Vui Yen  
 : APPLICANT: Nugent, No. 6121016een Patrice

```

: TITLE OF INVENTION: Human Follicle Stimulating
: TITLE OF INVENTION: Hormone Receptor
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Stephan P. Williams,
: ADDRESSEE: Ares-Serono, Inc.
: STREET: Exchange Place, 37th floor
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
: COMPUTER: IBM PS/2, model 55 SX
: OPERATING SYSTEM: MS-DOS version 4.0
: SOFTWARE: VAX/VMS Massill via Kermit to IBM MS-DOS
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/482,855
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/670,085
: FILING DATE: 15-MAR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams, Stephan P.
: REGISTRATION NUMBER: 28546
: REFERENCE/DOCKET NUMBER: US/252
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 723-1300
: TELEFAX: (617) 723-8923
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2179
: TYPE: Nucleic acid
: STRANDEDNESS: Double
: TOPOLOGY: Linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Homo. sapiens
: TISSUE TYPE: Testis
: IMMEDIATE SOURCE:
: LIBRARY: 19t11 cDNA library, Clontech #HL1010b
: CLONE: pFHSR11-11, pFHSR15-6
: FEATURE:
: NAME/KEY: protein coding region
: LOCATION: 75 to 2159
: US-08-482-855-1

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Query Match 70.98; Score 1677.6; DB 3; Length 2179;
Best Local Similarity 86.58; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 7 CTGGGAATCTGTGGAGTTTTCGCGCTGATGAGAAAGTGGTGAATGATGATAAT 66
DB 11 CTGAGATCTGTGGAGTTTTCGCGCTGATGAGAAAGTGGTGAATGATGATAAT 70
QY 67 AAGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126
DB 71 AATATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 130
QY 127 TCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186
DB 131 TCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190
QY 187 GATTCCGACCGACCTCCCGGAAAGTGGTGAATGAGTGGTGGTGGTGGTGGTGGTGG 246
DB 191 GATTCCGACCGACCTCCCGGAAAGTGGTGAATGAGTGGTGGTGGTGGTGGTGGTGG 250
QY 247 AGTCATCCCGAAAGGATCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
DB 251 AGTCATCCCAAAAGGTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
QY 307 GAATGATGCTTGGAAAGTAAATAGAGGAGATGTTCTTCCAACTACCCCAAGTTGCATGA 366

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311 GAATGATCTGTGGAGGTGATAGGAGAGATGTGTTCTCCCACTTCCCAATTTACTGGA 370  
367 AATTAGGATTAAGAGGCCAACATCTCTGTACATCAAGCGAGGCGCTTCAGAACT 426  
371 AATTAGGATTAAGAGGCCAACACCTGCTCTACATCAACCTCGAGGCGCTTCAGAACT 430  
427 CCCCAGCTCTCAGATATCTGTATATATCAACACAGGAGATTAAGCACTTCCCACTGTTCA 486  
431 TCCCACACCTCTCAATATCTGTATATCAACACAGGATTAAGCACTTCCCACTGTTCA 490  
487 CAGATCCAGCTCTCTCAAAAGGTTCTACTAGACATCAAGATTAACATTAACATCCACAT 546  
491 CAGATCTCTCTCAAAAGGTTCTACTAGACATCAAGATTAACATTAACATCCACAT 550  
547 CTTGCCAGACCTCTCTCAAGGAGCTGAGTTTGAAGGTGATATTTATGGCTGAGTAA 606  
551 AATTGAAGAAATCTCTGTGGGCGTGGCTTGAAGGTGATATTTATGGCTGAGTAA 610  
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611 GAATGGGATTAAGAAATCAACACTGATCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 670  
667 TCTAAGGATTAAGAAATCAACACTGATCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 726  
671 TCTAAGGATTAAGAAATCAACACTGATCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 730  
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731 ACAGTCAATCTAGATATTTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 790  
787 AATCTGAAGAGCTGAGGCGAGCTCAACATACGCTTGAAGGAGTCAAGGAGTCAAGGAG 846  
791 AATCTGAAGAGCTGAGGCGAGCTCAACATACGCTTGAAGGAGTCAAGGAGTCAAGGAG 850  
847 CAGTCTGACCTCAAGGAGGAGCTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGG 906  
851 AAGCTTGTGGGCTGATGAGGAGGAGCTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 910  
907 AAGCTTGAAGGAGGAGTCTGAAGTCTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 966  
911 AAGCTTGAAGGAGGAGTCTGAAGTCTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 970  
967 AGATATGATGATATGATCAATTTGGGATGATGATGATGATGATGATGATGATGATGAT 1023  
971 AGAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1030  
1024 AGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083  
1031 GTCCAGCTACAGCAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1090  
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1091 TGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1150  
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1151 CATGGGTACACATCTCTAGGCTTGTATGATGATGATGATGATGATGATGATGATGATGAT 1210  
1204 GAGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1263  
1211 GAGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1270  
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1271 CTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1330  
1324 ATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383  
1331 ATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1390  
1384 AGCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1443

1391 GGCAGGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1450  
1444 ATTGACAGGCTATCACCCTAGAAAGATGGGATACCATACATGATATGCACTGGAATG 1503  
1451 TCTGACAGCTATCACCCTAGAAAGATGGGATACCATACATGATATGCACTGGAATG 1510  
1504 CAGGCTGACGCTGCGGAGCTGCGAGGCTGATGATGATGATGATGATGATGATGATGATGAT 1563  
1511 CAGGCTGACGCTGCGGAGCTGCGAGGCTGATGATGATGATGATGATGATGATGATGATGAT 1570  
1564 AGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1623  
1571 AGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1630  
1624 CATGATATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1683  
1631 CATGATATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1690  
1684 CTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1743  
1691 CTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1750  
1744 TACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1803  
1751 CAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1810  
1804 CAGACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1863  
1811 CACTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1870  
1864 GCGGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1923  
1871 GCGGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1930  
1924 TTTGGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1983  
1931 CTTGGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1990  
1984 CTTGGCTGAGCAAGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2043  
1991 TCTGCTGAGCAAGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2050  
2044 ATCCGCTACCCCAACTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2103  
2051 ATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2110  
2104 CAAT-----AGTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2157  
2111 CAGTGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2170  
2158 GTGAAATG 2166  
2171 GTGAAATG 2179

RESULT 4  
US-08-474-986-1  
; Sequence 1, Application US/08474986  
; Patent No. 6372711

GENERAL INFORMATION:

APPLICANT: Kelson, Christie Ann  
Schweickhardt, Rene Lynn  
Cheng, Shirley Yui Yen  
Nugent, No. 6372711  
TITLE OF INVENTION: Human Pollicle Stimulating  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen P. Williams,  
Ares-Serono, Inc.  
STREET: Exchange Place, 37th floor  
CITY: Boston  
STATE: MA







[illegible]

RESULT B  
US-08-795-876-36  
Sequence 36, Application US/08795876  
Patent No. 1603105  
INVENTOR INFORMATION:  
INVENTOR: GERNARD, Marvin C.  
APPLICANT: GERBABA, Elizabeth  
APPLICANT: GERNBERG, Daniel R.  
APPLICANT: NUSSENSEVELD, Daniel R.  
TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795.876  
FILED DATE: 08/08/95  
CLASSIFICATION: 530  
CROSS-REFERENCE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BRAMAN, SUSAN J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/1280  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1636  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 36:

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; LENGTH: 1300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-795-876-36

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Query Match 33.8%; Score 799.8; DB 4; Length 1300;  
Best Local Similarity 87.4%; Pred. No. 1e-237;  
Matches 889; Conservative 0; Mismatches 122; Indels 6;

[illegible]

Db	1182	ACTTATCCACTGTCCACAACACCCACTCCGCGGAATGGCCACTGCTCTTTAGCTCCCGA	1241
Qy	2099	GTCCACCAAT-----AGTTACGTGCTGTGCCCTTTAATCATTCATCCACAGAACTAA	2149
Db	1242	GTCCACCAATGGTTCACCTTACATACCTGTGCCCTCTAAGTCATTATTAGCCAAAACCTAA	1298

## RESULTS

US-08-795-876-37/c  
 Sequence 37, Application US/08795876  
 Patent No. 6403305  
 GENERAL INFORMATION:  
 APPLICANT: Gershengorn, Marvin C.  
 APPLICANT: Geras-Raaka, Elizabeth  
 APPLICANT: Nussenzevig, Daniel R.  
 TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN  
 TITLE OF INVENTION: COUPLED RECEPTORS  
 NUMBER OF SEQUENCES: 44  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
 STREET: Clinton Square, P.O. Box 1051  
 CITY: Rochester  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 14603  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/795,876  
 FILING DATE:  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BRAMAN, SUSAN J.  
 REGISTRATION NUMBER: 34,103  
 REFERENCE/DOCKET NUMBER: 19603/1280  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 716-263-1636  
 TELEFAX: 716-263-1600  
 INFORMATION FOR SEQ ID NO: 37:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1300 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-795-876-37

Query Match 33.8%; Score 799.8; DB 4; Length 1300;  
Best Local Similarity 87.4%; Pred. NO. 1e-237;  
Matches 889; Conservative 0; Mismatches 122; Indels 6; Gaps 1;

Qy	1139	GATATCATGGGTAAACATCCTCAGGGTCTTGATATGGTTATTATAGCATCTCGGCCATT	1198
Db	1023	GGTTACCTGGGGTAAACAATCCTCAGAGTCTCTGATATGGTTTATCAGCATCTCGGCCATC	964
Qy	1199	ACTGGGAACACCAAGTGGTGGTCTGNACCACAGCCCAATCAAACTAACTGTGCC	1258
Db	963	ACTGGGAACATCATAGTGTAGTGATCCTAACTACCAGCCAAATAAACTCACAGTCCCC	904
Qy	1259	CGGTTTCTTATGTGTAACTCGCCTCGCTCGATCTCTGCATAGGCATCTACTTCTCACTT	1318
Db	903	AGGTTCTTATGTGCAACCTGGCCCTTGTCTGATCTCTGCATTGGAACTACTCTCGTCTC	844
Qy	1319	ATAGCATCAGTTGACATCCATACCAAGAGCCAGTACCACAACATATGCCATTGACTGGCAA	1378
Db	843	ATTGCATCAGTGTATATCCATACCAGAGCCAAATATCACAACTATGGATGATGGAGTGC	784
Qy	1379	ACAGGACGAGCTGTGATGCTGCTGGCTTTTTCATCTGTCTGGCAGTGAACCTGTCACTC	1438
Db	783	ACTGGGACAGCTCTGTAGTGTCTGGCTTTTTCATCTGTCTGGCAGTGAACCTGTCACTC	724







1428 AAAGCTGGATTAGACATGCCATCTGATTTGCTGGAGGATGGCTCTTTCTCTCT 1487  
1564 AGCTGCTCTCTCCCATCTTTGGCATCACTAGTACATGAAGTGGAGCATCTCCCTGCC 1623  
1488 AATTCATGATGTCCTCCCTCTGCTGGTGTAGCAATATACATGAAGTCAATTTCTCTCC 1547  
1624 CAGGATATGAGAGACCTCTGCTGACAGCTGTATGTATGGCCCTCTCTCTCAATGT 1683  
1548 CAGGATGAGAGACCTCTCTGACAGCTGTATGTATGGCCCTCTCTCTCAATGT 1607  
1684 CTTGGCTCTTTGGTCTGATGCTGCTGTATGACCATCTACCTCAAGTGGAGATCC 1743  
1608 GTGGCTCTCTCTCATATTTGCTGCTACATTAATTTATTTGCGATTCGAACCC 1667  
1744 TACCATTTGCTCTCATCAAGGACACAGATTTGCCAAGCCATGCGCACACTCTT 1803  
1668 AGAATTAATGGCTACCAATAAAGATTAAGATTTGCTAAGAAATGGCAATCTCATCTT 1727  
1804 CAGACATTTCTCTGCTGATGCTGCTGCTATTTGCTGCTGCTGCTGCTGCTGCTGCT 1863  
1728 CAGCATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1787  
1864 GCGCTCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1923  
1788 ACCTCTTACAGATTAAGCACTTAAGTTTACTGCTCTTTTATGCTGCTGCTGCTGCT 1847  
1924 TTGTCGCAATCTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1983  
1848 TTGTCGCAATCTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1907  
1984 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2043  
1908 TTGTCGCAATCTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2003  
2044 ATCCGCT 2050  
1968 TTCAGCT 1974

RESULT 12  
US-07-741-453A-57  
Sequence 57, Application US/07741453A  
Patent No. 6228597  
GENERAL INFORMATION:  
APPLICANT: PARMENTIER, MARC  
APPLICANT: LIBERT, FREDERIC  
APPLICANT: DUMONT, JACQUES  
APPLICANT: VASSART, GILBERT  
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABBY & CUSHMAN  
CITY: WASHINGTON, D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07741.453A  
FILING DATE: 1991015  
CLASSIFICATION: G06F 01/00  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16773  
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000



1657 GCGACTACAACTGAACTGCGCCGCTTCTCATGTGCAACCTGGCCCTTGGCGATTCT 1716  
1296 GCATAGCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 1355  
1717 GCGTGGGATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1776  
1356 ACACACTATGCCATGACTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1415  
1777 ACACACTATGCCATGACTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1836  
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1837 TCTTTCACAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1896  
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1957 TCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2016  
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2017 GCTATGCCAAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2076  
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1956 CCAGAACTTCCGAGGAGTCTTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2015  
2377 CCAGGCGTTCAGAGGAGTCTTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2436  
2016 AACGCGAGATTACAGG 2032  
2437 AGGCTAGCGCATACCG 2453

RESULT 14  
US-08-232-463-14  
: Sequence 14, Application US/08232463  
: Patent No. 5670367  
: GENERAL INFORMATION:  
: APPLICANT: DORNER, F.  
: APPLICANT: SCHREIFLINGER, F.  
: APPLICANT: FALKNER, F. G.  
: TITLE OF INVENTION: RECOMBINANT FOXP2 VIRUS  
: NUMBER OF SEQUENCES: 52  
: ADDRESS: 1800 Diagonal Road, Suite 500  
: CITY: Alexandria  
: STATE: VA  
: COUNTRY: USA  
: ZIP: 22313-0299

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT LOCATION DATA  
APPLICATION NUMBER: US/08/232.463  
FILING DATE: 05/08/2002  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
: APPLICATION NUMBER: US/07/935.313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
FAX: (703)836-9300  
TELEX: 695146  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-Fls  
US-08-232-463-14  
Query Match 3.1%, Score 72.2, DB 1, Length 7218;  
Best Local Similarity 6.4%, Prod. No. 1.2e-11;  
Matches 26; Conservative 228; Mismatches 151; Indels 0; Gaps 0;  
QY 1614 TCTGCTGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1673  
DB 1081 YY 1140  
QY 1674 TCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1733  
DB 1141 YY 1200  
QY 1734 TGAGGAATCTTACCATCTGCTGCTCATCAAGCAGCAGCAGCAGCAGCAGCAGCAG 1793  
DB 1201 YY 1260  
QY 1794 CACTCATCTTCAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1853  
DB 1261 YY 1320  
QY 1854 CCCTCAAGTCCGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1913  
DB 1321 YY 1380  
QY 1914 CCATCAATCTTGTGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1973  
DB 1381 YY 1440  
QY 1974 ACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2018  
DB 1441 AATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1485

RESULT 15  
US-08-866-757-1  
: Sequence 15, Application US/08866757  
: Patent No. 5670367  
: GENERAL INFORMATION:  
: APPLICANT: ELSHOURBAGY, NABIL A  
: APPLICANT: LI, XIAOTONG  
: APPLICANT: BERGSHA, DEREK J

```

: TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
:
: NUMBER OF SEQUENCES: 4
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: RATNER & PRESTIA
: STREET: P.O. BOX 980
: CITY: VALLEY FORGE
: STATE: PA
:
: COUNTRY: USA
:
: ZIP: 19482
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
:
: COMPUTER: IBM Compatible
:
: OPERATING SYSTEM: DOS
:
: SOFTWARE: FastSeq for Windows Version 2.0
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/866,757
:
: FILING DATE: 30-MAY-1997
:
: CLASSIFICATION: 536
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
:
: FILING DATE:
:
: ATTORNEY/AGENT INFORMATION:
: NAME: PRESTIA, PAUL F
:
: REGISTRATION NUMBER: 23,031
:
: REFERENCE/DOCKET NUMBER: GH-70055
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-407-0700
:
: TELEFAX: 610-407-0701
:
: TELEX: 846169
:
: INFORMATION FOR SEQ ID NO: 1:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4203 base pairs
:
: TYPE: nucleic acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: CDNA
:
: US-08-866-757-1

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Db	1606	TTCCATAGAGGGGAATATCTGCATCACCCCTTTGTGTGCATTTCTCAGGTGAACG	1665
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Db	1666	CCATCATTAGGATTCACTGTAAAGTTAGTGCTATTAACTCACTAGCATTTTATTATTAATG	1725
Qy	1703	TGTGGCTGCTATACCCACATCTTACCTCACAGTCAGGAATCCTACCAATGTGTCTCATCA	1762
Db	1726	GCGGTTATCTACACTAAGCTATACTGCACTTGGANAAGAGGACCTCTCAGAAAACTCA	1785
Qy	1763	AGGCACACCAAGATTGCCAAGCGCATGGCCACACTCATCTTCCACAGACTTTCTCTGATG	1822
Db	1786	CAATCTAGCATGATT---AAGCATGTGCGTTGGCTAATCTTCACCAATTGCATCTTTTTC	1842
Qy	1823	GCCCCCATTTCACTTTTGGCATTTCTGCCTCCCTCAAGGTGCCGTCACTCACTGTGTCC	1882
Db	1843	TGCCCTGTGGCGTTTTTTTCATTTGGACCAATGATCAGTCGAATCTATATACGCCCGAA	1902
Qy	1883	AAGGCCAAGATTCTCCTAGTTCCTGTGTTCTACCCCATCAATTTCTGTGCCAATCTTCTCCCTC	1942
Db	1903	ATAATGAAGTCCTTACTCTGATATTTTTCATTGCTTGCCTGAATCAGTCCTG	1962
Qy	1943	TAGCCCATTTTTCACCAAGAACTT	1965
Db	1963	TATGTTTCTTCTCAACCCAAAGTT	1985

Search completed: June 16, 2003, 11:39:46  
Job time : 143 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 07:25:51 : Search time 2993 Seconds  
(without alignments)  
12802.714 Million cell updates/sec

Title: US-09-877-804-5

Perfect score: 2366

Sequence: 1 agggactgggaattctgtg.....aaacaaagcaaaaccgcaca 2366

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapert 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum Match 100%

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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1: em\_estba:.\*  
2: em\_estba:.\*  
3: em\_estba:.\*  
4: em\_estba:.\*  
5: em\_estov:.\*  
6: em\_estpl:.\*  
7: em\_estro:.\*  
8: em\_hic:.\*  
9: gb\_estl:.\*  
10: gb\_est2:.\*  
11: gb\_hic:.\*  
12: gb\_est3:.\*  
13: gb\_est4:.\*  
14: gb\_est5:.\*  
15: em\_estfun:.\*  
16: em\_estom:.\*  
17: gb\_gss:.\*  
18: em\_gss\_hum:.\*  
19: em\_gss\_hum:.\*  
20: em\_gss\_plv:.\*  
21: em\_gss\_vrt:.\*  
22: em\_gss\_vrt:.\*  
23: em\_gss\_mam:.\*  
24: em\_gss\_mus:.\*  
25: em\_gss\_other:.\*  
26: em\_gss\_pro:.\*  
27: em\_gss\_rod:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	2037.6	85.7	2360	11	AK016635		Mus muscu
2	619	26.2	703	17	BH029943		BH029943 RPI-24-2
3	465.6	19.7	598	13	BM483278		BM483278 536539 MA
4	459.8	19.4	3015	11	AK014519		AK014519 Mus muscu
5	444	18.8	548	12	BF075894		BF075894 225322 MA
6	345.4	14.6	663	13	BM439989		BM439989 pgrin.pk0

7	306	12.9	591	13	BI186370		BI186370 UNL-P-FN-
8	305.4	12.9	711	13	BI185789		BI185789 UNL-P-FN-
9	282	12.1	253	10	AW358484		AW358484 42342 MAR
10	282	12.1	253	10	AW358484		AW358484 42342 MAR
11	228.2	9.6	142	13	BI171109		BI171109 RCO-H7061
12	218.6	9.2	142	13	BI171109		BI171109 RCO-H7061
13	210.4	8.9	294	10	BM553437		BM553437 AGSCCORT
14	208.8	8.8	885	17	CNS0300T		CNS0300T 22382 MAR
15	181.4	7.7	1113	13	BM454054		BM454054 AGSCCORT
16	181.4	7.7	1113	13	BM454054		BM454054 AGSCCORT
17	167.6	7.1	637	10	BF991227		BF991227 PM2-MT010
18	161	6.8	392	17	BF991227		BF991227 PM2-MT010
19	159.4	6.7	366	17	AZ717823		AZ717823 RPI-24-1
20	154.6	6.5	267	9	AZ717823		AZ717823 RPI-24-1
21	152.4	6.4	702	10	AV278732		AV278732 AV278732
22	141	6.0	181	13	BB617484		BB617484 BB617484
23	134	5.7	302	17	BM484173		BM484173 537925 MA
24	111.8	4.7	652	10	AF455800		AF455800 AF455800
25	110.8	4.7	678	10	BB666237		BB666237 BB666237
26	106.2	4.5	303	17	BB666237		BB666237 BB666237
27	106.2	4.5	303	17	BB666237		BB666237 BB666237
28	100.2	4.2	1087	9	AK016635		AK016635
29	98.6	4.2	568	13	CNS0589Y		CNS0589Y
30	96.2	4.1	427	12	BF508244		BF508244
31	89.4	3.8	437	12	BF523207		BF523207
32	87.6	3.7	761	12	BF036966		BF036966
33	84.8	3.6	913	17	CNS0404E		CNS0404E
34	83.2	3.5	628	13	BJ126800		BJ126800
35	82.2	3.5	932	11	AK021020		AK021020 Mus muscu
36	82	3.5	573	13	BI630907		BI630907 RH60250.5
37	82	3.5	610	13	BI628622		BI628622 RH57122.5
38	81.2	3.4	1101	17	CNS0181F		CNS0181F
39	80.6	3.4	397	10	AW174149		AW174149
40	79.8	3.3	515	9	AW177137		AW177137
41	77.2	3.2	127	12	BE707642		BE707642
42	75.4	3.2	101	17	CNS02UAM		CNS02UAM
43	75.4	3.2	891	17	CNS02UAM		CNS02UAM
44	74.2	3.1	465	13	BI792833		BI792833
45	74	3.1	249	10	BB608621		BB608621

## ALIGNMENTS

RESULT 1	AK016635	2360 bp	linear	HTC 19-JAN-2002
LOCUS	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933403107:follicle stimulating hormone receptor, full insert sequence.			
DEFINITION	AK016635			
ACCESSION	AK016635			
VERSION	AK016635.1			
KEYWORDS	HTC; CAP; trippase			
SOURCE	Mus musculus (strain: C57BL/6J) adult male testis cDNA to mRNA, clone:lib-RIKEN full-length enriched mouse cDNA library			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBLISHED	2			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, N., Kono, H., Oikawa, Y., Muramatsu, M., and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cDNAs from the RIKEN cDNA library to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBLISHED	11042159			



Db	242	TCATTCCAAAGGATCATTTTCTGGATTGGGACCTGGCAAAATAGAGATCTCTCA	301
Oy	309	ATGATGCTCTTGAAGTAATAGAGGAGATCTGCTCCAACTTACCAGTGGCAATGA	368
Db	302	ATGATGCTCTTGAAGTAATAGAGGAGATGCTGCTCCAACTTACCAGTGGCAATGA	361
Oy	369	TTAGGATTGAAGAGGCAACAATCTTCTGACATCAACCGGAGGCTTCCAGATCTCC	428
Db	362	TTAGGATTGAAGAGGCTAACAACTCTGCTGACATCAACCGTGAAGGCTTCCAGATCTTC	421
Oy	429	CAAGTCTCAGATCTCTTAAATATCCAAACAGGCAATTAAGCACTTGGCAGCTGTTC	488
Db	422	CAAGTCTCAGATCTCTTAAATATCCAAACAGGCAATTAAGCACTTGGCAGCTGTTC	481
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Db	482	AGATCCAGTCTCTCCAAAGGTTCTACTAGACATTAAGATTAACATCCACATG	541
Oy	549	TTGCCAGCAACTCTCTCATGCGAGTGTGTTTGAAGTGTATTTATGGCTGACGA	608
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Db	722	CAGTCATTTAGATATCTCAGGAGCAAGGTCATCTCTTACCAACCATGCTTGA	781
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Oy	909	ACTGAGCGGCAATCTCGAATCTATCCAAATTTGCAACAGTCTATTTAAGGCAG	968
Db	902	ACTGAGCGGCAATCTCGAATCTATCCAAATTTGCAACAGTCTATTTAAGGCAG	961
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Oy	1089	TTGTTGATGATGACTCTGATGATGATGATGATGATGATGATGATGATGATG	1148
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Oy	1209	CACAGTCTGCTGCTGCTGACCAACAGGCAATCAACATCACTGCTGCTGCTG	1268
Db	1202	CCACAGTCTGCTGCTGCTGACCAACAGGCAATCAACATCACTGCTGCTGCTG	1261
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Db	1262	TGTTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1321
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Db	1322	TTGATATCCATACCAAGAGCCATACCAACTATGCAATGACCTGCAACAGGAG	1381
Oy	1389	GCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1448
Db	1382	GCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1441
Oy	1449	CAGCATCACTAGAAAGATGGCATACATACATACATGCTATGCAATGCAATG	1508
Db	1442	CAGCATCACTAGAAAGATGGCATACATACATACATGCTATGCAATGCAATG	1501
Oy	1509	TGAGCTCTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1568
Db	1502	TGAGCTCTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1561
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Oy	1629	CTCTCTTCCCATCTTGGCATCAGTAGCTACATGAAAGTGAGCATCTGCTGCTG	1688
Db	1622	CTCTCTTCCCATCTTGGCATCAGTAGCTACATGAAAGTGAGCATCTGCTGCTG	1681
Oy	1689	CTCTCTTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1748
Db	1682	CTCTCTTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1741
Oy	1749	TTGTGCTCTCATCAAGGAGCAACCAAGATTTGCCAAGGCGCATGGCCACATCT	1808
Db	1742	TTGTGCTCTCATCAAGGAGCAACCAAGATTTGCCAAGGCGCATGGCCACATCT	1801
Oy	1809	ACTTCTCTGCAATGCGGCGCATCTTCTTGGCATTTTCTGCTGCTGCTGCTGCTG	1868
Db	1802	ACTTCTCTGCAATGCGGCGCATCTTCTTGGCATTTTCTGCTGCTGCTGCTGCTG	1861
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Db	1862	TCATCACTCTGTCGAGGCGCAAGATCTGCTAGTGTGCTTACCGCATCAATCT	1921
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Db	1922	CCATCTCTTCTCTAGGCGCATTTTCCCAAGCACTTTCCGCGGAGCTTCTGCTG	1981
Oy	1989	TGAGCAAGTTTGGCTGTATGAAATGCAAGCGGAGATTTACAGAGCAAGAACT	2048
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Oy	2049	CTACCCAACTTCCATGCGGCAAGAGCCACTGCTGCTGCTGCTGCTGCTGCTG	2108
Db	2042	CTACCCAACTTCCATGCGGCAAGAGCCACTGCTGCTGCTGCTGCTGCTGCTG	2101
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Oy	2169	TCTTCACTTGAAGAGCAATTTATGAC-TCTTCTGAGAGAGCGGCTTAAATGGC	2227
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Oy	2228	AATCTCTGACATCTCATCTAATTAATCTCTGCTGCTGCTGCTGCTGCTGCTG	2287
Db	2222	AGTGTGCTGACATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2281
Oy	2288	AGGAGCCATTAACACCCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2346
Db	2282	AGGAGCCATTAATCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2341
Oy	2347	AAAGAGCAAGCCG 2363	
Db	2342	AAATAGTGAACACTGCG 2358	

RESULT 2  
BH029943  
LOCUS

BH029943 703 bp DNA linear GSS 17-JUL-2001

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DEFINITION  RPCI-24-266J19.TJ RPCI-24 Mus musculus genomic clone RPCI-24-266J19
              , DNA sequence.
ACCESSION    BH029943
VERSION      BH029943.1 GI:14798113
KEYWORDS     GSS.
SOURCE       house mouse.
ORGANISM     Mus musculus

REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 703)
              Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
              Tsugeye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
              Russell,D., de Jong,P. and Fraser,C.M.
              Mouse BAC End Sequences from Library RPCI-24
              Unpublished (1999)
              Other_GSSs: RPCI-24-266J19.TV
              Contact: Shaying Zhao
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 0200
              Fax: 301 838 0208
              Email: szhao@tigr.org
              Clones are derived from the mouse BAC library RPCI-24. For BAC
              library availability, please contact Pieter de Jong
              (pjejong@mail.cho.org). Clones may be purchased from BACPAC
              Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
              page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
              Plate: 266 row: J column: 19
              Seq primer: SP6
              Class: BAC ends.
              Location/Qualifiers
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                  /strain="C57BL/6J"
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                  /clone_lib="RPCI-24"
                  /sex="Male"
                  /cell_type="Spleen/Brain"
                  /note="Vector: pTARBAC1; Site_1: BamHI; Site_2: BamHI; The
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                  BamHI sites using MboI partially digested male C57BL/6J
                  DNA."
BASE COUNT   175 a 174 c 156 g 198 t
ORIGIN
Query Match      26.2%; Score 619; DB 17; Length 703;
Best Local Similarity 92.8%; Pred. No. 3,6e-160;
Matches 649; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy  923 ATCTCTGAATTCATCAATTTGCAACAAGTCTATTTTAAGGCAAGATATTTGATGATG 982
Db  1 ATCTCTGAATTCATCAATTTGCAACAAGTCTATTTTAAGGCAAGATATTTGATGATG 64
Qy  983 ACTCAATTTGGGATCAGAGTCTCTCTGATGATGATCAACCCAGTTATGGAAGA 1042
Db  65 ACTCAGGCTGGGATCAGAGTCTCTCTGATGATGATCAACCCAGTTATGGAAGA 124
Qy  1043 TCTGACATGATGATCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1102
Db  125 TCTGACATGATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 184
Qy  1103 TGCTACCAAGCCAGATGATTTAATCCATGTGAAGATATCATGCGGTACCAACCTC 1162
Db  185 TGCTCGCAAGCCAGATGATTTAATCCATGTGAAGATATCATGCGGTACCAACCTC 244
Qy  1163 AGGCTCTGATGATGTTTATAGCATCTCTGCGCATTTACTGGACACACAGTCTGGTG 1222
Db  245 AGAGTCCTGATGATGTTTATAGCATCTCTGCGCATTTACTGGACACACAGTCTGGTG 304
Qy  1223 GTCCTGACCAAGCCAACTAACTGTGCCCGGGTTCTTTATGTGTAACTCGCC 1282

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305 GTCTGACCAAGCAATACAACTCACTGTGCCCGGTTCTTATGTGAACCTCGCC 364
1283 TTGCGTGATCTCTGCAATAGCATCTACTTGTCTACTTATAGCATGATTTGACATCCATACC 1342
365 TTTGCTGATCTTTGCAATGCGATCTACTTGTCTACTTATAGCATGATTTGACATCCATACC 424
1343 AAGAGCCATACCAACATATGCCATTGACTGGCAACAGGAGCGCTGTGATGCTGCT 1402
425 AAGAGCCATACCAACATATGCCATTGACTGGCAACAGGAGCGCTGTGATGCTGCT 484
1403 GGCCTTTTTCACATCTCTTTGCCAGTGAATCTGCTACACATTTGACAGCCATCACCCCTA 1462
485 GGCCTTTTTCACATCTCTTTGCCAGTGAATCTGCTACACATTTGACAGCCATCACCCCTA 544
1463 GAAAGATGCAATACCAATACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1522
545 GAAAGATGCAATACCAATACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 604
1523 GCTGCCAGCGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1582
605 GCTGCCAGCGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 664
1583 TTGGCATCAGTAGCTACATGAAGTGAGCATCTGCTG 1621
665 TTGGCATCAGTAGCTACATGAAGTGAGCATCTGCTG 703

RESULT 3
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LOCUS       BM483278 598 bp mRNA linear EST 05-FEB-2002
DEFINITION 536539 MARC. 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BM483278
VERSION     BM483278.1 GI:18533606
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
            Bovidae; Bovinae; Bos.
            1 (bases 1 to 598)
            Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keefe,J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
            21180013
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTCACAGTCACGACG
            Plate: 6 row: G column: 10
            Seq primer: ATTTAGTGACACTATAG.
            Location/Qualifiers
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                /db_xref="taxon:9913"
                /clone_lib="MARC 3BOV"
                /tissue_type="pooled"
                /lab_host="DH10B"
                /note="vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                Library made from pooled tissue from marrow, alveolar

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COMMENT Contact: Smith TPL  
USDA, Wildlife Research Center  
PO Box 156, Clinton Center, NE 68931-0156, USA  
Tel: 402 762 4356  
Fax: 402 762 4390  
Email: smith@email.merc.usda.gov  
Single pass sequencing. Bases called and alt. trimmed with phred  
v0.98004.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.  
PCR Primers  
FORWARD: AGCAACAGCTATACCAT  
BACKWARD: GTTTCCTCCAGTCAGCAGC  
Plate: 85 row: E column: 3  
Seq primer: ATTAGTGCACATATAG.  
Location/Qualifiers  
1. 348  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="PC-248"  
/lab\_host="DH109"  
/note="Vector: pCMVSPORT6"  
Library made from pooled tissue from testis, thymus,  
semintendous muscle, longissimus muscle, pancreas,  
adrenal, and endometrium."

BASE COUNT 107 a 187 c 103 g 151 t

FEATURES source  
Query Match 18.8% Score 444; DB 12; Length 548;  
Best Local Similarity 88.1%; Pred. No. 1.1e-111;  
Matches 483; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 1474 TACATCATCATATGATGCAATGGAATGCAAGTGCAGCTCCGGAGTGTGCGACGGT 1533  
Db 1 TACATCATCATATGATGCAATGGAATGCAAGTGCAGCTCCGGAGTGTGCGACGGT 60

Qy 1534 CAGCTATTCGGCTGGACCTTTGCTGCGAGCTGCTCTCCGCACTTTGGCATCTG 1593  
Db 61 CAGCTGCTGGCTGGATCTTGTCTTGGCACTGGCTCTTCCCATCTTTGGCATCTG 120

Qy 1594 TAGCTACATCAAGTGAAGCATCTGCTGCCCATGATATGACAGCCCTTTGTGACAGCT 1653  
Db 121 CAGCTACATCAAGTGAAGCATCTGCTGCCCATGATATGACAGCCCTTTGTGACAACT 180

Qy 1654 GTATGTATGGCCCTCTCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTA 1713  
Db 181 GTATGTATGCTGCTCTCTGCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTA 240

Qy 1714 TACCATCATCTACATGATGAGGATGCTACCATGCTGCTGCTGCTGCTGCTGCTGCTA 1773  
Db 241 CACTCATCATCTACATGATGAGGATGCTACCATGCTGCTGCTGCTGCTGCTGCTGCTA 300

Qy 1774 GATTGCCAAGCGCATGCGCACTATCTTCACAGACTTCTCTGATGCGCCCATTTTC 1833  
Db 301 GATAGCCAAAGCGCATGCGCATCTCTCTGATGCGCCCATTTTC 360

Qy 1834 ATTCTTTGCCATTTCTGCTCCCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1893  
Db 361 CTCTTTTGCCATTTCTGCTCCCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

Qy 1894 TCTCTTACTTCTTCTTACCCCATCAATTTCTGCGCAATCTTCTTCTCTAGCCCATTTT 1953  
Db 421 CTCTCTTCTGCTTCTTCTTACCCCATCAATTTCTGCGCAATCTTCTTCTCTAGCCCATTTT 480

Qy 1954 CACGAGAGAGTCTGCGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2013  
Db 481 CACGAGAGAGTCTGCGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

Qy 2014 CGAAGCCC 2021  
Db 541 CGAAGCCC 548

RESULT 6  
BM439989  
LOCUS 663 bp mRNA linear EST 01-FEB-2002  
DEFINITION BM439989.1 GI:18470764  
P311PK001.n16 Normalized Chicken Reproductive Tract cDNA Library  
P311PK001.n16 Normalized Chicken Reproductive Tract cDNA Library  
SP79763.FSHR.CHICK.FOLLICLE STIMULATING HORMONE RECEPTOR  
PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) dbj|BAAL3487.1| (087871)  
follicle-stimulating hormone receptor [Gallus gallus], mRNA  
sequence.  
ACCESSION BM439989  
VERSION BM439989.1 GI:18470764  
KEYWORDS EST  
SOURCE chicken.  
ORGANISM Gallus gallus  
REFERENCE 1 (bases 1 to 663)  
AUTHORS Cogburn, L.A. and Nys, Y.  
TITLE Estis from Normalized Chicken Reproductive Tract cDNA library-  
JOURNAL Nucleic Acids Res 30(2002)1167  
COMMENT University of Delaware  
Contact: Larry A. Cogburn  
University of Delaware  
Townsend Hall, Newark, DE 19717, USA  
Tel: 302-831-1335  
Fax: 302-831-2822  
Email: cogburn@udel.edu, www.chickest.udel.edu.  
FEATURES source  
1. 663  
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/strain="Commercial broiler and layer"  
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/clone\_lib="Normalized Chicken Reproductive Tract cDNA  
Library (pgrin) Female"  
/sex="Male and Female"  
/development="testis, ovary and oviduct"  
/stage="embryonic, post-hatch, immature  
and sexually-mature"  
/lab\_host="E. coli BMDH109"  
/note="Vector: pCMVSPORT6; Library made from three total  
RNA pools from each tissue (testis 25%, ovary 25%, and  
oviduct 50% of final RNA pool); Single pass sequencing  
from 5'-end"

BASE COUNT 176 a 145 c 141 g 197 t 4 others

Query Match 14.6% Score 345.4; DB 13; Length 663;  
Best Local Similarity 71.7%; Pred. No. 2.6e-84;  
Matches 464; Conservative 0; Mismatches 180; Indels 3; Gaps 1;

Qy 939 GAACCTTCATCCCAATTTGCAACAGCTATTTTAAGGCAAGATATGATATGATGACMA 988  
Db 16 GAATTTTACCANTATGATGATGCTCTCCGCAAGCAAGCTTGTGAGCAGACTGGC 75

Qy 989 ATTGGGATGACAGAGTCTCTCTGATGATGATGA---ACCCAGTTATGAAAGGATCT 1045  
Db 76 AAAAGAAACACAGACGATCTGCGAGCTGAAGATTATATTTCCCATATGCGACGGCTTT 135

Qy 1046 GACATGATGTACAATGAATTTGATATGATGATGATGATGATGATGATGATGATGATG 1105  
Db 136 GCGCCCTGCGGAGAACGAATTTGATGATGATGATGATGATGATGATGATGATGATG 195

Qy 1106 TCACCAAGCCAGATGCAATTTAATGATGATGATGATGATGATGATGATGATGATGATG 1165  
Db 136 GCGCCCTGCGGAGAACGAATTTGATGATGATGATGATGATGATGATGATGATGATG 255

Qy 1166 GTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1225  
Db 256 GTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 315

Qy 1226 CTGACCAAGCAAGCAATACAACTAAGTGTGCGCCGGTTTCTTATGATGATGATGATG 1285





Db 122 GAACCTTCCCAACCTCCGATATCTGTTAATATCCACACAGGTATTAAAGCACTTGCCAGC 181  
 QY 481 TGTTCACAAGATCCAGCTCTCTCCAAAGGTTCTTACTAGACATTCAGATAACATTAACAT 540  
 Db 182 TGTTCACAAGATTCAGCTCTCTCCAAAGGTTTACTAGATATTCAGATAAATATAACAT 241  
 QY 541 CCACATCGTGGCAGGAACCTCTTCATGGGAGTGGTGTGAAAGTGTGATTTATGGCT 600  
 Db 242 CCACACAGTGTGAAGAAATCTTTCATGGGGCTAAGTTTGAAGATGACACTGTATGGCT 301  
 QY 601 GAGTAGAATGGAGTGAAGAATAACACAACTGTGCAATTCACGGAACCTCA 651  
 Db 302 GAGTAGAATGGAGTGAAGAATAACACAACTGTGCAATTCACGGAACCTCA 352

RESULT 10  
 BE179105/c  
 LOCUS  
 DEFINITION RCO-HT0613-200300-031-a10 HT0613 Homo sapiens cDNA, mRNA sequence. EST 22-JUN-2000  
 ACCESSION BE179105  
 VERSION BE179105.1 GI:8658257  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 613)  
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RCO-HT0613-200300-031-a10st3-2000-03-20st4-1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 19  
 High quality sequence stop: 612.

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 source  
 1. .613  
 /organism="Homo sapiens"  
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 /dev\_stage="Adult"  
 /note="Organ: head\_neck; Vector: puc18; Site1: SmaI; Site2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
 BASE COUNT 168 a 132 c 178 g 135 t  
 ORIGIN

Query Match 10.2%; Score 242; DB 10; Length 613;  
 Best Local Similarity 64.4%; Pred. No. 1.2e-55;  
 Matches 362; Conservative 0; Mismatches 200; Indels 0; Gaps 0;  
 QY 1471 GCATACCATCACATGCTATGCAACTGGAATGCAAGGTGACGCTCGGCATCTGCCAG 1530

Db 612 GTATGCCATCACCTTCGCCATCGGCTGGACCGAAGATCCGCCTCAGGCACGCATGTGC 553  
 QY 1531 COTCATGGTATTGGGCTGGAGCTTTTGGCTTCCAGAGTGTCTCTCTTCCCATCTTTTGGCAT 1590  
 Db 552 CATCATGTTGGGGCTGGTGTCTCTTCCCTTCCGCCCTGCTTCCCTTGGTGGGAAT 493  
 QY 1591 CAGTAGCTACATGAAGTCAGCATCTGCTGCCATGGATATCGACAGCCCTTTGTCACA 1650  
 Db 492 AAGTAGCTATGCAAGTCAAGTATGCTGCTGACATGGACACCGAAACCCCTCTTGTCT 433  
 QY 1651 GCTGTATGTTATGGCCCTCTTGTCTCAATGTCTGCGCTTTTGGTGTCTATCTGTGCTG 1710  
 Db 432 GCATATATTGTTTGTCTGACGCTCAACATAGTTGCTTGGCTGCTATCTGTGCTGCTG 373  
 QY 1711 CTATACCCACATCTACCTCACAGTGAAGAACTCTTACCATTGTGCTCTCATCAAGCACAC 1770  
 Db 372 TTATGTGAAGATCTACATCACAGTCCGAATCCGAGTACAACCCAGGGGACAAGATAC 313  
 QY 1771 CAAGATTGCCAAGCGCATGCCACACTCATCTTACAGACTTCTCTGATGCGATGCGCCCAT 1830  
 Db 312 CAAGATTGCCAAGAGGATGGCTGTGTGATCTTACCGACTTCATATGATGCGCCCAT 253  
 QY 1831 TTCAATCTTTGGCCATTTCTGCTCCTCAAGGTGCGCTCATCACTGTGTCCAAGGCCAA 1890  
 Db 252 CTCAATCTATGCTCTGTGAGCAATTTGAAAGCGCTCTCATCACTGCTAGCACTCCAC 193  
 QY 1891 GATTCTCTAGTCTGTTCTTACCCCATCAATTTGTTGCAATCTCTTCTTACGCCCAT 1950  
 Db 192 AATCTTCTGCTGCTACTCTTATCCACTTAACCTCTGCAATCCATCTCTCTATGCTAT 133  
 QY 1951 TTTCACCAAGAACTTCCGAGGAGCTTCTTCACTCTGCTGAGCAAGTTTGGCTGTTATGA 2010  
 Db 132 TTTCACCAAGGCTCTCCAGGGGATGTGTTTCACTTACTCAGCAAGTTTGGCATCTGTAT 73  
 QY 2011 AATGCAAGCCCATTTACAGG 2032  
 Db 72 ACGCCAGGCTCAGGCATACCGG 51

RESULT 11  
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 DEFINITION AGENCOURT\_6419913 NCI\_CGAP\_Ov44 Mus musculus cDNA clone  
 IMAGE:5503889 5', mRNA sequence.  
 ACCESSION BM4611149  
 VERSION BM4611149.1 GI:18510189  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE 1 (bases 1 to 1142)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapus@mail.nih.gov  
 Tissue Procurement: Aaron Haueh  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM12144 row: f column: 18  
 High quality sequence start: 16  
 High quality sequence stop: 685.  
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FEATURES  
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FEATURES
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Query Match 8.8% Score 208.8; DB 17; Length 885;
Best Local Similarity 69.8%; Pred. No. 2,2e-46;
Matches 282; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
OY 1584 TTGGCAGCTAGCTACATGAAGTGAAGTCTCTGCTGCTCAATGTCTGGCCCTTTGGTGCATCT 1703
DB 424 TTTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 365
OY 1644 TGTACAGCTCTATGTTATGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1703
DB 11111111111111111111111111111111111111111111111111111111111111 365
OY 1704 GTGGCTGTATACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 305
DB 364 GTGGCTGTATACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 305
OY 1704 GTGGCTGTATACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 305
DB 364 GTGGCTGTATACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 305
OY 1764 GGGACACCACTGTCAGGCTGTCAGGCTGTCAGGCTGTCAGGCTGTCAGGCTGTCAGGCT 245
DB 304 GTGGCTGTATACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 245
OY 1764 GGGACACCACTGTCAGGCTGTCAGGCTGTCAGGCTGTCAGGCTGTCAGGCTGTCAGGCT 1823
DB 304 GTGGCTGTATACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1823
OY 1824 CCCCCATTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCAT 1883
DB 184 CTTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 125
OY 1884 AGGCCAAGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1943
DB 124 AGGCCAAGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 65
OY 1944 AGGCCAAGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1987
DB 64 AGGCCAAGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 21

RESULT 15
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ACENICOURT_6419563 NCI_CGAP_Ov44 Mus musculus cDNA clone
IMAGE:5504347 5', mRNA sequence.
BM454054
BM454054.1 GI:18503094
EST.
House mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases to 1113)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgep@femail.nih.gov
Tissue Procurement: Aaron Hsueh
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Date: 11/01/99 row: 1 column: 20
High quality sequence start: 14
High quality sequence end: 1072
High quality sequence length: 1072
Location/Qualifiers
1..1113
/organism="Mus musculus"
/db_xref="taxon:10090"
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/clone_lib="NCI_CGAP_Ov44"
/lab_host="DH10B (T1 phage-resistant)"
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/notes="Organ: ovary, PMSG-treated; Vector:
pCMV-SPORT6.cdb; Site_1: EcoRV; Site_2: NotI; Cloned
unidirectionally. Primer: Oligo dt. Average insert size
2.2 kb. Library constructed by Life Technologies. Note:
This is a NCI_CGAP Library."
BASE COUNT 318 a 253 c 180 g 382 t
ORIGIN

Query Match 7.7% Score 181.8; DB 13; Length 1113;
Best Local Similarity 68.3%; Pred. No. 7.6e-39;
Matches 252; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
OY 1665 CCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1724
DB 23 CCATCTTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 82
OY 1725 ACCTCAGAGTGAAGATCTCTACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1784
DB 83 ACTTTGAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 142
OY 1785 GGTTCGGCAGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1844
DB 143 AGTGGGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 202
OY 1845 TTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1904
DB 203 TCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 262
OY 1905 TGTTCACCCATCAATTTCTGTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1964
DB 263 TTTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 322
OY 1965 TCCGAGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2024
DB 323 TTCAGAGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 382
OY 2025 TTTACAGGA 2033
DB 383 TTTACAGGA 391
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Search completed: June 16, 2003, 11:37:14  
Job time : 2998 secs



XX Examples; Fig 12; 103pp; English.

PS This sequence represents the N-terminal of a novel protein having a

CC binding affinity for human chorionic gonadotropin (hCG), luteinising

CC hormone (LH), and follicle stimulating hormone (FSH). The protein

CC itself is a chimera having residues from both the FSH receptor,

CC and LH receptor. The receptor analogues can be used in bioassays

CC for the simultaneous detection of both LH (or hCG) and FSH as

CC well as their ratio of biological activities. The analogues can also

CC be used for raising, purifying and assaying antibodies to the

CC analogues. Coding sequence for the chimera was produced by two step

CC PCR.

XX Sequence 695 AA;

XX

Query Match 99.9%; Score 3589; DB 14; Length 695;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 691; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MALLVSLAFGLTSGCHHLCNSRVFLCQDSKVTEIPTDLPRNAIELRVLTCLR 60

Db 1 MALLVSLAFGLTSGCHHLCNSRVFLCQDSKVTEIPTDLPRNAIELRVLTCLR 60

Qy 61 IPKGSFAGFGLDKIEISQNDVLEADVFSLPKLHEIRIEKANNLLYINPEAFONLP 120

Db 61 IPKGSFAGFGLDKIEISQNDVLEADVFSLPKLHEIRIEKANNLLYINPEAFONLP 120

Qy 121 SLRYLLISNTGKIKHLPVAVHKIQSLQKVLDDIQDNINIHIVARNFMSGLSFESVILWLSKN 180

Db 121 SLRYLLISNTGKIKHLPVAVHKIQSLQKVLDDIQDNINIHIVARNFMSGLSFESVILWLSKN 180

Qy 181 GIEIHNCAFNQTQDLNLSNNLELNDVFGASGVVLDISTRTKVSHPNHGLEN 240

Db 181 GIEIHNCAFNQTQDLNLSNNLELNDVFGASGVVLDISTRTKVSHPNHGLEN 240

Qy 241 LKLRARSTYRLKLPNDKFTVLEASLYPSHCCAFANLKRQISELHPICNKSLIQD 300

Db 241 LKLRARSTYRLKLPNDKFTVLEASLYPSHCCAFANLKRQISELHPICNKSLIQD 300

Qy 301 IDDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPAFNPCEDIMG 360

Db 301 IDDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPAFNPCEDIMG 360

Qy 361 YNLRVLIWFISILAITGNTTVLVLTTSQYKLVTPRFLMCNLAFAADLCIGYLLLIASV 420

Db 361 YNLRVLIWFISILAITGNTTVLVLTTSQYKLVTPRFLMCNLAFAADLCIGYLLLIASV 420

Qy 421 DIHTKSOYHVAIDWQTGAGDAAGFTVFASLSVYTLTITLERWHTITHAMOLECKV 480

Db 421 DIHTKSOYHVAIDWQTGAGDAAGFTVFASLSVYTLTITLERWHTITHAMOLECKV 480

Qy 481 QLRHAASVMVLGWTFAFAALFPIFGISSYMKVSIKLPMDIDPSLSQLYNALLVNLVA 540

Db 481 QLRHAASVMVLGWTFAFAALFPIFGISSYMKVSIKLPMDIDPSLSQLYNALLVNLVA 540

Qy 541 FWTCGCTHYLYLVNPTIYSSSDTKIAKRMATLFTDFLCMAPISFFAISLKVPL 600

Db 541 FWTCGCTHYLYLVNPTIYSSSDTKIAKRMATLFTDFLCMAPISFFAISLKVPL 600

Qy 601 ITVSKAKILLVFPINSCANPFLYAIPTKFRDRDFILLSKFCGYEQAOIYRTETSSA 660

Db 601 ITVSKAKILLVFPINSCANPFLYAIPTKFRDRDFILLSKFCGYEQAOIYRTETSSA 660

Qy 661 THNFHARKSHCSSAPRVNTSYVLPLNHSSQN 692

Db 661 THNFHARKSHCSSAPRVNTSYVLPLNHSSQN 692

RESULT 2

AAR08038

ID AAR08038 standard; protein; 692 AA.

XX

AC AAR08038;

XX

DT 26-FEB-1991 (first entry)

XX

DE Rat testicular luteinising hormone/choriogonadotropin receptor.

XX

KW LH/CG receptor; FSH receptor; TSH receptor; fertility; breast cancer;

KW prostate cancer; thyroid cancer; osteoporosis; Graves disease;

KW polycystic ovarian disease; vasomotor instability.

XX

OS Rattus rattus.

XX

PN WO9013643-A.

XX

PD 15-NOV-1990.

XX

PF 04-MAY-1990; 90MO-US02488.

XX

PR 05-MAY-1989; 89US-0347683.

XX

PA (GETH ) GENENTECH INC.

XX

PI Nikolics K, McFarland KC, Segaloff DL, Seeburg PH;

XX

DR WPI; 1990-361478/48.

DR N-PSDB; AAQ06634.

XX

XX Pharmaceutical compsn. contg. hormone receptor mol - used for

PT treating fertility, breast-and prostate-cancer and osteoporosis,

PT etc.

XX

PS Disclosure; fig 6; 78pp; English.

XX

CC This rat testicular follicle-stimulating hormone (FSH) receptor.

CC This receptor is useful in a pharmaceutical compsn. for treating

CC e.g. breast-, prostate- and thyroid cancer, fertility, osteopor-

CC ois, vasomotor instability and polycystic ovarian disease.

CC LH/CG- or TSH-receptors can also be used, to treat e.g. Graves

CC disease. Abs can be used to inhibit receptor binding and for imag-

CC ing and therapy. See also AAR08015-23, AAR08035-36 and AAQ06633.

XX

SQ Sequence 692 AA;

Query Match 99.7%; Score 3585; DB 11; Length 692;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 690; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MALLVSLAFGLTSGCHHLCNSRVFLCQDSKVTEIPTDLPRNAIELRVLTCLR 60

Db 1 MALLVSLAFGLTSGCHHLCNSRVFLCQDSKVTEIPTDLPRNAIELRVLTCLR 60

Qy 61 IPKGSFAGFGLDKIEISQNDVLEADVFSLPKLHEIRIEKANNLLYINPEAFONLP 120

Db 61 IPKGSFAGFGLDKIEISQNDVLEADVFSLPKLHEIRIEKANNLLYINPEAFONLP 120

Qy 121 SLRYLLISNTGKIKHLPVAVHKIQSLQKVLDDIQDNINIHIVARNFMSGLSFESVILWLSKN 180

Db 121 SLRYLLISNTGKIKHLPVAVHKIQSLQKVLDDIQDNINIHIVARNFMSGLSFESVILWLSKN 180

Qy 181 GIEIHNCAFNQTQDLNLSNNLELNDVFGASGVVLDISTRTKVSHPNHGLEN 240

Db 181 GIEIHNCAFNQTQDLNLSNNLELNDVFGASGVVLDISTRTKVSHPNHGLEN 240

Qy 241 LKLRARSTYRLKLPNDKFTVLEASLYPSHCCAFANLKRQISELHPICNKSLIQD 300

Db 241 LKLRARSTYRLKLPNDKFTVLEASLYPSHCCAFANLKRQISELHPICNKSLIQD 300

Qy 301 IDDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPAFNPCEDIMG 360

Db 301 IDDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPAFNPCEDIMG 360

Qy 361 YNLRVLIWFISILAITGNTTVLVLTTSQYKLVTPRFLMCNLAFAADLCIGYLLLIASV 420

Db 361 YNLRVLIWFISILAITGNTTVLVLTTSQYKLVTPRFLMCNLAFAADLCIGYLLLIASV 420

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Db 361 YNLRVLNFIATIGTNTTVLVLTTSQYKLTVPFLMCNLAFAADLCIGIYLLIASV 420
Oy 421 DIHTKSOYHNTAIDMOTGACGDAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKV 480
Db 421 DIHTKSOYHNTAIDMOTGACGDAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKV 480
Oy 481 QLRHAASVWVLGHTFAAALPPIFGISSYKVSICLPMDIDSPLSQLYMALLVNLVLA 540
Db 481 QLRHAASVWVLGHTFAAALPPIFGISSYKVSICLPMDIDSPLSQLYMALLVNLVLA 540
Oy 541 FVVICGCTHYIYLVNPTIVSSSDTKIAKRMATLIPTDFLCMAPISFFAISASLKVPL 600
Db 541 FVVICGCTHYIYLVNPTIVSSSDTKIAKRMATLIPTDFLCMAPISFFAISASLKVPL 600
Oy 601 ITVSKAKILLVLYPINSKANPELYAIFTKNFRDRFFILLSKFCGYENQAIYRTETSSA 660
Db 601 ITVSKAKILLVLYPINSKANPELYAIFTKNFRDRFFILLSKFCGYENQAIYRTETSSA 660
Oy 661 TINFHARKSHCSSAPRVNTSVLVPLNHSQN 692
Db 661 TINFHARKSHCSSAPRVNTSVLVPLNHSQN 692

RESULT 3
AAR30524
ID AAR30524 standard; protein; 695 AA.
AC AAR30524;
XX
XX 10-MAY-1993 (first entry)
XX
XX N-terminal of LH receptor/FSH receptor chimera #33.
XX
XX Follicle stimulating hormone receptor; luteinising hormone receptor;
XX human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimera; chimera.
XX
XX Chimaeric; homo sapiens.
XX
XX W09222667-A.
XX
XX 23-DEC-1992.
XX
XX 12-JUN-1992; 92MO-US04987.
XX
XX 14-JUN-1991; 91US-0715911.
XX
XX (UYNE-) UNIV NEW JERSEY.
XX
XX Bernard M, Moyle WR, Myers R;
XX
XX MPI; 1993-018150/02.
XX
XX Glyco:protein hormone receptor analogues - having binding
XX affinity to human chorionic gonadotrophin, luteinising and
XX follicle stimulating hormones, useful in bio:immunoassays
XX
XX Examples; Fig 12; 103pp; English.
XX
XX This sequence represents the N-terminal of a novel protein having a
XX binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX hormone (LH) and follicle stimulating hormone (FSH). The protein
XX is a chimera of residues from both the FSH receptor,
XX and LH receptor. The detection of both LH (or hCG) and FSH
XX for the simultaneous detection of both LH (or hCG) and FSH
XX as well as their ratio of biological activities. The analogues can also
XX be used for raising, purifying and assaying antibodies to the
XX analogues. Coding sequence for the chimera was produced by two step
XX PCR.
XX
XX Sequence 695 AA;

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Query Match 98.3%; Score 3532; DB 14; Length 695;

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Best Local Similarity 98.1%; Pred. No. 0;
Matches 679; Conservative 6; Mismatches 7; Indels 0; Caps 0;
Oy 1 MALLVSLLAFLATGTCGCHHMLCHCSNRVFLCQDSKYTEIPTDLPNNAIELEFVLTJLV 60
Db 1 MALLVSLLAFLATGTCGCHHMLCHCSNRVFLCQDSKYTEIPTDLPNNAIELEFVLTJLV 60
Oy 61 IPKGSFAGCDLEKTEISONDVLEVIEADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120
Db 61 IPKGSFAGCDLEKTEISONDVLEVIEADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120
Oy 121 SLRYLLISMTGIXKHPAVHKIQSLQKVLDDIODNINIHIVARNSPMGSPESVILMSKN 180
Db 121 SLRYLLISMTGIXKHPAVHKIQSLQKVLDDIODNINIHIVARNSPMGSPESVILMSKN 180
Oy 181 GIEZHNCAFNQTODELNLSNNNLEELPNDVPOGASGPVILDISRTKVHSLPMHLEN 240
Db 181 GIEZHNCAFNQTODELNLSNNNLEELPNDVPOGASGPVILDISRTKVHSLPMHLEN 240
Oy 241 LKKLPARSTYRLKLLPNLDKFTVLTWEASLTYPSSHCCAFANLKROISELHPICNKLROD 300
Db 241 LKKLPARSTYRLKLLPNLDKFTVLTWEASLTYPSSHCCAFANLKROISELHPICNKLROD 300
Oy 301 IDDMTQIGDORVSLIDDEPSYKSGSDMYNEFDYDLCNEVYDVTCSPKPAFNPCEIDMG 360
Db 301 IDDMTQIGDORVSLIDDEPSYKSGSDMYNEFDYDLCNEVYDVTCSPKPAFNPCEIDMG 360
Oy 361 YNLRVLNFIATIGTNTTVLVLTTSQYKLTVPFLMCNLAFAADLCIGIYLLIASV 420
Db 361 YNLRVLNFIATIGTNTTVLVLTTSQYKLTVPFLMCNLAFAADLCIGIYLLIASV 420
Oy 421 DIHTKSOYHNTAIDMOTGACGDAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKV 480
Db 421 DIHTKSOYHNTAIDMOTGACGDAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKV 480
Oy 481 QLRHAASVWVLGHTFAAALPPIFGISSYKVSICLPMDIDSPLSQLYMALLVNLVLA 540
Db 481 QLRHAASVWVLGHTFAAALPPIFGISSYKVSICLPMDIDSPLSQLYMALLVNLVLA 540
Oy 541 FVVICGCTHYIYLVNPTIVSSSDTKIAKRMATLIPTDFLCMAPISFFAISASLKVPL 600
Db 541 FVVICGCTHYIYLVNPTIVSSSDTKIAKRMATLIPTDFLCMAPISFFAISASLKVPL 600
Oy 601 ITVSKAKILLVLYPINSKANPELYAIFTKNFRDRFFILLSKFCGYENQAIYRTETSSA 660
Db 601 ITVSKAKILLVLYPINSKANPELYAIFTKNFRDRFFILLSKFCGYENQAIYRTETSSA 660
Oy 661 TINFHARKSHCSSAPRVNTSVLVPLNHSQN 692
Db 661 TINFHARKSHCSSAPRVNTSVLVPLNHSQN 692

RESULT 4
AAR30525
ID AAR30525 standard; protein; 695 AA.
AC AAR30525;
XX
XX 10-MAY-1993 (first entry)
XX
XX N-terminal of LH receptor/FSH receptor chimera #34.
XX
XX Follicle stimulating hormone receptor; luteinising hormone receptor;
XX human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimera; chimera.
XX
XX Chimaeric; homo sapiens.
XX
XX W09222667-A.
XX
XX 23-DEC-1992.
XX
XX 12-JUN-1992; 92MO-US04987.

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XX PR 14-JUN-1991; 91US-0715911.
XX PA (UYNE-) UNIV NEW JERSEY.
XX PI Bernard M, Moyle WR, Myers R;
XX DR WPI; 1993-018150/02.
XX XX
XX PT Glyco:protein hormone receptor analogues - having binding
XX PT affinity to human chorionic gonadotrophin, luteinising and
XX PT follicle stimulating hormones, useful in bio:immunoassays
XX PS
XX PS Examples; Fig 12; 103pp; English.
XX CC
XX CC This sequence represents the N-terminal of a novel protein having a
XX CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX CC hormone (LH), and follicle stimulating hormone (FSH). The protein
XX CC itself is a chimera having residues from both the FSH receptor,
XX CC and LH receptor. The receptor analogues can be used in bioimmunoassays
XX CC for the simultaneous detection of both LH (or hCG) and FSH as
XX CC well as their ratio of biological activities. The analogues can also
XX CC be used for raising, purifying and assaying antibodies to the
XX CC analogues. Coding sequence for the chimera was produced by two step
XX CC PCR.
XX SQ Sequence 695 AA;

Query Match 98.0%; Score 3523; DB 14; Length 695;
Best Local Similarity 98.4%; Pred. NO. 0;
Matches 681; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

OY 1 MALLVSLAFLGTCGCHHLCCHSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKRV 60
DB 1 MALLVSLAFLGTCGCHHLCCHSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKRV 60
OY 61 IPKGSFAGFGLDKIEISQNDVLEIADVFSNLPKLEIRIEKANNLLYNPEAFQNL 120
DB 61 IPKGSFAGFGLDKIEISQNDVLEIADVFSNLPKLEIRIEKANNLLYNPEAFQNL 120
OY 121 SLRYLLISNTGKHLPAVHKTSQKVLQSLQKVLQDQNNINIHIVARNFPMGLSFESVILWLSK 180
DB 121 SLRYLLISNTGKHLPAVHKTSQKVLQSLQKVLQDQNNINIHIVARNFPMGLSFESVILWLSK 180
OY 181 GIEETHNCAFGTOLDLNLSDNNLELNDVFGAGSPVILDSRTKVSLSNPHGLE 240
DB 181 GIEETHNCAFGTOLDLNLSDNNLELNDVFGAGSPVILDSRTKVSLSNPHGLE 240
OY 181 GFEEVQSHAFNGTQDELNLSNNLELNDVFGAGSPVILDSRTKVSLSNPHGLE 240
DB 181 GFEEVQSHAFNGTQDELNLSNNLELNDVFGAGSPVILDSRTKVSLSNPHGLE 240
OY 241 LKLLRARSTYRLKLPNLDKFTVLTMEASLTYPSCCAFANLKROISELHPICNKSILROD 300
DB 241 LKLLRARSTYRLKLPNLDKFTVLTMEASLTYPSCCAFANLKROISELHPICNKSILROD 300
OY 301 IDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPDAPNCPEDIMG 360
DB 301 IDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPDAPNCPEDIMG 360
OY 361 YNLRVLWFLTSLAITNTVVLVLTTSQVKLTVPRFLMCLNLAFAADLCIGYILLTASV 420
DB 361 YNLRVLWFLTSLAITNTVVLVLTTSQVKLTVPRFLMCLNLAFAADLCIGYILLTASV 420
OY 421 DIHTKSOYHNYAIDMQTGAGDAAGFTVFASLSVYTLTTLERWHTITHAMOLECKV 480
DB 421 DIHTKSOYHNYAIDMQTGAGDAAGFTVFASLSVYTLTTLERWHTITHAMOLECKV 480
OY 481 QLRHAASVWLGWTFAPAAALFPIFGISSYKVSICLPMIDSPLSQLYVALLVNLVLA 540
DB 481 QLRHAASVWLGWTFAPAAALFPIFGISSYKVSICLPMIDSPLSQLYVALLVNLVLA 540
OY 541 FWIGCGYTHYLTVRNPTIVSSSDTKIARMTLIETDFLCNAPISFFAISLSKVP 600
DB 541 FWIGCGYTHYLTVRNPTIVSSSDTKIARMTLIETDFLCNAPISFFAISLSKVP 600
OY 601 ITVSKAKILLVFLYINSCANPFLYAIPTKFRDFFILLSKFCGYEMQAQIYRTETSSA 660
DB 601 ITVSKAKILLVFLYINSCANPFLYAIPTKFRDFFILLSKFCGYEMQAQIYRTETSSA 660

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OY 180 NGIEZHNCAFWGTQDELNLSDNNLEELPNDFVQAGSGPVILDI SRTKVSHPNIGLE 239  
 DB 181 NGIEZHNCAFWGTQDELNLSDNNLEELPNDFVQAGSGPVILDI SRTKVSHPNIGLE 240  
 OY 240 NLKLRARSTTRALKLPNDKPVTLKESALTPSHCCAFANLKRQISELHPICNKSLRQ 299  
 DB 241 NLKLRARSTTRALKLPNDKPVTLKESALTPSHCCAFANLKRQISELHPICNKSLRQ 300  
 OY 300 DIDDMTQIGDORVSLIDDEPSYKSGSDMKNFYDLCNEVDVTCSPKDFAPNCEIDM 359  
 DB 301 DIDDMTQIGDORVSLIDDEPSYKSGSDMKNFYDLCNEVDVTCSPKDFAPNCEIDM 360  
 OY 360 GYNILRVLPWFISLTAITGNTTVLVLTTSQYKLTVPRLMCLNAPADLCIGIYLLIAS 419  
 DB 361 GYNILRVLPWFISLTAITGNTTVLVLTTSQYKLTVPRLMCLNAPADLCIGIYLLIAS 420  
 OY 420 VOIHTKSOYHNTAIDMOTGACDAAGFTVPFASLSVYTLTAITLERHHTITHAMOLECK 479  
 DB 421 VOIHTKSOYHNTAIDMOTGACDAAGFTVPFASLSVYTLTAITLERHHTITHAMOLECK 480  
 OY 480 VOLRHAASVWVGLWTFAPAAALPPIFGISSYKVSICLPMIDISPLSOLYVALLVNL 539  
 DB 481 VOLRHAASVWVGLWTFAPAAALPPIFGISSYKVSICLPMIDISPLSOLYVALLVNL 540  
 OY 540 AFVVICGCTTHILTVRNPTIVSSSDTKIAKRNATLIFTDFLCHAPISFPFALSASLKV 599  
 DB 541 AFVVICGCTTHILTVRNPTIVSSSDTKIAKRNATLIFTDFLCHAPISFPFALSASLKV 600  
 OY 600 LITVSKAKILLVLYPINSKANPFLYAIPTKNFRDRDFILLSKFGCYEMOQIYRTETSS 659  
 DB 601 LITVSKAKILLVLYPINSKANPFLYAIPTKNFRDRDFILLSKFGCYEMOQIYRTETSS 660  
 OY 660 ATHNPHARKSHCSSAPRVNTNSYVLPJNHSSON 692  
 DB 661 ATHNPHARKSHCSSAPRVNTNSYVLPJNHSSON 693

## RESULT 6

AAR30519  
 ID AAR30519 standard; protein: 696 AA.

AC AAR30519;  
 DT 10-MAY-1993 (first entry)

DE N-terminal of LH receptor/FSH receptor chimera #28.  
 KW Follicle stimulating hormone receptor; luteinizing hormone receptor;  
 KW human chorionic gonadotrophin; glycoprotein hormone receptor;  
 KW chimera; chimera.

OS Chimeraic; homo sapiens.  
 XX MO9222667-A.

XX 23-DEC-1992.  
 XX 12-JUN-1992: 92MO-US04987.

XX 14-JUN-1991: 91US-0715911.  
 XX (UTNE-) UNIV NEW JERSEY/

XX Bernard M. Moyle WR, Myers R;  
 XX WPI; 1993-018150/02.

XX Glyco:protein human receptor analogues - having binding  
 PT affinity to human chorionic gonadotrophin, luteinizing and  
 PT follicle stimulating hormones, useful in bio:immunoassays

PS Examples: Fig 12; 103pp; English.

CC This sequence represents the N-terminal of a novel protein having a  
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinizing  
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein  
 CC itself is a chimera having residues from both the FSH receptor,  
 CC and LH receptor. The receptor analogues can be used in bioimmunoassays  
 CC for the simultaneous detection of both LH (or hCG) and FSH as  
 CC well as of biological activities. The analogues can also  
 CC be used for raising and purifying antibodies against the  
 CC analogues. Coding sequence for the chimera was produced by two step  
 CC PCR.

XX Sequence 696 AA;

SQ Query Match 93.1%; Score 3346.5; DB 14; Length 696;  
 Best Local Similarity 93.8%; Pred. No. 7.5e-316;  
 Matches 650; Conservative 13; Mismatches 29; Indels 1; Gaps 1;

OY 1 MALLVLSLLAPLQTSCHHMLCHSNNRVFLCQDSKVTEIPTOLPRNAIELRFLVTLKRV 60  
 DB 1 MALLVLSLLAPLQTSCHHMLCHSNNRVFLCQDSKVTEIPTOLPRNAIELRFLVTLKRV 60  
 OY 61 KPSFAGFGDLEKIEISONDVLEVPANVFNLSPLKHEIRIEKANLLYIMPFAONLP 120  
 DB 61 KPSFAGFGDLEKIEISONDVLEVPANVFNLSPLKHEIRIEKANLLYIMPFAONLP 120  
 OY 121 SURYLLISNTGIKHLPVAVHKIQSLQ-KVLLDIQDNINITHIVARNSPGLCSFESVILWLSK 179  
 DB 121 RUKYLSICHTGIRTPDVTKISSSFNFLEICDNLHRTTIPGNAFOCMNNEVTLKLYG 180  
 OY 180 NGIEZHNCAFWGTQDELNLSDNNLEELPNDFVQAGSGPVILDI SRTKVSHPNIGLE 239  
 DB 181 NGIEZHNCAFWGTQDELNLSDNNLEELPNDFVQAGSGPVILDI SRTKVSHPNIGLE 240  
 OY 240 NLKLRARSTTRALKLPNDKPVTLKESALTPSHCCAFANLKRQISELHPICNKSLRQ 299  
 DB 241 NLKLRARSTTRALKLPNDKPVTLKESALTPSHCCAFANLKRQISELHPICNKSLRQ 300  
 OY 300 DIDDMTQIGDORVSLIDDEPSYKSGSDMKNFYDLCNEVDVTCSPKDFAPNCEIDM 359  
 DB 301 DIDDMTQIGDORVSLIDDEPSYKSGSDMKNFYDLCNEVDVTCSPKDFAPNCEIDM 360  
 OY 360 GYNILRVLPWFISLTAITGNTTVLVLTTSQYKLTVPRLMCLNAPADLCIGIYLLIAS 419  
 DB 361 GYNILRVLPWFISLTAITGNTTVLVLTTSQYKLTVPRLMCLNAPADLCIGIYLLIAS 420  
 OY 420 VOIHTKSOYHNTAIDMOTGACDAAGFTVPFASLSVYTLTAITLERHHTITHAMOLECK 479  
 DB 421 VOIHTKSOYHNTAIDMOTGACDAAGFTVPFASLSVYTLTAITLERHHTITHAMOLECK 480  
 OY 480 VOLRHAASVWVGLWTFAPAAALPPIFGISSYKVSICLPMIDISPLSOLYVALLVNL 539  
 DB 481 VOLRHAASVWVGLWTFAPAAALPPIFGISSYKVSICLPMIDISPLSOLYVALLVNL 540  
 OY 540 AFVVICGCTTHILTVRNPTIVSSSDTKIAKRNATLIFTDFLCHAPISFPFALSASLKV 599  
 DB 541 AFVVICGCTTHILTVRNPTIVSSSDTKIAKRNATLIFTDFLCHAPISFPFALSASLKV 600  
 OY 600 LITVSKAKILLVLYPINSKANPFLYAIPTKNFRDRDFILLSKFGCYEMOQIYRTETSS 659  
 DB 601 LITVSKAKILLVLYPINSKANPFLYAIPTKNFRDRDFILLSKFGCYEMOQIYRTETSS 660  
 OY 660 ATHNPHARKSHCSSAPRVNTNSYVLPJNHSSON 692  
 DB 661 ATHNPHARKSHCSSAPRVNTNSYVLPJNHSSON 693

## RESULT 7

AAR30526  
 ID AAR30526 standard; protein: 696 AA.

AC AAR30526;  
 XX 10-MAY-1993 (first entry)

XX N-terminal of LH receptor/FSH receptor chimera #35.  
 XX Follicle stimulating hormone receptor; luteinising hormone receptor;  
 KW human chorionic gonadotrophin; glycoprotein hormone receptor;  
 KW chimera; chimera.  
 XX Chimeraic; homo sapiens.  
 XX W09222667-A.  
 XX 23-DEC-1992.  
 XX 12-JUN-1992; 92WO-US04987.  
 XX 14-JUN-1991; 91US-0715911.  
 XX (UYNE-) UNIV NEW JERSEY.  
 XX Bernard M, Moyle WR, Myers R;  
 XX WPI; 1993-018150/02.  
 XX Glyco:protein hormone receptor analogues - having binding  
 PT affinity to human chorionic gonadotrophin, luteinising and  
 PT follicle stimulating hormones, useful in bio:immunoassays  
 XX Examples; Fig 12; 103pp; English.  
 XX This sequence represents the N-terminal of a novel protein having a  
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinising  
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein  
 CC itself is a chimera having residues from both the FSH receptor,  
 CC and LH receptor. The receptor analogues can be used in bio:immunoassays  
 CC for the simultaneous detection of both LH (or hCG) and FSH as  
 CC well as their ratio of biological activities. The analogues can also  
 CC be used for raising, purifying and assaying antibodies to the  
 CC analogues. Coding sequence for the chimera was produced by two step  
 CC PCR.  
 XX Sequence 696 AA;

Query Match 91.1%; Score 3272.5; DB 14; Length 696;  
 Best Local Similarity 91.8%; Pred. No. 1.2e-308;  
 Matches 636; Conservative 17; Mismatches 39; Indels 1; Gaps 1;

Qy 1 MALLVSLAFLGTGSGCHWLCNSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKRV 60  
 Db 1 MALLVSLAFLGTGSGCHWLCNSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKRV 60  
 Qy 61 IPKGSFAGDLEKIEISQNDVLEIADVFNSLPKLHEIRIEKANNLLYINPEAFONLP 120  
 Db 61 IPKGSFAGDLEKIEISQSDLERIEANAFDNLNLSSELLIQNTKRLLYIEPGAFNLP 120  
 Qy 121 SLRYLLSNTGKIKLPAHVHTQSLQ-KVLDDIONINIHIVARNSEFMGLSFESVILWLSK 179  
 Db 121 RLKYLSCNTGIRLPDVTKISSEFNFLEICDNLHITIPGAFGMNNESTLYKLG 180  
 Qy 180 NGIEEINCAPNGTQDLDELNLSNNLEELPNDFVQASGSPVILDYISRTKVHSLPNHGLE 239  
 Db 181 NGFEVQSHAFNGTQDLDELNLSNNLEELPNDFVQASGSPVILDYISRTKVHSLPNHGLE 240  
 Qy 240 NLKRLARSTYRLAKLNLDKFTVIMEASLTYPHSCCAFANLKRQISELHPICKNSILRQ 299  
 Db 241 NLKRLARSTYRLAKLNLDKFTVIMEASLTYPHSCCAFANLKRQISELHPICKNSILRQ 300  
 Qy 300 DIDDMTQIGQVRSLIDDEPSYGGSDMYNEFDYDLNCEVVDVTCSPKDPDFNCPEDIM 359  
 Db 301 DIDDMTQIGQVRSLIDDEPSYGGSDMYNEFDYDLNCEVVDVTCSPKDPDFNCPEDIM 360  
 Qy 360 GYNILRVLIWIFISILATIGNTVTLVLTTSQYKLTVPFRLMCNLAFLADLCIGIYLLIAS 419  
 Db 361 GYNILRVLIWIFISILATIGNTVTLVLTTSQYKLTVPFRLMCNLAFLADLCIGIYLLIAS 420

Qy 420 VDIHTKSOYHNYAIDMOTGAGCDAAGFTTFVASELSVYTLTAITLERWHHTITHAMOLECK 479  
 Db 421 VDIHTKSOYHNYAIDMOTGAGCDAAGFTTFVASELSVYTLTAITLERWHHTITHAMOLECK 480  
 Qy 480 VOLRHAASVNVGLGWTFAFAAALPFIIGISSYMKVSIICPLMDIDSPLSOLYVMALLVNLV 539  
 Db 481 VOLRHAASVNVGLGWTFAFAAALPFIIGISSYMKVSIICPLMDIDSPLSOLYVMALLVNLV 540  
 Qy 540 AFVVICGCTHYIYLTVRNPTIVSSSDTKIAKRMATLIIFTDFLCMAPISFAISASLKV 599  
 Db 541 AFVVICGCTHYIYLTVRNPTIVSSSDTKIAKRMATLIIFTDFLCMAPISFAISASLKV 600  
 Qy 600 LITVSKAKILLVLFYPINSCANPFLYAIFTKNRRDFILLSKFGCYEMOAIYRTETSS 659  
 Db 601 LITVSKAKILLVLFYPINSCANPFLYAIFTKNRRDFILLSKFGCYEMOAIYRTETSS 660  
 Qy 660 ATHNFHARKSHCSSAPRVNTNSYVLVPLNHSSQN 692  
 Db 661 ATHNFHARKSHCSSAPRVNTNSYVLVPLNHSSQN 693

## RESULT 8

AA42082  
 ID AA42082 standard; Protein; 695 AA.

AC AA42082;

DT 05-MAY-1994 (first entry)

DE FSH receptor.

KW FSH; receptor; follicle stimulating hormone; GST;  
 KW glutathione-S-transferase; primer; PCR; amplification;  
 KW polymerase chain reaction; probe; antibody; overstimulation.

OS Homo sapiens.

PN W09320199-A.

PD 14-OCT-1993.

PF 29-MAR-1993; 93WO-EP00780.

PR 30-MAR-1992; 92EP-0200886.

XX (ALKU ) AKZO NV.

XX De Leeuw R, Dijkema R;

DR WPI; 1993-336907/42.

DR N-PSDB; AAQ50013.

PT New follicle stimulating hormone receptor - and derived  
 PT antibodies, anti-idiotypic antibodies, and transfected cells,  
 PT useful e.g. in diagnosis and as antidote for FSH overstimulation

PS Claim 7; Page 20-23; 42pp; English.

CC The primers given in AAQ50029-34 were used in the cloning of GST-FSH-  
 CC R1, GST-FSH-R2 and GST-FSH-R3 fusion protein constructs.  
 CC Screening of the human testis cDNA library with a hFSH-R specific  
 CC probe resulted in five recombinant phages positive in hybridisation.  
 CC Sequence analysis was performed of the 2222 bp fragment of pGEM3Zc1  
 CC (AAQ50013).

XX Sequence 695 AA;

Query Match 90.0%; Score 3235.5; DB 14; Length 695;  
 Best Local Similarity 89.5%; Pred. No. 4.6e-305;  
 Matches 622; Conservative 31; Mismatches 39; Indels 3; Gaps 2;

Qy 1 MALLVSLAFLGTGSGCHWLCNSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKRV 60

Db 1 MALLVSLAFSGGCHRRICHSNRVFLCQESKVTETPSDLPNNAIELRFLVTKLRV 60  
Oy 61 IPKGSFAGGQLEKIEISONDVLEIADVFSNPLKHEIRIEKANNLLYINPEAFONLP 120  
Db 61 IQKGFSGGQLEKIEISONDVLEIADVFSNPLKHEIRIEKANNLLYINPEAFONLP 120  
Oy 121 SRYLLISNTGIKHLPAYHVKIOSLOKVLDDIQDNIHIVARNSEFGLSFESVILWLSKN 180  
Db 121 NQYLLISNTGIKHLPAYHVKIOSLOKVLDDIQDNIHIVARNSEFGLSFESVILWLSKN 180  
Oy 181 GTEETHCAFNFTQDLELNSDNNLEELPNDVFGAGSPVILDISRTKVSHPNHLN 240  
Db 181 GTEETHCAFNFTQDLELNSDNNLEELPNDVFGAGSPVILDISRTKVSHPNHLN 240  
Oy 241 LKKLRARSTYRLKLPNDKPYTLMEASLTYPESHCCAFANLKRQISELHPICNKSILROD 300  
Db 241 LKKLRARSTYRLKLPNDKPYTLMEASLTYPESHCCAFANLKRQISELHPICNKSILROD 300  
Oy 301 IDDMTOIGDQVSLIDD-EPYSGKSDMYNEFDYDLCEVVDVTCSPKDAFNPCEIDM 359  
Db 301 IDDMTOIGDQVSLIDD-EPYSGKSDMYNEFDYDLCEVVDVTCSPKDAFNPCEIDM 359  
Oy 360 GYNILRVLWFIISLAIATGNTTVLVLTTSQTKLTPRFLMCLNAPADLCIGIYLLIAS 419  
Db 360 GYNILRVLWFIISLAIATGNTTVLVLTTSQTKLTPRFLMCLNAPADLCIGIYLLIAS 419  
Oy 420 VOIHTKSOYHNYAIDMOTGACDAGPFTVASELSVYTLTAITLERHHTITHAMQLECK 479  
Db 420 VOIHTKSOYHNYAIDMOTGACDAGPFTVASELSVYTLTAITLERHHTITHAMQLECK 479  
Oy 480 VOLRHAASVYVLGWTFAAALPPIFGISSYMKVSYCLPMDIDPSLSQLYVALLVNLV 539  
Db 480 VOLRHAASVYVLGWTFAAALPPIFGISSYMKVSYCLPMDIDPSLSQLYVALLVNLV 539  
Oy 540 AFVVICGCTHYLTVRNPTVSSSDTKAKRMATLIFTDFLCHAPISFFAISAKVP 599  
Db 540 AFVVICGCTHYLTVRNPTVSSSDTKAKRMATLIFTDFLCHAPISFFAISAKVP 599  
Oy 541 AFVVICGCTHYLTVRNPTVSSSDTKAKRMATLIFTDFLCHAPISFFAISAKVP 600  
Db 541 AFVVICGCTHYLTVRNPTVSSSDTKAKRMATLIFTDFLCHAPISFFAISAKVP 600  
Oy 600 LITVSKAKILLVLPINSCANPFLYALFTKRNFRDFFILLSKGCTEMOQAIYRTTSS 659  
Db 600 LITVSKAKILLVLPINSCANPFLYALFTKRNFRDFFILLSKGCTEMOQAIYRTTSS 659  
Oy 660 ATNHFARKSHCSSAPRVTN--SYVLVPLNHSSQN 692  
Db 660 ATNHFARKSHCSSAPRVTN--SYVLVPLNHSSQN 692  
Oy 661 TVNTHPRNGHCCSNAPRVINGSTYILVPLSHLAQN 695  
Db 661 TVNTHPRNGHCCSNAPRVINGSTYILVPLSHLAQN 695

RESULT 10  
AAR27558

PI Alttomaeki K, De La Chapelle A, Huhtaniemi I;  
DR WPI: 1997-202900/18.  
N-PSDB: AAT63181.  
XX Diagnosis of ovarian dysgenesis and carriers from DNA abnormalities  
XX by amplifying DNA including follicle stimulating hormone receptor  
XX allele(s). i.e. codon 189, cleaving fragments, and examination  
XX Disclosure: Page 18-21: 43pp; English.  
XX The human follicle stimulating hormone (FSH) receptor (AAM14782)  
XX is a G-protein coupled transmembrane receptor. A mutation in the  
XX fshr gene (see also AAT63181) is associated with ovarian dysgenesis,  
XX and methods for provided for the diagnosis of this disorder.  
XX Sequence 695 AA:  
SQ  
Query Match 90.0%; Score 3235.5; DB 18; Length 695;  
Best Local Similarity 89.5%; Pred. No. 4.6e-305;  
Matches 622; Conservative 31; Mismatches 39; Indels 3; Gaps 2;  
Oy 1 MALLVSLAFSGGCHRRICHSNRVFLCQESKVTETPSDLPNNAIELRFLVTKLRV 60  
Db 1 MALLVSLAFSGGCHRRICHSNRVFLCQESKVTETPSDLPNNAIELRFLVTKLRV 60  
Oy 61 IPKGSFAGGQLEKIEISONDVLEIADVFSNPLKHEIRIEKANNLLYINPEAFONLP 120  
Db 61 IQKGFSGGQLEKIEISONDVLEIADVFSNPLKHEIRIEKANNLLYINPEAFONLP 120  
Oy 121 SRYLLISNTGIKHLPAYHVKIOSLOKVLDDIQDNIHIVARNSEFGLSFESVILWLSKN 180  
Db 121 NQYLLISNTGIKHLPAYHVKIOSLOKVLDDIQDNIHIVARNSEFGLSFESVILWLSKN 180  
Oy 181 GTEETHCAFNFTQDLELNSDNNLEELPNDVFGAGSPVILDISRTKVSHPNHLN 240  
Db 181 GTEETHCAFNFTQDLELNSDNNLEELPNDVFGAGSPVILDISRTKVSHPNHLN 240  
Oy 241 LKKLRARSTYRLKLPNDKPYTLMEASLTYPESHCCAFANLKRQISELHPICNKSILROD 300  
Db 241 LKKLRARSTYRLKLPNDKPYTLMEASLTYPESHCCAFANLKRQISELHPICNKSILROD 300  
Oy 301 IDDMTOIGDQVSLIDD-EPYSGKSDMYNEFDYDLCEVVDVTCSPKDAFNPCEIDM 359  
Db 301 IDDMTOIGDQVSLIDD-EPYSGKSDMYNEFDYDLCEVVDVTCSPKDAFNPCEIDM 359  
Oy 360 GYNILRVLWFIISLAIATGNTTVLVLTTSQTKLTPRFLMCLNAPADLCIGIYLLIAS 419  
Db 360 GYNILRVLWFIISLAIATGNTTVLVLTTSQTKLTPRFLMCLNAPADLCIGIYLLIAS 419  
Oy 420 VOIHTKSOYHNYAIDMOTGACDAGPFTVASELSVYTLTAITLERHHTITHAMQLECK 479  
Db 420 VOIHTKSOYHNYAIDMOTGACDAGPFTVASELSVYTLTAITLERHHTITHAMQLECK 479  
Oy 480 VOLRHAASVYVLGWTFAAALPPIFGISSYMKVSYCLPMDIDPSLSQLYVALLVNLV 539  
Db 480 VOLRHAASVYVLGWTFAAALPPIFGISSYMKVSYCLPMDIDPSLSQLYVALLVNLV 539  
Oy 540 AFVVICGCTHYLTVRNPTVSSSDTKAKRMATLIFTDFLCHAPISFFAISAKVP 599  
Db 540 AFVVICGCTHYLTVRNPTVSSSDTKAKRMATLIFTDFLCHAPISFFAISAKVP 599  
Oy 541 AFVVICGCTHYLTVRNPTVSSSDTKAKRMATLIFTDFLCHAPISFFAISAKVP 600  
Db 541 AFVVICGCTHYLTVRNPTVSSSDTKAKRMATLIFTDFLCHAPISFFAISAKVP 600  
Oy 600 LITVSKAKILLVLPINSCANPFLYALFTKRNFRDFFILLSKGCTEMOQAIYRTTSS 659  
Db 600 LITVSKAKILLVLPINSCANPFLYALFTKRNFRDFFILLSKGCTEMOQAIYRTTSS 659  
Oy 660 ATNHFARKSHCSSAPRVTN--SYVLVPLNHSSQN 692  
Db 660 ATNHFARKSHCSSAPRVTN--SYVLVPLNHSSQN 692  
Oy 661 TVNTHPRNGHCCSNAPRVINGSTYILVPLSHLAQN 695  
Db 661 TVNTHPRNGHCCSNAPRVINGSTYILVPLSHLAQN 695

RESULT 9  
AAW14782  
ID AAW14782 standard; Protein; 695 AA.  
AC AAW14782;  
DE 20-JUN-1997 (first entry)  
XX FSH receptor.  
XX Follicle stimulating hormone receptor; FSH receptor;  
XX ovarian dysgenesis; hypogonadotropic hypogonadism; diagnosis.  
XX Homo sapiens.  
XX W09711194-A1.  
XX 27-MAR-1997.  
XX 20-SEP-1996; 96NO-FI00501.  
XX 20-SEP-1995; 95US-0531070.  
XX (UYHE-) UNIV HELSINKI LICENSING LTD Oy.  
XX





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XX 12-JUN-1992; 92WO-US04987.
XX
XX 14-JUN-1991; 91US-0715911.
XX
XX (UYNE-) UNIV NEW JERSEY.
XX
XX Bernard M. Moyle WR. Myers R;
XX
XX WPI; 1993-018150/02.
XX
XX Glyco:protein hormone receptor analogues - having binding
XX affinity to human chorionic gonadotrophin, luteinising and
XX follicle stimulating hormones, useful in bio:immunoassays
XX
XX Examples; Fig 12: 103pp: English.
XX
XX This sequence represents the N-terminal of a novel protein having a
XX binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX hormone (LH), and follicle stimulating hormone (FSH). The protein
XX itself is a chimera having residues from both the FSH receptor,
XX and LH receptor. The receptor analogues can be used in bio:immunoassays
XX for the simultaneous detection of both LH (or hCG) and FSH as
XX well as their ratio of biological activities. The analogues can also
XX be used for raising, purifying and assaying antibodies to the
XX analogues. Coding sequence for the chimera was produced by two step
XX PCR.
XX
XX Sequence 634 AA:
XX
XX Query Match 89.9%; Score 3229.5; DB 14; Length 634;
XX Best Local Similarity 91.0%; Pred. No. 1.5e-304;
XX Matches 630; Conservative 0; Mismatches 1; Indels 61; Gaps 1;
XX
XX 1 MALLVSLAFPLGTGSGCHHMLCHCNSRVFLCQDSKYTEIPTDLPNNAIELRVLTCLR 60
XX 1 MALLVSLAFPLGTGSGCHHMLCHCNSRVFLCQDSKYTEIPTDLPNNAIELRVLTCLR 60
XX
XX 61 IPKGSFAGFDLEKIEISQNDVLEADVFNLSNPKLHEIREKANLLYINPEAFONLP 120
XX 61 IPKGSFAGFDLEKIEISQNDVLEADVFNLSNPKLHEIREKANLLYINPEAFONLP 120
XX
XX 121 SLRYLLSNTGCKHLPVHKIOSLQKVLDDIQQNINIHIVARNFSGLSFESVILMSKN 180
XX 121 SLRYLLSNTGCKHLPVHKIOSLQKVLDDIQQNINIHIVARNFSGLSFESVILMSKN 180
XX
XX 181 GIEZHNKAPNGTOLDELNLSDNNLZELPNDFVQAGSGFVILDISRTKVHSLPHNGLEN 240
XX 181 GIEZHNKAPNGTOLDELNLSDNNLZELPNDFVQAGSGFVILDISRTKVHSLPHNGLEN 240
XX
XX 241 LKLRASSTYRLKLPNKLKPLVFLWELASLTYPSCCAPANLKRQISELHPYCHKSILROD 300
XX 241 LKLRASSTYRLKLPNKLKPLVFLWELASLTYPSCCAPANLKRQISELHPYCHKSILROD 300
XX
XX 301 IDDMTOIGDQVSLIDEPFSGKSDMMYNEFDVLCNEVDVTCSPKPAFNPCEIDMG 360
XX 301 IDDMTOIGDQVSLIDEPFSGKSDMMYNEFDVLCNEVDVTCSPKPAFNPCEIDMG 360
XX
XX 361 YNLRLVLPFISILATGMTVLVLTTSQKLTVPFLMCLNFAFADLCIGYLLLIASV 420
XX 361 YNLRLVLPFISILATGMTVLVLTTSQKLTVPFLMCLNFAFADLCIGYLLLIASV 420
XX
XX 421 DIHTSOTHTAINDGTGAGCDAAGFTFVASELSVYTLTATLERMHTITHAWOLECKV 480
XX 421 DIHTSOTHTAINDGTGAGCDAAGFTFVASELSVYTLTATLERMHTITHAWOLECKV 480
XX
XX 481 QLRHAASVYVLTGTPAALAPPICISYMKVSTCLPMDISPSQLYVALLVLYLTA 540
XX 481 QLRHAASVYVLTGTPAALAPPICISYMKVSTCLPMDISPSQLYVALLVLYLTA 540
XX
XX 541 FVVICCTTHYLVTRNPTIVSSSDTKIARMATLIFTDFLCHAPISFPAISAKVPL 600
XX 541 FVVICCTTHYLVTRNPTIVSSSDTKIARMATLIFTDFLCHAPISFPAISAKVPL 600
XX
XX 600 FVVICCTTHYLVTRNPTIVSSSDTKIARMATLIFTDFLCHAPISFPAISAKVPL 600
XX 600 FVVICCTTHYLVTRNPTIVSSSDTKIARMATLIFTDFLCHAPISFPAISAKVPL 600
```

```
OY 601 ITVSKAKILLVLPYPINSCAMPYLAIFTKNFRDRDFILLSKGCGYEQAIYRTETSSA 660
DB 540 ITVSKAKILLVLPYPINSCAMPYLAIFTKNFRDRDFILLSKGCGYEQAIYRTETSSA 599
OY 661 TINFHARKSKSSAPRYTNSVLYVPLHSSQN 692
DB 600 TINFHARKSKSSAPRYTNSVLYVPLHSSQN 631

RESULT 12
AAR30513
ID AAR30513 standard; protein: 696 AA.
XX
XX AAR30513;
XX
XX 10-MAY-1993 (first entry)
XX
XX N-terminal of LH receptor/FSH receptor chimera #22.
XX
XX Follicle stimulating hormone receptor; luteinising hormone receptor;
XX human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimera; chimera.
XX
XX Chimeraic; homo sapiens.
XX
XX WO9222667-A.
XX
XX 23-DEC-1992.
XX
XX 12-JUN-1992; 92WO-US04987.
XX
XX 14-JUN-1991; 91US-0715911.
XX
XX (UYNE-) UNIV NEW JERSEY.
XX
XX Bernard M. Moyle WR. Myers R;
XX
XX WPI; 1993-018150/02.
XX
XX Glyco:protein hormone receptor analogues - having binding
XX affinity to human chorionic gonadotrophin, luteinising and
XX follicle stimulating hormones, useful in bio:immunoassays
XX
XX Examples; Fig 12: 103pp: English.
XX
XX This sequence represents the N-terminal of a novel protein having a
XX binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX hormone (LH), and follicle stimulating hormone (FSH). The protein
XX itself is a chimera having residues from both the FSH receptor,
XX and LH receptor. The receptor analogues can be used in bio:immunoassays
XX for the simultaneous detection of both LH (or hCG) and FSH as
XX well as their ratio of biological activities. The analogues can also
XX be used for raising, purifying and assaying antibodies to the
XX analogues. Coding sequence for the chimera was produced by two step
XX PCR.
XX
XX Sequence 696 AA:
XX
XX Query Match 88.7%; Score 3187.5; DB 14; Length 696;
XX Best Local Similarity 89.6%; Pred. No. 2.1e-300;
XX Matches 621; Conservative 22; Mismatches 49; Indels 1; Gaps 1;
XX
XX 1 MALLVSLAFPLGTGSGCHHMLCHCNSRVFLCQDSKYTEIPTDLPNNAIELRVLTCLR 60
XX 1 MALLVSLAFPLGTGSGCHHMLCHCNSRVFLCQDSKYTEIPTDLPNNAIELRVLTCLR 60
XX
XX 61 IPKGSFAGFDLEKIEISQNDVLEADVFNLSNPKLHEIREKANLLYINPEAFONLP 120
XX 61 IPKGSFAGFDLEKIEISQNDVLEADVFNLSNPKLHEIREKANLLYINPEAFONLP 120
XX
XX 121 SLRYLLSNTGCKHLPVHKIOSLQKVLDDIQQNINIHIVARNFSGLSFESVILMSKN 179
XX 121 SLRYLLSNTGCKHLPVHKIOSLQKVLDDIQQNINIHIVARNFSGLSFESVILMSKN 179
```

Db 121 RLKYLSTCNCTGIRTPDVTWKISSEFNFILEICDNLHITTPGNAFOGMNNESTVTKLYG 180  
 Qy 180 NGIEEIHCAFNGTQDLDELNSDNNLEELPNDVFOGASGPVILDSRTKVSHPNHLG 239  
 Db 181 NGFEVQSHAFNGTTLISLEKENIYLEKHSAGFQATGPVILDSRTKVSHPNHLG 240  
 Qy 240 NLKRLARSTYRLKLLPNLDFVTLMEASITYPSCCAFANLKRQISELHPICNKSILRQ 299  
 Db 241 NLKRLARSTYRLKLLPNLDFVTLMEASITYPSCCAFANLKRQISELHPICNKSILRQ 300  
 Qy 300 DIDDMTOIGDORVSLIDDEPSYKSGSDMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIM 359  
 Db 301 DIDDMTOIGDORVSLIDDEPSYKSGSDMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIM 360  
 Qy 360 GYNILRLVLIWFISITLAIITGNTTVLVLTTSQYKLTVPREFLMCNLAFADLCIGIYLLIAS 419  
 Db 361 GYNILRLVLIWFISITLAIITGNTTVLVLTTSQYKLTVPREFLMCNLAFADLCIGIYLLIAS 420  
 Qy 420 VDIHTKSOYHNYAIDWOTGAGCDAAAGFTTFVASELSVYTLTALTLERWHTITHAMOLECK 479  
 Db 421 VDIHTKSOYHNYAIDWOTGAGCDAAAGFTTFVASELSVYTLTALTLERWHTITHAMOLECK 480  
 Qy 480 VOLRHAASVMVLGWTFAFAALPFIPIGSISSYKSVICLPMIDSPLSQLYMALLVLNLV 539  
 Db 481 VOLRHAASVMVLGWTFAFAALPFIPIGSISSYKSVICLPMIDSPLSQLYMALLVLNLV 540  
 Qy 540 AFVVICGCTHYIYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVP 599  
 Db 541 AFVVICGCTHYIYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVP 600  
 Qy 600 LITVSKAKILLVLPYIPINSCANPELYAIFTKNFRDRFFILLSKFCGYEMOQAIYRTETSS 659  
 Db 601 LITVSKAKILLVLPYIPINSCANPELYAIFTKNFRDRFFILLSKFCGYEMOQAIYRTETSS 660  
 Qy 660 ATHNFHARKSHCSSAPRVNTSYVLVPLNHSQN 692  
 Db 661 ATHNFHARKSHCSSAPRVNTSYVLVPLNHSQN 693

## RESULT 13

AAR30521

ID AAR30521 standard; protein: 696 AA;

XX AC

XX AAR30521;

XX 10-MAY-1993 (first entry)

XX DE N-terminal of LH receptor/FSH receptor chimaera #30.

XX KW Follicle stimulating hormone receptor; luteinising hormone receptor;

XX KW human chorionic gonadotrophin; glycoprotein hormone receptor;

XX KW chimaera; chimera.

XX OS Chimaeric; homo sapiens.

XX PN WO9222667-A.

XX XX 23-DEC-1992.

XX PF 12-JUN-1992; 92WO-US04987.

XX PR 14-JUN-1991; 91US-0715911.

XX XX (UYNE-) UNIV NEW JERSEY.

XX PA Bernard M, Moyle WR, Myers R;

XX PI WPI; 1993-018150/02.

XX XX

PT Glyco:protein hormone receptor analogues - having binding

PT affinity to human chorionic gonadotrophin, luteinising and

PT follicle stimulating hormones, useful in bio:immunoassays

XX

PS Examples; Fig 12; 103pp; English..

XX This sequence represents the N-terminal of a novel protein having a  
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinising  
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein  
 CC itself is a chimaera having residues from both the FSH receptor,  
 CC and LH receptor. The receptor analogues can be used in bio:immunoassays  
 CC for the simultaneous detection of both LH (or hCG) and FSH as  
 CC well as their ratio of biological activities. The analogues can also  
 CC be used for raising, purifying and assaying antibodies to the  
 CC analogues. Coding sequence for the chimaera was produced by two step  
 CC PCR.

XX Sequence 696 AA;

Query Match 88.7%; Score 3187.5; DB 14; Length 696;

Best Local Similarity 89.6%; Pred. No. 2.1e-300;

Matches 621; Conservative 22; Mismatches 49; Indels 1; Gaps 1;

Qy 1 MALLLVSLAFLGTCGCHHWLCHCSNRVFLCQDSKVTETPTDLPRNAIELRFLVTKLV 60

Db 1 MALLLVSLAFLGTCGCHHWLCHCSNRVFLCQDSKVTETPTDLPRNAIELRFLVTKLV 60

Qy 61 IPKGSFAGFGDLEKIEISQSDSLERIEANAFDNLNLSSELLIQNTKLLYIEPCAFNLP 120

Db 61 IPKGSFAGFGDLEKIEISQSDSLERIEANAFDNLNLSSELLIQNTKLLYIEPCAFNLP 120

Qy 121 SLRYLLSNTGKIKLPAVHKIQSLQ-KVLLDIDQINIHIVARNSFGLSPESVILWLSK 179

Db 121 RLKYLSTCNCTGIRTPDVTWKISSEFNFILEICDNLHITTPGNAFOGMNNESTVTKLYG 180

Qy 180 NGIEEIHCAFNGTQDLDELNSDNNLEELPNDVFOGASGPVILDSRTKVSHPNHLG 239

Db 181 NGFEVQSHAFNGTTLISLEKENIYLEKHSAGFQATGPVILDSRTKVSHPNHLG 240

Qy 240 NLKRLARSTYRLKLLPNLDFVTLMEASITYPSCCAFANLKRQISELHPICNKSILRQ 299

Db 241 NLKRLARSTYRLKLLPNLDFVTLMEASITYPSCCAFANLKRQISELHPICNKSILRQ 300

Qy 300 DIDDMTOIGDORVSLIDDEPSYKSGSDMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIM 359

Db 301 DIDDMTOIGDORVSLIDDEPSYKSGSDMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIM 360

Qy 360 GYNILRLVLIWFISITLAIITGNTTVLVLTTSQYKLTVPREFLMCNLAFADLCIGIYLLIAS 419

Db 361 GYNILRLVLIWFISITLAIITGNTTVLVLTTSQYKLTVPREFLMCNLAFADLCIGIYLLIAS 420

Qy 420 VDIHTKSOYHNYAIDWOTGAGCDAAAGFTTFVASELSVYTLTALTLERWHTITHAMOLECK 479

Db 421 VDIHTKSOYHNYAIDWOTGAGCDAAAGFTTFVASELSVYTLTALTLERWHTITHAMOLECK 480

Qy 480 VOLRHAASVMVLGWTFAFAALPFIPIGSISSYKSVICLPMIDSPLSQLYMALLVLNLV 539

Db 481 VOLRHAASVMVLGWTFAFAALPFIPIGSISSYKSVICLPMIDSPLSQLYMALLVLNLV 540

Qy 540 AFVVICGCTHYIYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVP 599

Db 541 AFVVICGCTHYIYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVP 600

Qy 600 LITVSKAKILLVLPYIPINSCANPELYAIFTKNFRDRFFILLSKFCGYEMOQAIYRTETSS 659

Db 601 LITVSKAKILLVLPYIPINSCANPELYAIFTKNFRDRFFILLSKFCGYEMOQAIYRTETSS 660

Qy 660 ATHNFHARKSHCSSAPRVNTSYVLVPLNHSQN 692

Db 661 ATHNFHARKSHCSSAPRVNTSYVLVPLNHSQN 693

## RESULT 14

AAR30522

ID AAR30522 standard; protein: 620 AA.

XX AC

XX AAR30522;



```
Query Match      86.6%; Score 3112; DB 14; Length 689;
Best Local Similarity 87.3%; Pred. No. 4.6e-293;
Matches 607; Conservative 32; Mismatches 44; Indels 12; Gaps 3;

Qy 1 MALLVSLAFLGTGSGCHHLCNSNRVFLCODSKVTEIPTDLPRNAIELRVLTCLR 60
Db 1 MALLVSLAFLGTGSGCHHLCNSNRVFLCODSKVTEIPTDLPRNAIELRVLTCLR 60

Qy 61 IPKGSFAGDLEKIEISONDVLEIVADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120
Db 61 IPKGSFAGDLEKIEISONDVLEIVADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120

Qy 121 SLRYLLISNTGIRKHLPAVHKIQSLQKVLDDIQDNINIHIVARNSEFGLSFESVILWLSKN 180
Db 121 SLRYLLISNTGIRKHLPAVHKIQSLQKVLDDIQDNINIHIVARNSEFGLSFESVILWLSKN 180

Qy 181 GIEIHNCAPNGTQDELNLSNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLE 240
Db 181 GIEIHNCAPNGTQDELNLSNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLE 240

Qy 241 LKILRASTYRLAKLPNLDKFTVLMASLTYPHSCCAFANLKRQISELHPICHNKSILRQD 300
Db 241 IQTLIALUSSYSLTKPLPSKERFTSLLVATLTPSHCCAFRLPKK-----EQNFSESI 292

Qy 301 IDDMTQIGDQVRSLIDDEPSYG---KGSMDMYNEFDYDLCLNEVVVDVTCSPKPDAPNCPED 357
Db 293 FENFSKQCESTVRKADNETLYSAIFEENELSGWDYDYGFCSPKT-LOCAPEPDAPNCPED 351

Qy 358 IMGYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPRLMCNLAFAADLCIGIYLLI 417
Db 352 IMGYAFRLVLIWFISTLAITGNTTVLVLTTSQYKLTVPRLMCNLAFAADLCIGIYLLI 411

Qy 418 ASVDIHTKSOYHNVAIDMQTGACGDAAGFTVFASLSVYTLTAITLERWHTITHAMOLE 477
Db 412 ASVDIHTKSOYHNVAIDMQTGACGDAAGFTVFASLSVYTLTAITLERWHTITHAMOLE 471

Qy 478 CKVQLRHAASVMVLGWTFAFAALFPFIFGISSYMKVSIKLPMDIDSPLSQLYVWALLVLN 537
Db 472 CKVQLRHAASVMVLGWTFAFAALFPFIFGISSYMKVSIKLPMDIDSPLSQLYVWALLVLN 531

Qy 538 VLFVWICGCTHYIYLVNRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFFAISASLK 597
Db 532 VLFVWICGCTHYIYLVNRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFFAISASLK 591

Qy 598 VPLITVSKATILLVFPINSCANPFLYAIFTKFRERDFFILLSKFCGYEQAOIYRTET 657
Db 592 VPLITVSKATILLVFPINSCANPFLYAIFTKFRERDFFILLSKFCGYEQAOIYRTET 651

Qy 658 SSATHNPHARKSHCSSAPRVNTSNVYVPLNHSQN 692
Db 652 SSATHNPHARKSHCSSAPRVNTSNVYVPLNHSQN 686
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Search completed: June 16, 2003, 13:33:19  
Job time : 49.5845 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2003, 13:31:41 : Search time 21.7674 Seconds  
(without alignments)  
935.375 Million cell updates/sec

Title: US-09-877-804-6

Perfect score: 3594

Sequence: 1 MALLVSLAPLTGSGCHH.....SAPRTNSVLYPLNHSQN 692

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/laa/3A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/laa/3A.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/laa/3A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/laa/3A.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/laa/3A.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/laa/3A.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	3594	100.0	682	US-07-757-342D-6
2	3235.5	90.0	685	US-08-497-886-2
3	3235.5	90.0	685	US-08-492-885-2
4	3235.5	90.0	695	US-08-474-986-2
5	1817.5	50.6	764	US-07-741-453A-60
6	1807.5	50.3	696	US-07-757-342D-3
7	1797	50.0	700	US-07-757-342D-3
8	1776	49.4	674	US-07-757-342D-10
9	1674	46.6	699	US-07-757-342D-2
10	1673.5	46.6	764	US-07-741-453A-61
11	1670	46.5	782	US-07-741-453A-54
12	1659	46.2	764	US-07-741-453A-56
13	1658	46.1	764	US-07-741-453A-59
14	1634.5	46.0	785	US-07-757-342D-5
15	1628.5	44.8	390	US-08-460-576-2
16	1598	44.5	423	US-08-735-876-33
17	1598	44.5	423	US-08-735-876-2
18	1598	44.5	436	US-08-735-876-2
19	1567.5	43.6	611	US-07-757-342D-8
20	1567.5	43.6	636	US-07-757-342D-7
21	1542	42.9	764	US-07-741-453A-29
22	1474.5	41.0	337	US-08-118-270-55
23	1474.5	41.0	337	US-08-118-270-55
24	1474.5	41.0	337	US-08-118-270-55
25	1037.5	28.6	336	US-08-118-270-54
26	1037.5	28.6	336	US-08-118-270-54
27	983.5	27.4	332	US-08-118-270-53

Sequence 53, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 58, Appl  
Sequence 35, Appl  
Sequence 4, Appl  
Sequence 6, Appl  
Sequence 4, Appl  
Sequence 6, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 16, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-07-757-342D-6  
: Sequence 6, Application US/07757342D  
: Patent No. 6218509  
: GENERAL INFORMATION:  
: APPLICANT: IGARASHI, Masao  
: MINEGISHI, Takashi  
: NAKAMURA, Kazuto  
: TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
: NUMBER OF SEQUENCES: 10  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
: USMAN  
: STREET: 130 Water Street  
: CITY: Boston  
: STATE: Massachusetts  
: COUNTRY: US  
: ZIP: 02109  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07757,342D  
: FILING DATE: 10-Sep-1991  
: CLASSIFICATION: <Unknown>  
: ATTORNEY/AGENT INFORMATION:  
: NAME/REGISTRATION NUMBER: 51003  
: REFERENCE/DOCKET NUMBER: 41226  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (617)523-3400  
: TELEFAX: (617)523-6440  
: TELEX: 200291 STRE UR  
: INFORMATION FOR SEQ ID NO: 6:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 692 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-07-757-342D-6

Query Match 100.0%; Score 3594; DB 4; Length 692;  
Best Local Similarity 100.0%; Prod. No. 8e-284; 0;  
Matches 692; Conservative 0; Mismatches 0; Gaps 0;  
OY 1 MALLVSLAPLTGSGCHHLCNSRVFLCQDSKYTEIPTDLPRLNLEFLVTLKLV 60  
|||||

Db 1 MALLVSLAFLGTSGCHHLCNSNRVFLQDSKVTEIPTOLPRNAIELRVLTCLR 60  
Qy 61 IPKGSFAGDLEKIEISQNDVLEIADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120  
Db 61 IPKGSFAGDLEKIEISQNDVLEIADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120  
Qy 121 SLRYLLISNTGKIHLPVAVHQLQSLQKVLDDIQDNIHIVARNFMSFESVILWLSKN 180  
Db 121 SLRYLLISNTGKIHLPVAVHQLQSLQKVLDDIQDNIHIVARNFMSFESVILWLSKN 180  
Qy 181 GIEIHNCARNGTQDELNLSDDNNLEELPNVFGASGPVILDISRTKVHSLPNHGLEN 240  
Db 181 GIEIHNCARNGTQDELNLSDDNNLEELPNVFGASGPVILDISRTKVHSLPNHGLEN 240  
Qy 241 LKLRARSTYRLKLPNLDKFTVLTMEASLTYPSCCAFANLKROISELHPICNKSILROD 300  
Db 241 LKLRARSTYRLKLPNLDKFTVLTMEASLTYPSCCAFANLKROISELHPICNKSILROD 300  
Qy 301 IDDMTOIGDQVSLIDDEPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPAFNPCEIMG 360  
Db 301 IDDMTOIGDQVSLIDDEPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPAFNPCEIMG 360  
Qy 361 YNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPRLMCNLAFAADLCIGIYLLIASV 420  
Db 361 YNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPRLMCNLAFAADLCIGIYLLIASV 420  
Qy 421 DIHTKSOYHVAIDWQAGCDAAGFTVFASLSVYTLTAITLERWHTITHAMOLECKV 480  
Db 421 DIHTKSOYHVAIDWQAGCDAAGFTVFASLSVYTLTAITLERWHTITHAMOLECKV 480  
Qy 481 QLRHAASVMVLGTFVFAAALFFPIFGISSYKMSVICLPMDDSPLSQLYVALLVNLVA 540  
Db 481 QLRHAASVMVLGTFVFAAALFFPIFGISSYKMSVICLPMDDSPLSQLYVALLVNLVA 540  
Qy 541 FWICGCTHYLYVRNPVTVSSSDTKIAKRMATLIPTDFLCNAPISFFAISASLKVPL 600  
Db 541 FWICGCTHYLYVRNPVTVSSSDTKIAKRMATLIPTDFLCNAPISFFAISASLKVPL 600  
Qy 601 ITVSKAKILLVLPINSCANPFLYAITKFRDRDFILLSKFCYEMQAOIYRTETSSA 660  
Db 601 ITVSKAKILLVLPINSCANPFLYAITKFRDRDFILLSKFCYEMQAOIYRTETSSA 660  
Qy 661 THNPHARKSHCSSAPRVNTSYLVPLNHSQN 692  
Db 661 THNPHARKSHCSSAPRVNTSYLVPLNHSQN 692

## RESULT 2

US-08-487-886-2  
; Sequence 2, Application US/08487886  
; Patent No. 5744448  
; GENERAL INFORMATION:  
; APPLICANT: Kelton, Christie Ann  
; APPLICANT: Schweickhardt, Rene Lynn  
; APPLICANT: Cheng, Shirley Vui Yen  
; APPLICANT: Nugent, No. 5744448een Patrice  
; TITLE OF INVENTION: Human Follicle Stimulating  
; TITLE OF INVENTION: Hormone Receptor  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Stephan P. Williams,  
; STREET: Exchange Place, 37th floor  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density  
; COMPUTER: IBM PS/2, model 55 SX  
; OPERATING SYSTEM: MS-DOS version 4.0  
; SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,886  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA: 07/670,085  
; APPLICATION NUMBER: 15-MAR-1991  
; FILING DATE: 15-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams, Stephan P.  
; REGISTRATION NUMBER: 28546  
; REFERENCE/DOCKET NUMBER: US/252  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 723-1300  
; TELEFAX: (617) 723-8923  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 695  
; TYPE: Amino acid  
; TOPOLOGY: Linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: signal sequence  
; LOCATION: -17 to -1  
; IDENTIFICATION METHOD: hydrophobic  
; FEATURE:  
; NAME/KEY: putative amino-terminal extracellular domain  
; LOCATION: 1 to 349  
; IDENTIFICATION METHOD: similarity with other  
; IDENTIFICATION METHOD: dimeric glycoprotein receptor extracellular  
; IDENTIFICATION METHOD: domains, hydrophilic  
; FEATURE:  
; NAME/KEY: transmembrane domain  
; LOCATION: 350 to 613  
; IDENTIFICATION METHOD: similarity to other G  
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane domains  
; FEATURE:  
; NAME/KEY: putative transmembrane region I  
; LOCATION: 350 to 370  
; IDENTIFICATION METHOD: similarity to other G  
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
; FEATURE:  
; NAME/KEY: putative transmembrane region II  
; LOCATION: 382 to 404  
; IDENTIFICATION METHOD: similarity to other G  
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
; FEATURE:  
; NAME/KEY: putative transmembrane region III  
; LOCATION: 427 to 448  
; IDENTIFICATION METHOD: similarity to other G  
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
; FEATURE:  
; NAME/KEY: putative transmembrane region IV  
; LOCATION: 469 to 491  
; IDENTIFICATION METHOD: similarity to other G  
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
; FEATURE:  
; NAME/KEY: putative transmembrane region V  
; LOCATION: 512 to 533  
; IDENTIFICATION METHOD: similarity to other G  
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
; FEATURE:  
; NAME/KEY: putative transmembrane region VI  
; LOCATION: 557 to 580  
; IDENTIFICATION METHOD: similarity to other G  
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
; FEATURE:  
; NAME/KEY: putative transmembrane region VII  
; LOCATION: 592 to 613

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IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
FEATURE:
NAME/KEY: putative carboxy-terminal intracellular
NAME/KEY: domain
LOCATION: 614 to 678
US-08-487-886-2

Query Match          90.0%  Score 3235.5;  DB 1;  Length 695;
Best Local Similarity 89.5%  Pred. No. 1.1e-254;
Matches 622;  Conservative 31;  Mismatches 39;  Indels 3;  Gaps 2;

OY 1 MALLVSLFALATGSGCHRLCHSRVFLCDSKVTETPTDLPRAIELRFLVTLKRV 60
DB 1 MALLVSLFALFSLGSGCHRLCHSRVFLCDSKVTETPTDLPRAIELRFLVTLKRV 60
OY 61 IPKSGPAGDLEKLEISONDVLEVEDVSNLPHLEIRIEKANMLYINPEAFONP 120
DB 61 IQGNSGPDGKLEISONDVLEVEDVSNLPHLEIRIEKANMLYINPEAFONP 120
OY 121 SLRYLLSGTCKIKHLPVHKSQKVLQDQNNIHRIVARNSPMGLSPESVILWLN 180
DB 121 SLRYLLSGTCKIKHLPVHKSQKVLQDQNNIHRIVARNSPMGLSPESVILWLN 180
OY 121 NLOVLLISGTCIKHLPVHKSQKVLQDQNNIHRIVARNSPMGLSPESVILWLN 180
OY 181 GTEETHKCAFNGTQDDELNLSDNNHLEELPNDVFGASGVPVLDLSRTKVSLSLPHGLN 240
DB 181 GTEETHKCAFNGTQDDELNLSDNNHLEELPNDVFGASGVPVLDLSRTKVSLSLPHGLN 240
OY 241 LKKURARSTYRLKLPNDKFLVTLMEASLTYPSCCAFANLKRQISELHPICNKSILROD 300
DB 241 LKKURARSTYRLKLPNDKFLVTLMEASLTYPSCCAFANLKRQISELHPICNKSILROE 300
OY 301 IDDTQIGQORVSLIDD-EPSTGKSGDMYNEFYDLCNEVDVTCSPKDPAPNCPEDIM 359
DB 301 VDTWTGTCROSSLADNESSTGSPDHTTETFDLCLNEVDVTCSPKDPAPNCPEDIM 360
OY 360 GYNILRVLIWPLISTALITNTVTVLVLTISQYKLPVPLFNCNAPADLCIGVILLIAS 419
DB 361 GYNILRVLIWPLISTALITNTVTVLVLTISQYKLPVPLFNCNAPADLCIGVILLIAS 420
OY 420 VDIHTKSOYHNATIDMOTGAGCDAAAGFTVPASELSVYTLTATILRHHITHAMOLCK 479
DB 421 VDIHTKSOYHNATIDMOTGAGCDAAAGFTVPASELSVYTLTATILRHHITHAMOLCK 480
OY 480 VOLRDAASVYVLGTFAPAAALFPIGISTMYKSYICLDPIDSPLSQLYMALLVNLYL 539
DB 481 VOLRDAASVYVNGVTFAPAAALFPIGISTMYKSYICLDPIDSPLSQLYMALLVNLYL 540
OY 540 AFVVICGCTTHILTVRNPTVYSSSDTKIAKNATLIPTOFICHAPISTFPAISGLKVP 599
DB 541 AFVVICGCTTHILTVRNPTVYSSSDTKIAKNATLIPTOFICHAPISTFPAISGLKVP 600
OY 600 LITVSKAKILLVLPYINSCANPFLYALPTKRNFRDPTLLSKFGCYEMQAQIVRTETSS 659
DB 601 LITVSKAKILLVLPYINSCANPFLYALPTKRNFRDPTLLSKFGCYEMQAQIVRTETSS 660
OY 660 ATNHFHARKSHCCSAPRVTN--SYVLVPLHSSQN 692
DB 661 TVNTHPRNGHCCSAPRVTVNGSYVLVPLSHLQON 695
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## RESULT 3

```
US-08-482-855-2
Sequence 2, Application US/08482855
Patent No. 6121016
GENERAL INFORMATION:
APPLICANT: Kelton, Christie Ann
APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 6121016een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
```

```
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen P. Williams,
ADDRESSEE: Area-Serono, Inc.
CITY: Exchange Place, 37th floor
STATE: Boston
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Massill via Kermit to IBM MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482.855
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 07/670,085
APPLICATION NUMBER: 8-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephen P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/252
TELEPHONE: (617) 723-1300
TELEFAX: (617) 723-8923
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 695
TYPE: Amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: 1 to 23
IDENTIFICATION METHOD: hydrophobic
FEATURE:
NAME/KEY: putative amino-terminal extracellular domain
LOCATION: 1 to 349
IDENTIFICATION METHOD: similarity with other
IDENTIFICATION METHOD: dimeric glycoprotein receptor extracellular
IDENTIFICATION METHOD: domains, hydrophilic
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 350 to 613
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane domains
FEATURE:
NAME/KEY: putative transmembrane region I
LOCATION: 350 to 404
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
FEATURE:
NAME/KEY: putative transmembrane region II
LOCATION: 382 to 404
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
FEATURE:
NAME/KEY: putative transmembrane region III
LOCATION: 427 to 448
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
FEATURE:
NAME/KEY: putative transmembrane region IV
LOCATION: 469 to 491
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
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FEATURE:  
NAME/KEY: putative transmembrane region V  
LOCATION: 512 to 533  
IDENTIFICATION METHOD: similarity to other G  
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
FEATURE:  
NAME/KEY: putative transmembrane region VI  
LOCATION: 557 to 580  
IDENTIFICATION METHOD: similarity to other G  
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
FEATURE:  
NAME/KEY: putative transmembrane region VII  
LOCATION: 592 to 613  
IDENTIFICATION METHOD: similarity to other G  
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
FEATURE:  
NAME/KEY: putative carboxy-terminal intracellular  
NAME/KEY: domain  
LOCATION: 614 to 678  
US-08-482-855-2

Query Match 90.0%; Score 3235.5; DB 3; Length 695;  
Best Local Similarity 89.5%; Pred. No. 1.1e-254;  
Matches 622; Conservative 31; Mismatches 39; Indels 3; Gaps 2;  
Qy 1 MALLVSLAPLGTGSGCHHCHCSNRVFLCQSKVTEIPDLPRNAIELRFLVTLKRV 60  
Db 1 MALLVSLAPLGTGSGCHHCHCSNRVFLCQSKVTEIPDLPRNAIELRFLVTLKRV 60  
Qy 61 IPKGSFAGFGLKIEISQNDVLEIADVFNPLKHEIRKANNLLYINPEAFQNL 120  
Db 61 IQKAFSGFGLKIEISQNDVLEIADVFNPLKHEIRKANNLLYINPEAFQNL 120  
Qy 121 SLRYLLISNTGKILPAVKHKTQSLQKVLDDQDNIHIVARNSPFGLSFESVILWLSKN 180  
Db 121 NLQYLLISNTGKILPAVKHKTQSLQKVLDDQDNIHIVARNSPFGLSFESVILWLSKN 180  
Qy 181 GIEIHNCFAFNGTQDELNDLSDNNLELNDVFGAGSPVILDSRTKVKHSLPNHGLN 240  
Db 181 GIOEIHNCFAFNGTQDELNDLSDNNLELNDVFGAGSPVILDSRTKVKHSLPNHGLN 240  
Qy 241 LKLLRARSTYRLKLPNDKFTVLEASLTYPSCCAFANLKRQISELHPTCNKSLRQ 300  
Db 241 LKLLRARSTYRLKLPNDKFTVLEASLTYPSCCAFANLKRQISELHPTCNKSLRQ 300  
Qy 301 IDDMTQIGDQVSLDD--EPSYKGSMDMYNEFDYDLCNEVVDVTCSPKPAFNPCE 359  
Db 301 VDYMTQTRGQRSSLAEDNESSYRGFDYDLCNEVVDVTCSPKPAFNPCE 359  
Qy 360 GYNILRVLIWISILATGNTVLTYSQYKLTVPRLMCLNLAFAADLCIGVLLIAS 419  
Db 361 GYNILRVLIWISILATGNTVLTYSQYKLTVPRLMCLNLAFAADLCIGVLLIAS 419  
Qy 420 VDIHTKQYHNYADWGTGACDAGFTVFASELSVYTLTAILERWHHTTHAMOLECK 479  
Db 421 VDIHTKQYHNYADWGTGACDAGFTVFASELSVYTLTAILERWHHTTHAMOLECK 480  
Qy 480 VOLRHAASVMVLTFAFAALFFIFGISSYKMYKISCLPMDIDSPLSQLYMALLVNLV 539  
Db 481 VOLRHAASVMVLTFAFAALFFIFGISSYKMYKISCLPMDIDSPLSQLYMALLVNLV 540  
Qy 540 AFVVICGTYHILTVRNPTIVSSSDTKIAKRMTLIFTDFLCMAPISFPAISAKVP 599  
Db 541 AFVVICGTYHILTVRNPTIVSSSDTKIAKRMTLIFTDFLCMAPISFPAISAKVP 600  
Qy 600 LITVSKAKILLVLPINSCANPELYAIFTNFRDRDFILLKSGCYEMQAQIYRTSS 659  
Db 601 LITVSKAKILLVLPINSCANPELYAIFTNFRDRDFILLKSGCYEMQAQIYRTSS 660  
Qy 660 ATHNFHARKSHCSSAPRVN--SYVLVPLNHSQN 692

Db 661 TVNTHPRNGHCSSAPRVNNGSTYILVPLSLAON 695  
RESULT 4  
US-08-474-986-2  
GENERAL INFORMATION:  
APPLICANT: Kelton, Christie Ann  
Schweickhardt, Rene Lynn  
Cheng, Shirley Vui Yen  
Nugent, No. 637271leen Patrice  
TITLE OF INVENTION: Human Follicle Stimulating  
Hormone Receptor  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephan P. Williams,  
Ares-Serono, Inc.  
STREET: Exchange Place, 37th floor  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density  
COMPUTER: IBM PS/2, model 55 SX  
OPERATING SYSTEM: MS-DOS version 4.0  
SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,986  
FILING DATE: 07-Jun-1995  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/670,085  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Stephan P.  
REGISTRATION NUMBER: 28546  
REFERENCE/DOCKET NUMBER: US/252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 723-1300  
TELEFAX: (617) 723-8923  
LOCATION: 614 to 678  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-08-474-986-2

Query Match 90.0%; Score 3235.5; DB 4; Length 695;  
Best Local Similarity 89.5%; Pred. No. 1.1e-254;  
Matches 622; Conservative 31; Mismatches 39; Indels 3; Gaps 2;  
Qy 1 MALLVSLAPLGTGSGCHHCHCSNRVFLCQSKVTEIPDLPRNAIELRFLVTLKRV 60  
Db 1 MALLVSLAPLGTGSGCHHCHCSNRVFLCQSKVTEIPDLPRNAIELRFLVTLKRV 60  
Qy 61 IPKGSFAGFGLKIEISQNDVLEIADVFNPLKHEIRKANNLLYINPEAFQNL 120  
Db 61 IQKAFSGFGLKIEISQNDVLEIADVFNPLKHEIRKANNLLYINPEAFQNL 120  
Qy 121 SLRYLLISNTGKILPAVKHKTQSLQKVLDDQDNIHIVARNSPFGLSFESVILWLSKN 180  
Db 121 NLQYLLISNTGKILPAVKHKTQSLQKVLDDQDNIHIVARNSPFGLSFESVILWLSKN 180  
Qy 181 GIEIHNCFAFNGTQDELNDLSDNNLELNDVFGAGSPVILDSRTKVKHSLPNHGLN 240  
Db 181 GIOEIHNCFAFNGTQDELNDLSDNNLELNDVFGAGSPVILDSRTKVKHSLPNHGLN 240  
Qy 241 LKLLRARSTYRLKLPNDKFTVLEASLTYPSCCAFANLKRQISELHPTCNKSLRQ 300  
Db 241 LKLLRARSTYRLKLPNDKFTVLEASLTYPSCCAFANLKRQISELHPTCNKSLRQ 300  
Qy 301 IDDMTQIGDQVSLDD--EPSYKGSMDMYNEFDYDLCNEVVDVTCSPKPAFNPCE 359  
Db 301 VDYMTQTRGQRSSLAEDNESSYRGFDYDLCNEVVDVTCSPKPAFNPCE 360

QY	4	LLVSLLAFLGTCGGCHMLCHCSN---RVFLQCDQSKVTEIPTDLPNAIRFVLTKLR	59
DB			
QY	11	LLLAFLPSRLG-KGCGSPCECHOEDFRV-TCKD--IHRIFT-LPSTOTLAFIETOLK	65
DB			
QY	60	VPKGSPAGCQDLEKILISONDVLEVLADVFNPSLKLHEIRKANKLLIINPEAFOL	119
DB			
QY	66	TIPSAFSLNPLSVISIDATLQRLSESLNKLHETIRNRESUTSIDPDALEKL	125
DB			
QY	120	ESRLYLLISNTGIKHLPAVHKIQSLQAK-VLLDIOINIIHIVARNSPGLSFSFVILML	178
DB			
QY	126	PLKFLGIFNTGLGVDPDTKVYSDVDFEILEITDNPVMASIPANAFQGLCNETLTKLY	185
DB			
QY	179	KGLEIRHCAFNFGLODELNLSDNNLEELPNDVQCA-SGPVLDLSIRTKVHSLPHNG	237
DB			
QY	186	NGPFTSIOGHAFKGLDVAIVLKNKYLSHIDKDAFGVYSGPLLDVDSVTVTALP	245
DB			
QY	238	LENLKLKLRASVTRLLKLDKNDKFTVLMEASLTSPHCCAPANKLRQISELHPT-CN	296
DB			
QY	246	LEHLKELIARNTWLKGLPLSLPLHTRADLSYPSHCCAFNKKIRGILESILMCNESS	305
DB			
QY	297	LRO-----DIDDDTQIGDRVSLIDDEPSYKGKSDMWT-----	329
DB			
QY	306	IRSLRQKSVNTLPGPDTGVEYLGDSHAGYKDNQSDPOTDSHSHYFFEQDEITLG	365
DB			
QY	330	-----NFEVDYLCNEVNVCTSCPKDPANFCEDINGNTLRVLNVLWIFIS	372
DB			
QY	366	FQGLKLNQBEETLQAFDISHDYTVCGSNEEDMAYCTPKSIDNEEDINGTKFLAVYH	425
DB			
QY	373	ILATIGNTTVLVYLTTSQKLTVPRFLMCNLADFLCIGIYLLIASVDIHTKSOYHNYA	432
DB			
QY	426	LLAALGNVFLVILVLTSHRKLTVPRFLMCNLADFQCIYIYLLIASVDIHTKSOYHNYA	485
DB			
QY	433	IDMTQAGCQDAGPPTVFASLSYTLTAITLERNHTITRANQLECKVOLRAASVYVLG	492
DB			
QY	486	IDMTQAGCQDAGPPTVFASLSYTVITFLERHTITRANQLECKVOLRAHSAVGM	545
DB			
QY	493	WTFAPAAALPIPIGLISSYKVKVETCLPMDISPLSQLYKVALYLVNLPVYICGVTIHY	552
DB			
QY	546	WTFAPAAALPIPIGLISSYKVKVETCLPMDISPLSQLYVILLJLLNLVNLVYICSVYKLY	605
DB			
QY	553	LYTRNPTPTVSSSSDPTKAKRMATVITFDPLCHAPISFPAISLAKVPLTYSKAKTLVL	612
DB			
QY	606	LYTRNPTQPNQDKDQTKAKRMATVITFDPLCHAPISFPAISLAKVPLTYSKAKTLVL	665
DB			
QY	613	YYPINSCANPFLYATFKTRPROFFLTKLPGCYQMAQVYRTTSTATHPN-----HAR	667
DB			
QY	666	FPYFSCASAPRVNLYVPLNHSOON-----	725
DB			
QY	668	FPYFSCASAPRVNLYVPLNHSOON	692
DB			
QY	726	RDNRQSLNMODEYELLENLSLTPN	750
DB			

RESULT 6  
US-07-757-342D-4  
Sequence 4, Application US/07757342D  
Patent No. 6218509  
GENERAL INFORMATION:  
APPLICANT: IGARASHI, Masao  
MINEGISHI, Takashi  
NAKAMURA, Kazuto  
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
CUSHMAN  
STREET: 110 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:

Query Match	50.6%	Score 1817.5;	DB 4;	Length 764;
Best Local Similarity	51.7%	Pred. No. 2.1e-139;		
Matches 388; Conservative	94;	Mismatches 205;	Indels 61;	Gaps 11;

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/07/757,342D

APPLICATION NUMBER: US/07/757,342D

FILING DATE: 10-Sep-1991

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: BUCKLEY, Linda M.

REGISTRATION NUMBER: 31003

REFERENCE/DOCKET NUMBER: 41226

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)523-3400

TELEFAX: (617)523-6440

TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 696 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-07-757-342D-4

Query Match 50.3%; Score 1807.5; DB 4; Length 696;  
Best Local Similarity 55.1%; Pred. No. 1.2e-138;  
Matches 373; Conservative 103; Mismatches 154; Indels 47; Gaps 13;

QY 1 MALLV-----SLAFLGTGSGCHHWHCHSNRVFLQDSKVTEIPTDLPNAELRFV 54  
DB 12 LALLLPPLPOTLL-----GAPCE---PCS-----CRPDGALCPG--PRAGLS-RLS 55  
QY 55 LKFL--RVIPKSPAGFGLDEKIEISONDVLEIADVFNSLPKLEHRIEAKNLLYN 112  
DB 56 LYLTKVPSQAFGLNEVVKIEISQSDSEKIEANAFDNLNLSEILQIKNLYTE 115  
QY 113 PFAONLPSRLYLLSNTGKIKHLPVHKIQSLQ-KVLLDIQDNIHIVARNSEMGSLPE 171  
DB 116 PGFTNLPRLKYLSCNTGIRLPDVKIFSEFNFLEICDNLHTTVPANAFQGMNE 175  
QY 172 SVILMLSKNGIEIHNCAPNGTOLDNLSDNNLEELPNDFVQSGGVILDIRKVVH 231  
DB 176 SITLKGNGFEEIQSHAFNGTLLISLEKNAHLKKMHNDAFRGARGPSILDISTKLQ 235  
QY 232 SLPNHGLENLKRLARSTYRLAKLNLDFVTLMEASLYPSHCCAFANL--KQ----- 284  
DB 236 ALPSYGLESIQTLIATSSYSLKPLSREKFTNLLDNLATLTPSHCCAFANLPTKEQNFSS 295  
QY 285 -ISELHPICNKSILRODIDMTQIGDQVSLDDEPSYKSGSDMMYNEFDYDLCEVVDV 343  
DB 296 IFKNFSKQCESTARPNNETL-----YSAFAE-----SELSDWDYDGCSPKT-L 341  
QY 344 TCSKPKDAPNCPEDINGYNILRVLIWFISILAITGNTVVLVLTTSQYKLTVPRLMCLN 403  
DB 342 QCAPEPAENCPEDINGYDLRVLIWLINILAIMGNVTFLVLLTSHYKLTVPRLMCLN 401  
QY 404 AFADLCIGYLLLIASVDIHTSOVHNYAIDNQTGAGCDAAAGFTTFVASELSYTLTAT 463  
DB 402 SFADFCMGYLLLIASVDAQTGQYHNAIDNQTGNCVAGFTTFVASELSYTLTAT 461  
QY 464 LERWHTTHAMOLECKVQLRHAASVNLGWTAFAAALPFIIGISYKMSVCLPMDIDS 523  
DB 462 LERWHTTAYIQDLRLRHAIPIMLGWLSTLIAMLPVGVSYKMSVCLPMDVET 521  
QY 524 PLSQYVMALLVNLVAFVIGCGYTHYLTVRNPTIVSSSDTIKAKMATLIETDFLC 583  
DB 522 TISQYVILITILNVVAFIICACYIKIYFQVNPENMATNKDKTKAKMVAVLIFTDFC 581  
QY 584 MAPISFAISAKVPLIVSVKAKILLVLFYVNSCANPFLYAIPTKFRPDRFFILLSKF 643  
DB 582 MAPISFAISAKVPLIVTNSKILLVLFYVNSCANPFLYAIPTKFRPDRFFILLSKS 641

QY 644 GCYEMQAQIYRTETSSA 660  
DB 642 GCCKHQAEYLRKDFSA 658

## RESULT 7

US-07-757-342D-3

Sequence 3, Application US/07757342D

Patent No. 6218509

GENERAL INFORMATION:

APPLICANT: IGARASHI, Masao

MINEGISHI, Takashi

NAKAMURA, Kazuto

TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

CUSHMAN

STREET: 130 Water Street

CITY: Boston

STATE: Massachusetts

COUNTRY: US

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/757,342D

FILING DATE: 10-Sep-1991

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: BUCKLEY, Linda M.

REGISTRATION NUMBER: 31003

REFERENCE/DOCKET NUMBER: 41226

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)523-3400

TELEFAX: (617)523-6440

TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 700 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3;

US-07-757-342D-3

Query Match 50.0%; Score 1797; DB 4; Length 700;

Best Local Similarity 56.5%; Pred. No. 8.5e-138;

Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

QY 45 PRNAIELREVLRKL--RVIPKSFAGFGLDEKIEISONDVLEIADVFNSLPKLEHRI 102  
DB 51 PRAGL-ARLSLTVLPVKVPSQAFRGLENEVKIEISQSDSLERIEANAFDNLNLSLI 109  
QY 103 EKANNLLYNPFAQNLPSRLYLLISNTGKIKHLPVHKIQSLQ-KVLLDIQDNIHIVA 161  
DB 110 QNTKNLLYEPGAFTNLPRLKYLSCNTGIRLPDVKTKISSSEFNFLEICDNLHTTIP 169  
QY 162 RNSFMGLSPESVILMLSKNGIEIHNCAPNGTOLDNLSDNNLEELPNDFVQSGGPV 221  
DB 170 GNAFOGMNNESTVTKLYGNGFEEVSHAFNGTLLISLEKNIYLEKMHSGAFQAGTGS 229  
QY 222 ILDIRTKVHSLPNHGLENLKRLARSTYRLAKLNLDFVTLMEASLYPSHCCAFANL 281  
DB 230 ILDISSTKQALPSHGLESIQTLIALSSYSLTKLPSKERFTSLVATLTPSHCCAFANL 289  
QY 282 KQOISELHPICNKSILRQDIDMTQIGDQVSLDDEPSYG---KQSDMMYNEFDYDLN 338  
DB 290 PKK-----EQNFSSIFENFSKQCESTVRKADNETLYSAIFEENELSGMDYDGFCS 341

OY 339 EVVDYTCSPDAPNCDINGNYLRLVLIWFIISALITGNTVVLVLTTSYKLYVPRF 398  
DB 342 PNT-LOCAPDAPNCDINGNYLRLVLIWFIISALITGNTVVLVLTTSYKLYVPRF 400  
OY 399 LACNLAPADLCIGYILLIIVSDIHTKSOYHNYAIDWOTGAGDGAAGFFTVFASLSVYT 458  
DB 401 LACNLSPADFCNGLYLLIIVSDIHTKSOYHNYAIDWOTGAGDGAAGFFTVFASLSVYT 460  
OY 459 LTAITLERHRTITHAMOLECKVOLRHAASVYVLTGTFAPAAALPFIIGISSYMKVSYCLP 518  
DB 461 LVYITLERHRTITHAMOLECKVOLRHAASVYVLTGTFAPAAALPFIIGISSYMKVSYCLP 520  
OY 519 MOIDPSOLYVLLVLIWFIISALITGNTVVLVLTTSYKLYVPRF 578  
DB 521 MOIDPSOLYVLLVLIWFIISALITGNTVVLVLTTSYKLYVPRF 580  
OY 579 TQPCMAPISPAISASVYVLTGTFAPAAALPFIIGISSYMKVSYCLP 638  
DB 581 TQPCMAPISPAISASVYVLTGTFAPAAALPFIIGISSYMKVSYCLP 640  
OY 639 LLSAFGCEYMAQIYRTTSSATHNFHAKSHCS 673  
DB 641 LLSAFGCEYMAQIYRTTSSATHNFHAKSHCS 673

## RESULT 8

US-07-757-3420-10  
Sequence 10, Application US/077573420  
Patent No. 6218509  
GENERAL INFORMATION:  
APPLICANT: IGARASHI, Masao  
INVENTOR: IGARASHI, Masao  
NAKAMURA, Kazuo  
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
MEDIUM SIZE: 5.25 inch  
OPERATING SYSTEM: PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07757.3420  
FILING DATE: 10-Sep-1991  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: BUCKLEY, Linda M.  
REGISTRATION NUMBER: 31003  
REFERENCE/DOCKET NUMBER: 41226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-3400  
FAX: 00251 STRE. OR  
INFORMATION FOR SEQUENCE CHARACTERISTICS:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 674 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:

## US-07-757-3420-10

Query Match 49.4% Score 1776; DB 4; Length 674;  
Best Local Similarity 55.4%; Pred. No. 4.1e-136;  
Matches 349; Conservative 107; Mismatches 148; Indels 26; Gaps 6;

OY 55 LTKL-----RVIPKSGAGFGDLEKIEISQNVLEIVADVFNPNKLEIREKANN 107  
DB 26 LRLSLAYLPVYISQAGLNEVYKIEISQNVLEIVADVFNPNKLEIREKANN 85  
OY 108 LLYINPEAPNLSRLYLLISNTGIKHLPVAKTI-OSLQKVLDDIODNINHIIVARNSP 166  
DB 86 LRYTECAPINLPLGLKYLISICNTGIRKFPDVTKVPSSENFLEICDNLJHTTIPGNAFO 145  
OY 167 GLSPESVILWLSKNGIEIHNKCAFNGTQDDELNLSNNNNLEELPNDVFOGASGPVILDIS 226  
DB 146 GNNNESVYTKLYNGEVEVOSHAFNGTTLTSLKENVHLEKMHGAPGATGPKTLDIS 205  
OY 227 RPKVHSLPHGLNKLKLRARSTYKRLKLPNDKPFVTLMEASUTYPSHCCAFANLKRQIS 286  
DB 206 STKQALPSTGLESIORLATSYSYSLAKLPSTRETFYNLELATUTYPSHCCAFANL----- 260  
OY 287 ELHPCNKSLRDDDDMTQIDQDQVSLIDDEPSYCK---GSDMYNEFDYDLNEVDV 343  
DB 261 ---PYKDFNFSHSISENSEKQCESTVYKVSNTLYSSMLAESGMDTETGCLPKTP- 316  
OY 344 TCSKPKDAPNCDINGNYLRLVLIWFIISALITGNTVVLVLTTSYKLYVPRF 403  
DB 317 RCAPDAPNCDINGNYLRLVLIWFIISALITGNTVVLVLTTSYKLYVPRF 376  
OY 404 AFADLCIGYILLIIVSDIHTKSOYHNYAIDWOTGAGDGAAGFFTVFASLSVYT 463  
DB 377 SPADFCNGLYLLIIVSDIHTKSOYHNYAIDWOTGAGDGAAGFFTVFASLSVYT 436  
OY 464 LERHRTITHAMOLECKVOLRHAASVYVLTGTFAPAAALPFIIGISSYMKVSYCLP 523  
DB 437 LERHRTITHAMOLECKVOLRHAASVYVLTGTFAPAAALPFIIGISSYMKVSYCLP 496  
OY 524 PLSOLYVLLVLIWFIISALITGNTVVLVLTTSYKLYVPRF 583  
DB 497 TQPCMAPISPAISASVYVLTGTFAPAAALPFIIGISSYMKVSYCLP 556  
OY 584 MAPISPAISASVYVLTGTFAPAAALPFIIGISSYMKVSYCLP 643  
DB 557 MAPISPAISASVYVLTGTFAPAAALPFIIGISSYMKVSYCLP 616  
OY 644 GCEYMAQIYRTTSSATHNFHAKSHCS 673  
DB 617 GCKRRRAELRYRK-----DFSAYTSNCKN 640

## RESULT 9

US-07-757-3420-2  
Sequence 2, Application US/077573420  
Patent No. 6218509  
GENERAL INFORMATION:  
APPLICANT: IGARASHI, Masao  
INVENTOR: IGARASHI, Masao  
NAKAMURA, Kazuo  
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
MEDIUM SIZE: 5.25 inch  
OPERATING SYSTEM: PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07757.3420  
FILING DATE: 10-Sep-1991  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: BUCKLEY, Linda M.  
REGISTRATION NUMBER: 31003  
REFERENCE/DOCKET NUMBER: 41226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 699 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-07-757-342D-2

Query Match 49.4%; Score 1776; DB 4; Length 699;  
Best Local Similarity 55.4%; Pred. No. 4.3e-136;  
Matches 349; Conservative 107; Mismatches 148; Indels 26; Gaps 6;  
Qy 55 LTKL-----RVIPKGFAGFGDLEKIEISQNDVLEIADVFESNPKLHEIRKANN 107  
Db 51 LTRLSLAYLPVKVPSQAFRLNEVIEKIEISQDSLEIEANAFDNLNLSEILIQNTKN 110  
Qy 108 LLYINPEAFONPLSRYLLISNTGKIKHLPVHKI-QSLQKVLDDIODNINIHVARNSEFM 166  
Db 111 LRYIEPGAFINPLGLKYLSCITGIRKFPDVTKYFSSSENFLEICDNLHTTIPGNAFQ 170  
Qy 167 GLSFESVILWLSKNGIEIHNCAFNQGLDELNLSDNNLEELPNDVFGASGVILDIS 226  
Db 171 GNNESVTLKLYNGFEEVQSHAFNGTTLTSLEKENVHLEKMHNGAFRGATGPKTLDIS 230  
Qy 227 RTKVHSLPNHGLENLKLLARSTYRLKLPNLDKFTVLMESLTYPSSHCCAFANLKQIS 286  
Db 231 STKLQALPSYGLSIOQLIATSSLSLKLPSRETFVNLLEATLTPSHCCAFRL----- 285  
Qy 287 ELHPICNKSILRQDQMTQIGDQVRSIDIDEPSYGR---GSDMMYNEFFDLCNEVVDV 343  
Db 286 ---PTKEQNFHSHISENFSCQESTVRKVSNTLYSSMLAESLSGWDYEGFCLPKTP- 341  
Qy 344 TCSKPDPAFNCEIDINGNIRLVLIWISILAITGNTVTLVLTSTQYKLTVPRLMCNL 403  
Db 342 RCAPEPAFNCEIDINGYDFLRVLINILINILAINGNMTVFLVLTSTQYKLTVPRLMCNL 401  
Qy 404 AFADLCIGYLLIASVDIHTKSOYHNVAIDWQTGAGDAAGFTTFVASELSVYTLTAIT 463  
Db 402 SFADFCLYLLIASVDSQTKQYHNVAIDWQTGAGDAAGFTTFVASELSVYTLTAIT 461  
Qy 464 LERWHTTHAMOLECKVOLRHAASVWVLGWTFAFAAALPPIFGISSYMKVSCICLPMIDIS 523  
Db 462 LERWHTITYAHLQKLRHAILIMLGGWLFSSLIAMLPVGVSNYMKVSCICFPMDET 521  
Qy 524 PLSQLYMALVNLVNLVAVVVICGCTHYTLVTRNPTVSSSDTKIAKRMATLITFDPLC 583  
Db 522 TLSQVYITILINVAFFIICACYIKIYFAVRPELMAKNDKIAKMAILITDFTC 581  
Qy 584 MAPISFFAISASLKVPLTISKAILLVLPINSCANPELYAIFTKFRDRDFILLSKF 643  
Db 582 MAPISFFAISAEKVPPLTIVNSKVLVLPINSCANPELYAIFTFTQDFDILLSKF 641  
Qy 644 GCYEQAOIYRTETSSATHNPHARKSHCS 673  
Db 642 GCCRRRAELRYRK-----DPSAVTSNCKN 665

RESULT 10  
US-07-741-453A-61  
Sequence 61, Application US/07741453A  
Patent No. 6228597  
GENERAL INFORMATION:  
APPLICANT: PARMENTIER, MARC  
APPLICANT: LIBERT, FREDERIC  
APPLICANT: DUMONT, JACQUES

APPLICANT: VASSART, GILBERT  
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1615 L STREET, N.W.  
CITY: WASHINGTON, D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0; Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07741.453A  
FILING DATE: 19911015  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16773  
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 764 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-741-453A-61

Query Match 46.6%; Score 1674; DB 4; Length 764;  
Best Local Similarity 49.4%; Pred. No. 9.5e-128;  
Matches 34; Conservative 112; Mismatches 186; Indels 56; Gaps 12;  
Qy 3 LLYVSLAFLGTGSGCHHMLCHCSN---RVFLQDSKVTEIPTDLPNALTELRFVLTKL 58  
Db 10 VLLDLPRDLG-GMGSSPPCEHQEDFRV-TCKD--IQRIPS-LPSTOTLKLIELHL 64  
Qy 59 RVIPKGFAGDLEKIEISQNDVLEIADVFESNPKLHEIRKANNLIYINPEAFON 118  
Db 65 RTPSHAFSNLPNISRIYVSDLTLOQLESHSFYNLSKVTHIEIRNTRNLTYIDPDALKE 124  
Qy 119 LPSRLYLLISNTGKIKHLPVHKIOSLO-KVLLDIDODNINIHVARNSEFMGLSFESVILWL 177  
Db 125 LPLKLFICFTNGKAMPDLTKVSTDIFFILEITDNPYMTSIPVNAFOGCLNETFLTUKL 184  
Qy 178 SKNGIEITHCAFNQTQDLDELNLSDNNLEELPNDVFOGA-SGPVILDISRTKVHSLPNH 236  
Db 185 YNNGFTSVQGVAFNGTKLDAYLNKNKYLTVIDDAFGVYSGPSLLDVSTVYALPSK 244  
Qy 237 GLENLKLARSTYRLKLPNLDKFTVLMESLTYPSSHCCAFANLKROISELHPI-CNKS 295  
Db 245 GLEHLKELIARNTWTLKPLSLSLFLHLTRADLSYPHSCCAFKKQKIRGILESMLCNES 304  
Qy 296 IL-----RODIDDMT-----QIGDQVSLID-----DEPSY 321  
Db 305 SMQSLRQKSVNALNSPLHQEYENLGDSIVGYKEKSFQDTHNNAHYVVFEEQDEII 364  
Qy 322 GKSDM-----MYNEFDYDLCEVVDVTCSPKPDPAFNCEIDINGNIRLVLIWFI 371  
Db 365 GFGQELKNPQEBETLQAFDSHYDYTCGSDSEDMVCTPKSDENPCEDINGYKFLRVVWF 424  
Qy 372 SILAITGNTTVLVLTSTQYKLTVPRLMCNLAFLADLCIGYLLIASVDIHTKSOYHN 431  
Db 425 SLLALIGNVFVLLILLTSHYKLVNVPRLMCNLAFLADFCMGMWYLLIASVDLYTHSEYHN 484

432 AIDQGTGACDAGFTTFASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVWVL 491  
Db 485 AIDQGTGACDAGFTTFASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVWVL 544  
Qy 492 GWTAFAPALPPIPGISYKVSICLPMDSPLSOLYVALLVNLVAFVYVCCGYTHI 551  
Db 545 GWVCCFLALLPLVGSISYKVSICLPMDSPLSOLYVALLVNLVAFVYVCCGYTHI 604  
Qy 552 YLTVRNPITVSSSDTKAKRMATLFTDFLCHAPISFAISAKVPLITYSKAKILLV 611  
Db 605 YLTVRNPITVSSSDTKAKRMATLFTDFLCHAPISFAISAKVPLITYSKAKILLV 664  
Qy 612 LPTVNSCANPFLITAFTRNFRDRDFILLSKFCGYCMAOYIR 654  
Db 665 LPTVNSCANPFLITAFTRNFRDRDFILLSKFCGYCMAOYIR 707

RESULT 11  
US-07-741-453A-54  
Sequence 54, Application US/07741453A  
Patent No. 6228597  
GENERAL INFORMATION:  
APPLICANT: PARMENTIER, MARC  
APPLICANT: LIBERT, FREDERIC  
APPLICANT: DUMONT, JACQUES  
APPLICANT: VASSART, GILBERT  
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
CITY: WASHINGTON, D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/07741453A  
FILING DATE: 19911015  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
REGISTRATION NUMBER: 916773  
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEO ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 764 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-741-453A-54

Query Match 46.64; Score 1673.5; DB 4; Length 764;  
Best Local Similarity 47.44; Procl. No. 16-127;  
Matches 35; Conservative 116; Mismatches 217; Indels 61; Gaps 11;

Qy 4 LVLALAFGLTGSCGHHNLCHSN----RVFLCDGSKVTEIPTDLPRLNATELRVUTKLR 59  
Db 11 LLLALPRLSG-GAGCSPCECHQEDDFV-TCRD--IIRIPT-LPPSTQTLKFIEQLK 65  
Qy 60 VIPAGSFGAGDKEIETLSONDVEADWPSLKPJHEIRIEKANNLLYNPEAPOML 119  
Db 66 TIPSRAFSLNPISRIYLSIDATLQRLSHSFPNLSKMTHEIRNTRSLSDPDALKEL 125

Qy 120 PSRLYLLISMTGKHLPAVKHTOSLOK-VLLDIOODNINIHAVRNSPMGLSFESVILMS 178  
Db 126 PLKFGIFNTGKLVGFDVTKYVSTVDFLEITDNPYMASIPANAPQGLNETLTKLY 185  
Qy 179 KNGIEELHNCAPNGTOLDDELANSNNLEELPDVDEQA-SGRVILDISRTKHSPLNIG 237  
Db 186 NNGFTSIQHAPNSTKLDAYLNNKYLNSAIDKARFGVYSGPTLLDVSYTSVTPALPSG 245  
Qy 238 LENLKKLARASTYRLKLLPNLKDQVTLMEASLTPSHCCAPANLAKROISELHPI-CNKS 296  
Db 246 LEHLKELIARTMTLKLPLSLSLHLTRADLSYPSHCAPKNOKKIRGILESIMCNES 305  
Qy 297 LRO-----DIDDMTOIGDORVSLDDDEPSYKGSDDMY----- 329  
Db 306 IRLRQRKSVNTLNGPFDQDEYELGDSHAGYKDNQFODTDSNHYTVFEEDEDEILG 365  
Qy 330 -----NEFDYDLGNEVDVTCSPKPDAPNFCEDINGYNILRVLIWFTIS 372  
Db 366 FGQELNQPQETLOAFUSHDYTVCGGNEDMWCPTKASDFNFCEDINGYKFLRVWVFS 425  
Qy 373 ILAIGTNTVVLVTSQKLYTRPLKCNLADGICIGYLLIASVDIHTKSOHYNA 432  
Db 426 LLALLGNFVLIVLTSYKLYTRPLKCNLADGICIGYLLIASVDIHTKSOHYNA 485  
Qy 433 IDMTGACGACDAGFTTFASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVWVL 492  
Db 486 IDMTGACGACDAGFTTFASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVWVL 545  
Qy 493 MTEFAAPALPPIPGISYKVSICLPMDSPLSOLYVALLVNLVAFVYVCCGYTHI 552  
Db 546 WCCFLALLPLVGSISYKVSICLPMDSPLSOLYVALLVNLVAFVYVCCGYTHI 605  
Qy 553 LTVRNPITVSSSDTKAKRMATLFTDFLCHAPISFAISAKVPLITYSKAKILLV 612  
Db 606 LTVRNPITVSSSDTKAKRMATLFTDFLCHAPISFAISAKVPLITYSKAKILLV 665  
Qy 613 FYPVNSCANPFLITAFTRNFRDRDFILLSKFCGYCMAOYIR 654  
Db 666 FYPVNSCANPFLITAFTRNFRDRDFILLSKFCGYCMAOYIR 707

668 KSHCSAPRVTNSYVLPVPLNHSN 692  
726 RDMRQSLPNMDEYELLENHSLTPN 750

RESULT 12  
US-07-741-453A-56  
Sequence 56, Application US/07741453A  
Patent No. 6228597  
GENERAL INFORMATION:  
APPLICANT: PARMENTIER, MARC  
APPLICANT: LIBERT, FREDERIC  
APPLICANT: DUMONT, JACQUES  
APPLICANT: VASSART, GILBERT  
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
CITY: WASHINGTON, D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/07741453A  
FILING DATE: 19911015  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
REGISTRATION NUMBER: 916773  
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEO ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 764 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-741-453A-56

```
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-741-453A-56

Query Match 46.5%; Score 1670; DB 4; Length 792;
Best Local Similarity 50.3%; Pred. No. 2.1e-127;
Matches 368; Conservative 100; Mismatches 166; Indels 98; Gaps 21;

Qy 45 PRNAIEELFVTLK--RVIPKGFAGDGLKIEISONDVLE-----VIEADVSNLPK 96
Db 59 PRAGLS-RLSLTYLPKIPVISOAFRLNVEVVKIEISQDSLEPTGHCCKTEANAFNLN 117
Qy 97 LHEIRIEKANNLLVINPEAFONLPSRLYLISNTGIKH-----LPAVHKIOSLO-KVLL 149
Db 118 LSELIQNTNLVIEGATNPRLKYLISCTGIRKPIGHGCLPQVTKIFSEFNIL 177
Qy 150 DIQDNIHIVARNFMSGLSFESVILWLSKNGIEIHNC-----AFNGTQDLNLSDN 203
Db 178 EICNLHITVPANAFQGMNESITLKYNGFEPIGHGCIQSHAFNGILLISLEKEN 237
Qy 204 NLEELPNVFOGASGVILDISTKVHS-----LPNHGLENLKKURARSTYRLKKLPN 257
Db 238 AHLKMHNDAPRGARGLISLISSTKLOAPIGHGCLPSYGLSITQTLIATSSYSLKPLS 297
Qy 258 LDKVETLMEASLTVPSCCAFANL-----KQ-----ISELHPICNKSILRODID 303
Db 298 REKTNLDAFLTPSHCCAFRNPPIPGHGTKEQNFSEIFKNFSKQCESTARPNNT 357
Qy 304 MTQIGDQSVLIDDEPSYKGSMDMYNEFDY-DLCNEVDVDTCSKPDPAFNPCEDIMGYN 362
Db 358 LYSALFAESELSDWDPIGHGCDY--YGPIGHGFCSPKT-LQCAPEDAFNPCEDIMGYD 414
Qy 363 ILRVLIWFISLATGNTVLV-----LTTQYKLTVPRLMCLNFAFADLCIGIYLL 416
Db 415 FLRVLIWLIINLAINGNVTVLFAPIGHGCLLTSHYKLTVPRLMCLNLSFADFCMLYLL 474
Qy 417 IASVDIHTKSOYHNAIDW-----OTCAGCDAAGFETVFASELSVYTLTATILRHWTI 470
Db 475 IASVDAOTKGYHNAIDWPIGHGCGTNGCGSVAGFTVFASELSVYTLTATILRHWTI 534
Qy 471 THAMQLECKVOLRHA-----ASYMVLGWTFAFAALFPFIFGISSYKMKVSCICLPMDIDSP 524
Db 535 TYAIQDQKRLRHAPIGHGCGIPIMLGWLFSTLIAMLPVGVSSYKMKVSCICLPMDVETT 594
Qy 525 LSQLYTMALLV-----LNVAFVVCGYTHIYLTVRNPVIVSSSDTKAKRMATLIIF 578
Db 595 LSQVYILTILPIGHGCLNVAFTIICACIYKIYFAVQNPMLMATNKDTKIAKKMAVLIF 654
Qy 579 TDFLCMA-----PISFPAISAKLVPLITVSKAKILLVLEVPYNSCANPELYAIFTKNF 632
Db 655 TDFTCMAPIGHGCGIPISFPAISAKLVPLITVSKAKILLVLEVPYNSCANPELYAIFTKAF 714
Qy 633 RRD-----FFILSKFCYEQMAQIYRTETSSATHNPHARKSHC-----SSAP-RVTN 679
Db 715 RRDPIGHGCGFFLLLSKSCCKHQALRYRKDFSA-----YCKNGFTGSKNFSRSTL 765
Qy 680 SYVLVPLNHSQ 691
Db 766 KLTTLPIGHGCG 777

RESULT 13
US-07-741-453A-59
Sequence 59, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/07/741,453A
APPLICATION NUMBER: 19911015
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-741-453A-59

Query Match 46.2%; Score 1659; DB 4; Length 764;
Best Local Similarity 48.9%; Pred. No. 1.6e-126;
Matches 344; Conservative 112; Mismatches 191; Indels 56; Gaps 12;

Qy 3 LLLVSLAFATGTGGCGHHWCHCSN-----RVFLQDSKVTEIPTDLPNATELRFVLTKL 58
Db 10 VLLDLPRDLG-GMGCSSPPECHEQEDFRV-TCKD--IQRIPS-LPESTQTLKLIETHL 64
Qy 59 RVIPKGFAGDGLKIEISONDVLEADVFNLPKLHIEIRKANNLLVINPEAFON 118
Db 65 RTIPSHAFSNLPNISRIVTSIDLTQQLESHSFNLKSVTHIEIRNTRNLYIDPAUKE 124
Qy 119 LPSLYLLISNTGKHLPAVHKIOSLO-KVLLDIQDNIHIVARNFMSGLSFESVILWL 177
Db 125 LPLKFLGIFNTGLKMFDPDLTKVYSTDIFFILEITDNPYMTSIPVNAFQGLCNETLTLLK 184
Qy 178 SKNGIEIHNCAFNQGLDELNLSNDNNLEELPNDFOGA-SGPVILDISRTKVVHSLPNH 236
Db 185 YNNGFTSVQGFAYFNGTKLDVYLNKNKYLTVIDKDAFGVYSGPSLDVQSOTSVTALPSK 244
Qy 237 GLENLKKLRARSTYRLKKLPNLDKFTVLMASLTPSHCCAFANLKRQISELHPI-CNKS 295
Db 245 GLEHLKELIARTNTLTKKLPUSLSFLHLTRADLSTYPSHCCAFKNOKKIRGILES LMCNES 304
Qy 296 IL-----RODIDDMT-----QIGDQVSLID-----DEPSY 321
```

Db 305 SMOSLRQKSVNALNSPLHOFYENKNSGIVGKESKFOOTHNNHHYVFFEEQDEII 364  
Oy 322 GKGSOW-----MYNEFDYDLCNEVDVTCSPKPAFNPCEIDIMGYILNRLVWFI 371  
Db 365 GFGOELKMPQOETLQAFDSHYDVTICGSEDWYCTPKSDEFNPCEIDIMGYILNRLVWFI 424  
Oy 372 SILAITGNTVLVLTTSOYKLTVPRLKCNLAFADLCIGIYLLIASYDIHTKSOYHNY 431  
Db 425 SLLALGHVFLVLLTSHYKLVNPRFLKCNLAFADFCMGNVLLIILIASYDLYTHSEYTHN 484  
Oy 432 AIDMOTGAGCDAAGFFTFVASELSVTLTILERHMTITHAMOLECKVQLRHAASVWL 491  
Db 485 AIDMOTGAGCDAAGFFTFVASELSVTLTILERHMTITHAMOLECKVQLRHAASVWL 544  
Oy 492 GWTFAPAAALPFIIGISSYMKVSCICLPMIDISPLSOLYVALLVNLVAFVYVCCGYTHI 551  
Db 545 GWCCFLLALLPLVIGISSYMKVSCICLPMIDISPLSOLYVALLVNLVAFVYVCCGYTHI 604  
Oy 552 YLVRNPTIVSSSOTKIARMAVLIPTDFLCMAPIFAISAIKYLPTVSKAKILLV 611  
Db 605 YLVRNPTIVSSSOTKIARMAVLIPTDFLCMAPIFAISAIKYLPTVSKAKILLV 664  
Oy 612 LFTYPLNSCANPFLYAITFTRPDRPFIILSKFCYEQMOAQIYR 654  
Db 665 LFTYPLNSCANPFLYAITFTRPDRPFIILSKFCYEQMOAQIYR 707

RESULT 14  
US-07-757-342D-5  
: Sequence 5, Application US/07737342D  
: Patent No. 6218509  
: GENERAL INFORMATION:  
: APPLICANT: IGARASHI, Masao  
: INVENTOR: IGARASHI, Masao  
: TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
: NUMBER OF SEQUENCES: 10  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
: CUSHMAN  
: STREET: 130 Water Street  
: CITY: Boston  
: STATE: Massachusetts  
: COUNTRY: US  
: ZIP: 02109  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: SOFTWARE: PILEUP, A-DOS/MS-DOS  
: CURRENT APPLICATION DATA:  
: PILING DATE: 10-Sep-1991  
: CLASSIFICATION: <Unknown>  
: ATTORNEY/AGENT INFORMATION:  
: NAME: BUCKLEY, Linda M.  
: REGISTRATION NUMBER: 31003  
: REFERENCE/DOCKET NUMBER: 41226  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (617)523-3400  
: TELEFAX: (617)523-6440  
: INFORMATION FOR SEQ ID NO: 5:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 764 amino acids  
: TYPE: linear  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-07-757-342D-5  
Query Match 46.1%; Score 1658; DB 4; Length 764;  
Best Local Similarity 48.9%; Pred. No. 1.9e-126;

Matches 344: Conservative 112; Mismatches 191; Indels 56; Gaps 12:  
Oy 3 LLLVSLAFILCTGCGCHUHLCHSN-----RVFLCDSKVTETPDLPRLNAIEARFVTKL 58  
Db 10 VLLDLPRLDLC-GACSSPCEQOEQFRV-TCAD--IQRIPS-LPPSTOTLLEIETHL 64  
Oy 59 RVTPKGSFAGCDLKELEISONDVLEADVFNPKLHEIRKANNLLYINPEAFON 118  
Db 65 RTIPSHAFSLNPNISRIYVSDVTLQOLESHPYNSKLVTHIEIRNRLTYIDPDALKE 124  
Oy 119 LPSRLYLLISNTGKHLPAVAKHQISQ-KVLLDIODINIHIVARNSPMGLSPESVILWL 177  
Db 125 LPLALGIFNTGLKMPOLTKVYSTDFIIFILEITDNPYMTSIPVNAPOGLCNETLTKL 184  
Oy 178 SKNGIEETHCAFNQTQLODELNSDNNLEELPNDFQGA-SGPVILDISRTKSHSLPNH 236  
Db 185 YNNGFTSVQGYAFNPETKLDAYLKNKRYLVITYKDAFGVYSGPSLLDSVTSYALPSK 244  
Oy 237 GLENKLRARSTYRLKLPNDKFTVTLKASUTYPSHCCAPANKKQISELHPI-CNKS 295  
Db 245 GLEHLELIARNTMTLAKLPLLSLFLHTRADUSTPSHCCNFKKQIRKIGLESACRES 304  
Oy 296 TL-----RODIDDMT-----QTGQDVSLID-----DEPSY 321  
Db 305 SMOSLRQKSVNALNSPLHOFYENKNSGIVGKESKFOOTHNNHHYVFFEEQDEII 364  
Oy 322 GKGSOW-----MYNEFDYDLCNEVDVTCSPKPAFNPCEIDIMGYILNRLVWFI 371  
Db 365 GFGOELKMPQOETLQAFDSHYDVTICGSEDWYCTPKSDEFNPCEIDIMGYILNRLVWFI 424  
Oy 372 SILAITGNTVLVLTTSOYKLTVPRLKCNLAFADLCIGIYLLIASYDIHTKSOYHNY 431  
Db 425 SLLALGHVFLVLLTSHYKLVNPRFLKCNLAFADFCMGNVLLIILIASYDLYTHSEYTHN 484  
Oy 432 AIDMOTGAGCDAAGFFTFVASELSVTLTILERHMTITHAMOLECKVQLRHAASVWL 491  
Db 485 AIDMOTGAGCDAAGFFTFVASELSVTLTILERHMTITHAMOLECKVQLRHAASVWL 544  
Oy 492 GWTFAPAAALPFIIGISSYMKVSCICLPMIDISPLSOLYVALLVNLVAFVYVCCGYTHI 551  
Db 545 GWCCFLLALLPLVIGISSYMKVSCICLPMIDISPLSOLYVALLVNLVAFVYVCCGYTHI 604  
Oy 552 YLVRNPTIVSSSOTKIARMAVLIPTDFLCMAPIFAISAIKYLPTVSKAKILLV 611  
Db 605 YLVRNPTIVSSSOTKIARMAVLIPTDFLCMAPIFAISAIKYLPTVSKAKILLV 664  
Oy 612 LFTYPLNSCANPFLYAITFTRPDRPFIILSKFCYEQMOAQIYR 654  
Db 665 LFTYPLNSCANPFLYAITFTRPDRPFIILSKFCYEQMOAQIYR 707  
RESULT 15  
US-07-741-453A-55  
: Sequence 55, Application US/07741453A  
: Patent No. 6228597  
: GENERAL INFORMATION:  
: APPLICANT: PARMENTIER, MARC  
: APPLICANT: LIBERT, FREDERIC  
: APPLICANT: DUMONT, JACQUES  
: APPLICANT: VASSART, GILBERT  
: TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
: TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
: NUMBER OF SEQUENCES: 62  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: CUSHMAN, ARBY & CUSHMAN  
: STREET: 1611 K STREET, N.W.  
: CITY: WASHINGTON, D.C.  
: COUNTRY: U.S.A.  
: ZIP: 20036  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: disk  
: COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/741.453A  
FILING DATE: 19911015  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16773  
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 795 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-741-453A-55

Query Match 46.08; Score 1652.5; DB 4; Length 795;

Best Local Similarity 50.7%; Pred. No. 5.6e-126;  
Matches 360; Conservative 96; Mismatches 159; Indels 95; Gaps 17;

Qy	45	PRNAIELRFLVTKL--RVIPKSPAGFGDLEKIEISQNDVLE-----VIEADVFSNLPK 96
Db	63	PRAGL-ARLSUTYLPVKVPSQAPRGVNEVVKIEISQSDSLERATHCGRIEAFDNLN 121
Qy	97	LHEIRIEKANMLLYINPEAFONLPSRLYLISNTGIK-----HLPVAVHKIQSLQ-KVLL 149
Db	122	LSELLQNTKLLYIEGAFNLRLKYLISCTGIRATHCGLPDVTKISSSEFNIL 181
Qy	150	DIQNIINIHVARNSFGLSPESVILMSKNGIEIHN-----AFNGTOLDENLSDN 203
Db	182	EICDNLHITTPGNAFOGMNNESTLKLYNGFERATHCGEVQSHAFNGTTLISLEKEN 241
Qy	204	NNLELPNDVFOGASGPVILDISTKVHS-----LPNHGLENLKLRLARSTYRLKKLPN 257
Db	242	IYLEKMHGAFQAGSGSILDISTKLOARATHCGLPESHGLESQTLLALSSYSKLTLP 301
Qy	258	LDFVTLMEASLYPSHCAPANKRQ-----ISELHPICNKSILRODIDD 303
Db	302	KEKTSLLVATLYPSHCAPRNLPRATHCGKKEQNFSEFENFSKQCESTVRKADNET 361
Qy	304	MTQIGDQSVLIDEPSYKGSDMYNEFDYDLQNEV-----VDVTCSPKPDAPNCEDEM 359
Db	362	L-----YSAIFEENELSGMDRATHCGYDYGRATHCGFSPKTLQCAPEPDAPNCEDEM 414
Qy	360	GYNILRLVIEISILAITGNTVLV-----LTSQYKLTVPRLMCLNLAFAADLCIGIY 413
Db	415	GYAFRLVLIWILINILATFGNLTFLVRATHCGLLTSRYKLTVPRLMCLNSFADFQCMGLY 474
Qy	414	LLLIASVDIHTKSYHNYAIDW-----QTGAGCDAAGFTVFASLSVYTLTATTLERW 467
Db	475	LLLIASVDSQTKGYYNHAIWRATHCGQOTGGCGAGFTVFASLSVYTLTATTLERW 534
Qy	468	HTITHAMOLECKVQLRHAAS-----VMVLGWTFAFAALPFIIGISSYMKVSIKLPMDI 521
Db	535	HTIYAVOLDQKLRLHARATHCGIPIMLGGWLFSTLIATMPLVGISNYMKVSIKLPMDV 594
Qy	522	DSPLSOLVYVALLV-----LNVLAFFVICCYTHIYLTVRNPTIVSSSDTKAKRMAT 575
Db	595	ESTLSQVYLSILIRATHCGNLNVAFVVICACIYIRIVFAVQNPETLAPNKTAKKMAI 654
Qy	576	LIFTDFLCMA-----PISFPAISLAKVPLITVSKAKILLVLFYPIVNSCANPFLYAIT 629
Db	655	LIFTDFTCMARATHCGPISFPAISAKVPLITVNSKILLVLFYPIVNSCANPFLYAIT 714
Qy	630	KNFRD-----FFILLSKFCYEMQAOIYRTETSSATHNFHARKSCSS 673

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Job time : 23.7674 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2003, 13:36:01 : Search time 170.089 Seconds  
(without alignments)  
434.981 Million cell updates/sec

Title: US-09-877-804-6  
Perfect score: 3594  
Sequence: 1 MALLVSLAFITGSGCHH.....SAPRTNSTYLVLPINHSQN 692

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:

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- 2: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3594	100.0	692	9	US-09-965-536A-11
2	3594	100.0	692	10	US-09-877-804-6
3	3594	99.1	688	9	US-09-965-536A-12
4	3516	97.8	675	10	US-09-877-804-7
5	3215.5	89.5	695	10	US-09-804-626-8
6	3076.5	85.6	687	9	US-09-965-536A-13
7	2605.5	72.5	693	9	US-09-965-536A-14
8	2107.5	58.6	458	10	US-09-862-767A-9
9	1932	51.0	348	10	US-09-877-804-8
10	1797	50.0	700	10	US-09-877-804-3
11	1797	50.0	700	10	US-09-877-804-4
12	1783	49.6	699	9	US-09-965-536A-15
13	1776	49.4	699	10	US-09-804-626-6
14	1653.5	46.0	764	9	US-10-045-6248-2
15	1505.5	41.9	516	10	US-09-862-767A-4
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17	1191	33.1	359	10	US-09-862-767A-7
18	810.5	22.6	861	10	US-09-804-5518-20
19	675	18.8	341	10	US-09-877-804-4

ALIGNMENTS

RESULT 1  
US-09-965-536A-11  
: Sequence 11, Application US/09965536A  
: Publication No. US20030027323A1  
: GENERAL INFORMATION:  
: APPLICANT: FEDER, J. N.  
: APPLICANT: MINIER, G.  
: APPLICANT: HANSEN, C. S.  
: APPLICANT: HANSEN, C. S.  
: TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGBRMS,  
: FILE REFERENCE: DOOLNP  
: CURRENT APPLICATION NUMBER: US/09/965.536A  
: CURRENT FILING DATE: 2001-09-26  
: PRIOR APPLICATION NUMBER: 60/235.713  
: PRIOR FILING DATE: 2000-09-27  
: PRIOR APPLICATION NUMBER: 60/261.781  
: PRIOR FILING DATE: 2001-01-16  
: PRIOR APPLICATION NUMBER: 60/306.605  
: PRIOR FILING DATE: 2001-07-19  
: PRIOR APPLICATION NUMBER: 60/310.436  
: PRIOR FILING DATE: 2001-08-03  
: NUMBER OF SEQ ID NOS: 6  
: SOFTWARE: Patent In Ver. 2.1  
: SEQ ID NO 11  
: LENGTH: 692  
: TYPE: PRT  
: ORGANISM: RAT  
US-09-965-536A-11

Query Match 100.0%; Score 3594; DB 9; Length 692;  
Best Local Similarity 100.0%; Pred. No. 3e-287;  
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MALLVSLAFITGSGCHHCHSRVFLCDSKVTEIPTDLPNRIELRFLVTKLRV 60  
Db 1 MALLVSLAFITGSGCHHCHSRVFLCDSKVTEIPTDLPNRIELRFLVTKLRV 60  
QY 61 IPKSGFAGDLEKIEISONDVLEIYADVSNLPKLTETRIKANNLYINPEAFONLP 120  
Db 61 IPKSGFAGDLEKIEISONDVLEIYADVSNLPKLTETRIKANNLYINPEAFONLP 120

Sequence 2, Appl1  
Sequence 16, Appl1  
Sequence 264, App  
Sequence 278, App  
Sequence 2, Appl1  
Sequence 10, Appl1  
Sequence 3, Appl1  
Sequence 30, Appl1  
Sequence 7, Appl1  
Sequence 6, Appl1  
Sequence 2, Appl1  
Sequence 24, Appl1  
Sequence 21, Appl1  
Sequence 20, Appl1  
Sequence 3, Appl1  
Sequence 6, Appl1  
Sequence 3, Appl1  
Sequence 2, Appl1  
Sequence 8, Appl1  
Sequence 7, Appl1  
Sequence 8, Appl1  
Sequence 4, Appl1

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QY 121 SLRYLLISNTGIGKHLPAVHKIQSLQKVLDDIQDNNINIHIVARNSPMGLSFESVILWLSKN 180
DB 121 SLRYLLISNTGIGKHLPAVHKIQSLQKVLDDIQDNNINIHIVARNSPMGLSFESVILWLSKN 180
QY 181 GIEEIHNCFAFNGTQDDELNLSNNLELNDVFOGASGPVILDSRTKVVHSLPNHGLE 240
DB 181 GIEEIHNCFAFNGTQDDELNLSNNLELNDVFOGASGPVILDSRTKVVHSLPNHGLE 240
QY 241 LKLRARSTYRLKLLPNLDKFTVTLMEASLTYPSSHCCAFANLKRQISELHPICNKSILROD 300
DB 241 LKLRARSTYRLKLLPNLDKFTVTLMEASLTYPSSHCCAFANLKRQISELHPICNKSILROD 300
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DB 301 IDDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMG 360
QY 361 YNLRVLWFTSILAITGNTTVLVLTTSOYKLVTPVPRFLMCLNLAFAADLCIGIYLLIASV 420
DB 361 YNLRVLWFTSILAITGNTTVLVLTTSOYKLVTPVPRFLMCLNLAFAADLCIGIYLLIASV 420
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DB 421 DIHTKSOYHNAIDQMGAGDAAGFTVFASLSVYTLTATILRWHITITHAMOLECKV 480
QY 481 QLRHAASVWVLGWTFAFAAALFPPIFGISSYMKVSIKCLPMDIDSPLSQLYVMALLVNLVA 540
DB 481 QLRHAASVWVLGWTFAFAAALFPPIFGISSYMKVSIKCLPMDIDSPLSQLYVMALLVNLVA 540
QY 541 FWICGCGYTHIYLVTRNPTIYSSSDTKIAKRMATLIPTDFLCNAPISFAISLKVPL 600
DB 541 FWICGCGYTHIYLVTRNPTIYSSSDTKIAKRMATLIPTDFLCNAPISFAISLKVPL 600
QY 601 ITVSKAKILLVLFYPIVNSCANPFLYAIPTKFRDRDFILLSKFGCYEMOAIYRTETSSA 660
DB 601 ITVSKAKILLVLFYPIVNSCANPFLYAIPTKFRDRDFILLSKFGCYEMOAIYRTETSSA 660
QY 661 THNFHARKSHCSSAPRVNTNSYLVPLNHSN 692
DB 661 THNFHARKSHCSSAPRVNTNSYLVPLNHSN 692
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## RESULT 2

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US-09-877-804-6
; Sequence 6, Application US/09877804
; Patent No. US20020061557A1
; GENERAL INFORMATION:
; APPLICANT: Nikolics, Karoly
; APPLICANT: McFarland, Keith C.
; APPLICANT: Segalo, Deborah L.
; APPLICANT: Seeburg, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
; FILE REFERENCE: P0576P1C2
; CURRENT APPLICATION NUMBER: US/09-04
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 08/207,814
; PRIOR FILING DATE: 1994-03-07
; PRIOR APPLICATION NUMBER: US 07/781,153
; PRIOR FILING DATE: 1991-10-31
; PRIOR APPLICATION NUMBER: US 07/347,683
; PRIOR FILING DATE: 1989-05-05
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 6
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: deduced sequence
US-09-877-804-6
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Query Match 100.0% Score 3594; DB 10; Length 692;
Best Local Similarity 100.0%; Pred. No. 3e-287;
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MALLVSLAF LGTSGCHHHLCHCSNRVFLCQDSKVTEIPTDLPRNAIELRVLTCLR 60
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DB 61 IPKGSFAGFGOLEKIEISQNDVLEVIADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120
QY 121 SLRYLLISNTGIGKHLPAVHKIQSLQKVLDDIQDNNINIHIVARNSPMGLSFESVILWLSKN 180
DB 121 SLRYLLISNTGIGKHLPAVHKIQSLQKVLDDIQDNNINIHIVARNSPMGLSFESVILWLSKN 180
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DB 181 GIEEIHNCFAFNGTQDDELNLSNNLELNDVFOGASGPVILDSRTKVVHSLPNHGLE 240
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DB 361 YNLRVLWFTSILAITGNTTVLVLTTSOYKLVTPVPRFLMCLNLAFAADLCIGIYLLIASV 420
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DB 481 QLRHAASVWVLGWTFAFAAALFPPIFGISSYMKVSIKCLPMDIDSPLSQLYVMALLVNLVA 540
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DB 541 FWICGCGYTHIYLVTRNPTIYSSSDTKIAKRMATLIPTDFLCNAPISFAISLKVPL 600
QY 601 ITVSKAKILLVLFYPIVNSCANPFLYAIPTKFRDRDFILLSKFGCYEMOAIYRTETSSA 660
DB 601 ITVSKAKILLVLFYPIVNSCANPFLYAIPTKFRDRDFILLSKFGCYEMOAIYRTETSSA 660
QY 661 THNFHARKSHCSSAPRVNTNSYLVPLNHSN 692
DB 661 THNFHARKSHCSSAPRVNTNSYLVPLNHSN 692
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## RESULT 3

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US-09-965-536A-12
; Sequence 12, Application US/09965536A
; Publication No. US20030027323A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D. R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY5,
; EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
; FILE REFERENCE: D0041NP
; CURRENT APPLICATION NUMBER: US/09/965,536A
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,781
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/306,605
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/310,436
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 12
; LENGTH: 688
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-804-626-12

Query Match      99.1%; Score 3560; DB 9; Length 688;
Best Local Similarity 99.3%; Pred. No. 1.9e-284;
Matches 687; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 MALLVSLVLAFLGTSGCHHLCNHRVFLCODSKVTEIPTDLPNNAIELRFLVTKLRV 60
DB 1 MALLVSLVLAFLGTSGCHHLCNHRVFLCODSKVTEIPTDLPNNAIELRFLVTKLRV 60
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DB 61 IPKGSFAGGDEKIEISONDVLEIADVSNPLKHEIRIEKANNLLYINPEAFONLP 120
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DB 121 SLRYLLSHTGIEKHPNKHQKQVLDQDNINHHIVARNSEFGLSPESVILWLSKN 180
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DB 177 GTEIHNCAFGTQDDELNSDNNHLELNDVDFOGASGVILDSRTKVSHPNHLGLEN 236
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DB 297 IDMTQIGQDQVSLDDSPSTGKSDMHYNEFDYDLCNEVDVYDTCSPKDAFNPCEDING 356
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DB 357 YHLRVLWLPISILATGNTVTVLVLTTSQKLVTPRFLMCLNLAFCIGIYLLLSY 416
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DB 417 DIHTKSYHTAIDMTGAGCDAGGFTVFASELSVTLTAITLERHHTITHAMQLECKV 476
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DB 477 QLRHAASVWYLGMTFAAALPTFGISSTYKVSICLPHMDIDSPLSQLYVALLVLA 536
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DB 537 PVVICGCTHIYLVPRNPTIVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKVPL 596
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DB 657 THNPHARKSHCSSAPRTNVTSLVPLNHSN 688

RESULT 4
US-09-877-804-7
; Sequence 7, Application 05/09877804
; Patent No. US20020061557A1
; GENERAL INFORMATION:
; APPLICANT: Nikolic, Karoly
; APPLICANT: Szele, Randolph C.
; APPLICANT: Szele, Peter H.
; APPLICANT: Soeburg, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor molecules
; FILE REFERENCE: P0576PIC2
; CURRENT APPLICATION NUMBER: US/09/877,804
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 08/207,814
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; PRIOR FILING DATE: 1994-03-07
; PRIOR APPLICATION NUMBER: US 07/781,153
; PRIOR FILING DATE: 1991-10-31
; PRIOR APPLICATION NUMBER: US 07/347,683
; PRIOR FILING DATE: 1989-05-05
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 7
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: deduced sequence
US-09-877-804-7

Query Match      97.8%; Score 3516; DB 10; Length 675;
Best Local Similarity 100.0%; Pred. No. 7.6e-281;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CHHWCHCNRVFLCODSKVTEIPTDLPNNAIELRFLVTKLRVIPKGSFAGGDEKIEI 77
DB 1 CHHWCHCNRVFLCODSKVTEIPTDLPNNAIELRFLVTKLRVIPKGSFAGGDEKIEI 60
QY 78 SONOVLEVLEADVSNPLKHEIRIEKANNLLYINPEAFONHLSRLYLLSHTGIEKHP 137
DB 61 SONOVLEVLEADVSNPLKHEIRIEKANNLLYINPEAFONHLSRLYLLSHTGIEKHP 120
QY 138 VHKIOSLQKVLDDQDNINHHIVARNSEFGLSPESVILWLSKNGTIEIHNCAFNCTOLDE 197
DB 121 VHKIOSLQKVLDDQDNINHHIVARNSEFGLSPESVILWLSKNGTIEIHNCAFNCTOLDE 180
QY 198 LNLSDNNHLELNDVDFOGASGVILDSRTKVSHPNHLGLENLKKLRARSTYRLKLPN 257
DB 181 LNLSDNNHLELNDVDFOGASGVILDSRTKVSHPNHLGLENLKKLRARSTYRLKLPN 240
QY 258 LDKFVTLMEASLTTPSHCCAFANLKRQISELHPICNKSILRODIDMTQIGQDQVSLDD 317
DB 241 LDKFVTLMEASLTTPSHCCAFANLKRQISELHPICNKSILRODIDMTQIGQDQVSLDD 300
QY 318 EDSYKSDMHYNEFDYDLCNEVDVYDTCSPKDAFNPCEDINGYNTLVLPISILAT 377
DB 301 EDSYKSDMHYNEFDYDLCNEVDVYDTCSPKDAFNPCEDINGYNTLVLPISILAT 360
QY 378 GNTTVLVLTTSQKLVTPRFLMCLNLAFCIGIYLLLSYVDIHTKSYHTAIDMTQ 437
DB 361 GNTTVLVLTTSQKLVTPRFLMCLNLAFCIGIYLLLSYVDIHTKSYHTAIDMTQ 420
QY 438 GAGDAAGFTVFASELSVTLTAITLERHHTITHAMQLECKVQLRHAASVWYLGMTFAF 497
DB 421 GAGDAAGFTVFASELSVTLTAITLERHHTITHAMQLECKVQLRHAASVWYLGMTFAF 480
QY 498 AALPPIFGISSTYKVSICLPHMDIDSPLSQLYVALLVLAFTVVICGCTHIYLVPRN 557
DB 481 AALPPIFGISSTYKVSICLPHMDIDSPLSQLYVALLVLAFTVVICGCTHIYLVPRN 540
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DB 541 PTVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKVPLITVSKAKILLVLPYIN 600
QY 618 SCANPFLYAIFTKRNFRDFFILLSKFCGYEMQAIYRTETSSATHNPHARKSHCSSAPRV 677
DB 601 SCANPFLYAIFTKRNFRDFFILLSKFCGYEMQAIYRTETSSATHNPHARKSHCSSAPRV 660

RESULT 5
US-09-804-626-8
; Sequence 8, Application US/09804626
; Patent No. US20020128190A1
; GENERAL INFORMATION:
; APPLICANT: Lobel, Leslie
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; APPLICANT: Lustbader, Joyce  
; TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF  
; FILE OF INVENTION: GONADOTROPIN RECEPTOR  
; FILE REFERENCE: 0575/62259/JPW/SHS  
; CURRENT APPLICATION NUMBER: US/09/804,626  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 695  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-804-626-8

Query Match 89.5%; Score 3215.5; DB 10; Length 695;  
Best Local Similarity 88.9%; Pred. No. 4.2e-256;  
Matches 618; Conservative 33; Mismatches 41; Indels 3; Gaps 2;  
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DB 1 MALLVSLAFSLGSGCHHCHCSNRVFLCQESKVTEIPSDLPNAIELRFVLTCLR 60  
QY 61 IPKSGFAGDLEKTEISQNDVLEIADVFSNPKLHEIRIEKANNLLYINPEAFQNL 120  
DB 61 IQKGFAGDLEKTEISQNDVLEIADVFSNPKLHEIRIEKANNLLYITPEAFQNL 120  
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DB 121 NLOYLLISNTGKHLPAVKHQSLOKVLDDODNINIHIVARNSPMGSLFESVILWLSKN 180  
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DB 241 LKLRARSTYRLKLPNDKFTVLMASLTYPSSHCCAFANLKRQISELHPICNKSILROE 300  
QY 301 IDDMTOIGDQVSLDD--EPVSGKSDMMYNEFDYDLCEVVDVTCSPKPAFNPCE 359  
DB 301 VDMTOIGDQVSLDD--EPVSGKSDMMYNEFDYDLCEVVDVTCSPKPAFNPCE 360  
QY 360 GYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPFLMCLNFAFADLCIGYLLIAS 419  
DB 361 GYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPFLMCLNFAFADLCIGYLLIAS 420  
QY 420 VDIHTKQSYHNYAIDWQTGAGCDAAGFTTVFASLSVYTLTAITLERWHTITHAMOLECK 479  
DB 421 VDIHTKQSYHNYAIDWQTGAGCDAAGFTTVFASLSVYTLTAITLERWHTITHAMOLECK 480  
QY 480 VOLRHAASVWVLGWTFAFAAALFPFGISYMKVSIKLPMDIDSPLSOLYVWALLVNLV 539  
DB 481 VOLRHAASVWVWGHWFATAAALFPFGISYMKVSIKLPMDIDSPLSOLYVWALLVNLV 540  
QY 540 AFVWICGCTHYIYLVTRNPTIVSSSDTKIAKRMATLIETDFLCNAPISFAISASLKV 599  
DB 541 AFVWICGCTHYIYLVTRNPTIVSSSDTKIAKRMATLIETDFLCNAPISFAISASLKV 600  
QY 600 LITVSKAKILLVLPINSCANPFLYIAFTKNFRDRFFILLSKFCGYEQMAQIYRTETSS 659  
DB 601 LITVSKAKILLVLPINSCANPFLYIAFTKNFRDRFFILLSKFCGYEQMAQIYRTETSS 660  
QY 660 ATHNHARKSHCSSAPRYT--NSYVLVPLNHSQN 692  
DB 661 TVNTHPRNGHSCSSAPRYTSGSTYILVPLSHLAQN 695

## RESULT 6

US-09-965-536A-13  
; Sequence 13, Application US/09965536A  
; Publication No. US2003002732A1  
; GENERAL INFORMATION:  
; APPLICANT: FEDER, J. N.

; APPLICANT: MINTIER, G.  
; APPLICANT: RAMANATHAN, C. S.  
; APPLICANT: HAWKEN, D. R.  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBWMV5,  
; FILE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES  
; FILE REFERENCE: DCO41NP  
; CURRENT APPLICATION NUMBER: US/09/965,536A  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/235,713  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/261,781  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/306,605  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/310,436  
; PRIOR FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 687  
; TYPE: PRT  
; ORGANISM: Equus asinus  
US-09-965-536A-13

Query Match 85.6%; Score 3076.5; DB 9; Length 687;  
Best Local Similarity 86.0%; Pred. No. 1.1e-244;  
Matches 597; Conservative 38; Mismatches 50; Indels 9; Gaps 3;  
QY 1 MALLVSLAFGLTSGCGHHLCHCSNRVFLCQDSKVTEIPTDLPRNAIELRFVLTCLR 60  
DB 1 MALLVSLAFSLGSGCHHCHCSNRVFLCQESKVTEIPSDLPNAIELRFVLTCLR 60  
QY 61 IPKSGFAGDLEKTEISQNDVLEIADVFSNPKLHEIRIEKANNLLYINPEAFQNL 120  
DB 61 IPKGFAGDLEKTEISQNDVLEIADVFSNPKLHEIRIEKANNLLYIOHDAFQNL 120  
QY 121 SLRYLLISNTGKHLPAVKHQSLOKVLDDODNINIHIVARNSPMGSLFESVILWLSKN 180  
DB 121 NLOYLLISNTGKHLPAVKHQSLOKVLDDODNINIHIVARNSPMGSLFESVILWLSKN 180  
QY 181 GIEETHNCAFNGTQDLDELNLSDNNLEELPNDVFOGASGPVILDSRTKVSHPNHLGN 240  
DB 181 GIEETHNCAFNGTQDLDELNLSDNNLEELPNDVFOGASGPVILDSRTKVSHPNHLGN 240  
QY 241 LKLRARSTYRLKLPNDKFTVLMASLTYPSSHCCAFANLKRQISELHPICNKSILROD 300  
DB 241 LKLRARSTYRLKLPNDKFTVLMASLTYPSSHCCAFANLKRQISELHPICNKSILROE 300  
QY 301 IDDMTOIGDQVSLDD--EPVSGKSDMMYNEFDYDLCEVVDVTCSPKPAFNPCE 360  
DB 301 VDMTOIGDQVSLDD--EPVSGKSDMMYNEFDYDLCEVVDVTCSPKPAFNPCE 353  
QY 361 GYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPFLMCLNFAFADLCIGYLLIASV 420  
DB 361 GYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPFLMCLNFAFADLCIGYLLIASV 413  
QY 421 DIHTKQSYHNYAIDWQTGAGCDAAGFTTVFASLSVYTLTAITLERWHTITHAMOLECKV 480  
DB 421 DIHTKQSYHNYAIDWQTGAGCDAAGFTTVFASLSVYTLTAITLERWHTITHAMOLECKV 473  
QY 481 OLRRHAASVWVLGWTFAFAAALFPFGISYMKVSIKLPMDIDSPLSOLYVWALLVNLV 540  
DB 474 OLRRHAASVWVLGWTFAFAAALFPFGISYMKVSIKLPMDIDSPLSOLYVWALLVNLV 533  
QY 541 FVWICGCTHYIYLVTRNPTIVSSSDTKIAKRMATLIETDFLCNAPISFAISASLKVPL 600  
DB 534 FVWICGCTHYIYLVTRNPTIVSSSDTKIAKRMATLIETDFLCNAPISFAISASLKVPL 593  
QY 601 LITVSKAKILLVLPINSCANPFLYIAFTKNFRDRFFILLSKFCGYEQMAQIYRTETSSA 660  
DB 594 LITVSKAKILLVLPINSCANPFLYIAFTKNFRDRFFILLSKFCGYEQMAQIYRTETSS 653  
QY 661 THNHARKSHCSSAPRYT--NSYVLVPLNHSQN 692



RESULT 9  
US-09-877-804-8  
; Sequence 8, Application US/09877804  
; Patent No. US20020061557A1  
; GENERAL INFORMATION:  
; APPLICANT: Nikolics, Karoly  
; APPLICANT: McFarland, Keith C.  
; APPLICANT: Segalo, Deborah L.  
; APPLICANT: Seeburg, Peter H.  
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules  
; FILE REFERENCE: P0576P1C2  
; CURRENT APPLICATION NUMBER: US/09/877,804  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: US 08/207,814  
; PRIOR FILING DATE: 1994-03-07  
; PRIOR APPLICATION NUMBER: US 07/781,153  
; PRIOR FILING DATE: 1991-10-31  
; PRIOR APPLICATION NUMBER: US 07/347,683  
; PRIOR FILING DATE: 1989-05-05  
; NUMBER OF SEQ ID NOS: 22  
; SEQ ID NO 8  
; LENGTH: 348  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: deduced sequence  
US-09-877-804-8

Query Match 51.0%; Score 1832; DB 10; Length 348;  
Best Local Similarity 100.0%; Pred. No. 1.1e-142;  
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 CHWLVCHSNNRVFCQDSKVTETDLPRAIELRFLVTLKRLVPKSGFAGFGLKIEI 77  
Db 1 CHWLVCHSNNRVFCQDSKVTETDLPRAIELRFLVTLKRLVPKSGFAGFGLKIEI 60

Qy 78 SONDLVEIADVSNLPKLEIRKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 137  
Db 61 SONDLVEIADVSNLPKLEIRKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 120

Qy 138 VHKQSLQKVLDDODNINIHIARNSPMGUSFESVILWLSKNGIEETHNCAFNGLD 197  
Db 121 VHKQSLQKVLDDODNINIHIARNSPMGUSFESVILWLSKNGIEETHNCAFNGLD 180

Qy 198 LNLSDNNLEELPNDVFGAGSPVLDLSRTKVSHPNHLNKKLRARSTYRLKLPN 257  
Db 181 LNLSDNNLEELPNDVFGAGSPVLDLSRTKVSHPNHLNKKLRARSTYRLKLPN 240

Qy 258 LDKFVTLMEASLTYPSSHCCAFANLKRQISELHPICNKSILRQDIDDMTQIGDQVSLIDD 317  
Db 241 LDKFVTLMEASLTYPSSHCCAFANLKRQISELHPICNKSILRQDIDDMTQIGDQVSLIDD 300

Qy 318 EPSYKSGSDMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNILR 365  
Db 301 EPSYKSGSDMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNILR 348

RESULT 10  
US-09-877-804-3  
; Sequence 3, Application US/09877804  
; Patent No. US20020061557A1  
; GENERAL INFORMATION:  
; APPLICANT: Nikolics, Karoly  
; APPLICANT: McFarland, Keith C.  
; APPLICANT: Segalo, Deborah L.  
; APPLICANT: Seeburg, Peter H.  
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules  
; FILE REFERENCE: P0576P1C2  
; CURRENT APPLICATION NUMBER: US/09/877,804  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: US 08/207,814  
; PRIOR FILING DATE: 1994-03-07  
; PRIOR APPLICATION NUMBER: US 07/781,153

; PRIOR FILING DATE: 1991-10-31  
; PRIOR APPLICATION NUMBER: US 07/347,683  
; PRIOR FILING DATE: 1989-05-05  
; NUMBER OF SEQ ID NOS: 22  
; SEQ ID NO 3  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: deduced sequence  
US-09-877-804-3

Query Match 50.0%; Score 1797; DB 10; Length 674;  
Best Local Similarity 56.5%; Pred. No. 2e-139;  
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

Qy 45 PRNAIELRFLVTKL--RVIPKSGFAGFGLKIEISQNDVLEIEADVSNLPKLEIRI 102  
Db 25 PRAGL-ARLSITVLPVKVIPSQAFRGLNEVVKIEISQSDSLERIEANAFDNLNLSLLI 83

Qy 103 EKANNLLYINPEAFONLPSRLYLLISNTGKHLPAVHKIOSLO-KVLLDQDNINIHI 161  
Db 84 QNTKNLLYIEPGAFTNLPRLKYLISICNTGIRTPDVTKISSERFLEICDNLHITIP 143

Qy 162 RNSFMGLSFESVILWLSKNGIEETHNCAFNGLDDELNDNNLEELPNDVFGAGSPV 221  
Db 144 GNAFQGMNNEVSLKLYGNGFEEVQSHAFNGTTLSLELKENIYLEKMHSGAFGATGPS 203

Qy 222 ILDISRTKVSHPNHLNKKLRARSTYRLKLPNLDKFTVLMASLTYPSSHCCAFANL 281  
Db 204 ILDISRTKVSHPNHLNKKLRARSTYRLKLPNLDKFTVLMASLTYPSSHCCAFANL 263

Qy 282 KRQISELHPICNKSILRQDIDDMTQIGDQVSLIDDPSYV---KSDMYNEFDYDLN 338  
Db 264 PKK-----EQNFSEFSEFENFSKQCESTVRKADNETLYSAIFEENELSGWDYDGPCS 315

Qy 339 EVDVTCSPKPDAPNCPEDIMGYNILRVLWIFISILAITGNTTVLVLTTSQYKLTVPFR 398  
Db 316 PKT-LQCAPEPAENPCEDIMGYAFRLWILWILAILAIFGNLTVLVLTTSYKLTVPFR 374

Qy 399 LMCNLAFLADLCIGYLLLIASVDIHTKSOYHNYAIDMTQAGCDAAGFTVFASLSVYT 458  
Db 375 LMCNLSFADFCMGLYLLLIASVDISQTKGOYVNHAIQMTQSGCAGAGFTVFASLSVYT 434

Qy 459 LTATLTERWHITTHAMOLECKVQLRHAASVWVLGWTAFAAALPFIQGISYMKVSLCP 518  
Db 435 LTVTLEWHITTYAVQLDQKLRHAIPIMLGGMLFSTLIATMPLVGISYMKVSLCP 494

Qy 519 MDIDPSQLVYVALLVNLVLAFFVVICGYTHYLTVRNPTIVSSSDTKAKRMATLIF 578  
Db 495 MDVESTLSQVILSILINLVAVFVICACYIRIYFVONPELTAPNKDTRAKKMAILIF 554

Qy 579 TDFLCMAPISPFAISASLKVPLITVSKAKILLVLFYFIPNSCANPFLYAIFTKFRDRPFI 638  
Db 555 TDFTCMAPISPFAISAAFKVPLITVTSKILLVLFYFIPVNSCANPFLYAIFTKAFQDRELL 614

Qy 639 LLSKFGCYEMOQAIYRTETSSATNFHARKSHCSS 673  
Db 615 LLSRFGCCRRAELYRRK-----EFSAYTSNCKN 643

RESULT 11  
US-09-877-804-2  
; Sequence 2, Application US/09877804  
; Patent No. US20020061557A1  
; GENERAL INFORMATION:  
; APPLICANT: Nikolics, Karoly  
; APPLICANT: McFarland, Keith C.  
; APPLICANT: Segalo, Deborah L.  
; APPLICANT: Seeburg, Peter H.  
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules  
; FILE REFERENCE: P0576P1C2  
; CURRENT APPLICATION NUMBER: US/09/877,804

APPLICANT: JANKEN, D. B.  
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGBRHW'S,  
FILE REFERENCE: DQOJNP  
CURRENT APPLICATION NUMBER: US/09/965,536A  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/235,713  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/261,781  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/306,605  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: 60/310,436  
PRIOR FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 676  
ORGANISM: Gallitrix jacobus  
US-09-877-804-2

Query Match 50.0% Score 1797; DB 10; Length 700;  
Best Local Similarity 56.5% Pred. No. 2,1e-139;  
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

QY 45 PRNAIELRFLVTLK--RVIPKGSFAGDLEKIEISONDVLEIADVFNSLPLKRIEIRI 102  
DB 51 PRAGL-ARLSLTLPVKVPSOAFRGNEVVKIEISQDSLERIEANAFDNLNLSLI 109  
QY 103 EKANNLLYNPEAFONLPSRLYLISMTGKILPAVHKIQSLQ-KVLLDQDNIHIVA 161  
DB 110 QMTKLLYEPGAPNLPRLKYLISCTGRTLPDVKISSSEFNFILEICDNLHITTP 169  
QY 162 RNSPGLSPESIVIMLSKNGIEIHCNCFNGQDELKNSDNNLEELPNDVFGAGPV 221  
DB 170 GNAQGMNSESIVLTKNGFEVQSHAFNGTIVLSLEKENTYLERKHSAGPAGTGS 229  
QY 232 ILDISRTKVSPLHGLENLKILBARSTYRLKLPNDKFTYLMKASLTYPHCCAFNL 281  
DB 230 ILDISRTKLOALPSHGLESIOTLIATSSYSLATLPSKEKFTSLVATLTPSHCCAFNL 289  
QY 282 KROISELPHCKNSILRODIDMTQIGDQVSLDDDEPSY---XGSDMNYEFDYLCN 338  
DB 290 PKK-----EONFSFIPENFSKQESTVAKADNETLYSAIFEENELSGMDYDGC 341  
QY 339 EYVDYSCPKDAPNCPEDINGNIRLVLPISLAIATGNTTVLVLTSTYKLTVPFR 398  
DB 342 PRT-LQCAPEPDAPNCPEDINGVAPLRVLIHILAIPLGRLVLTSTYKLTVPFR 400  
QY 399 LACNLAPADIGIKILLIASVDIHTSKOYHNADQGTGACDAGPFTVPASELSVT 458  
DB 401 LACNLSTADCKGLYLLIASVDSQGTQYHNALDQGTGCGAGPFTVPASELSVT 460  
QY 459 LTAITLERWHITTHAMOLECKVOLRHAASVYVLTGTFAPAAALPFGISSYMKV 518  
DB 461 LTVITLERWHITTAVOLDKLRLHAIPIMLGOMLESTLIATMTPLVGISNTMKV 520  
QY 519 MDIDPSLSQTYMALLVLNLPVFCGCTTHIYTVRNPTIVSSSDTKIAKRMATLIF 578  
DB 521 MDVESTLSQTYVLSILNVPVYVYACVIRIYAVQNPBLTAPNKOTKIAKRMATLIF 580  
QY 579 TDFLCHAPISFALSASUKVPLTVSKAKILLVLPYINSCAMPFLYAIPTKPRDPFI 638  
DB 581 TDFLCHAPISFALSASUKVPLTVSKAKILLVLPYINSCAMPFLYAIPTKPRDPFI 640  
QY 639 ILSEKPCETEMOAOIYRTETSSATHPHARKSCSS 673  
DB 641 ILSRFGCCRRRAELTRK-----EFSNYSNCLN 669

RESULT 12  
US-09-965-536A-15  
Sequence 15, Application US/09965536A  
Publication No. US20030027323A1  
GENERAL INFORMATION:  
APPLICANT: FEDER, J. N.  
MINTIER, G.  
APPLICANT: RAMANATHAN, C. S.

APPLICANT: JANKEN, D. B.  
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGBRHW'S,  
FILE REFERENCE: DQOJNP  
CURRENT APPLICATION NUMBER: US/09/965,536A  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/235,713  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/261,781  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/306,605  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: 60/310,436  
PRIOR FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 676  
ORGANISM: Gallitrix jacobus  
US-09-965-536A-15

Query Match 49.6% Score 1783.5; DB 9; Length 676;  
Best Local Similarity 55.8% Pred. No. 2.6e-138;  
Matches 359; Conservative 99; Mismatches 140; Indels 45; Gaps 6;

QY 55 LTKL-----RVIPKGSFAGDLEKIEISONDVLEIADVFNSLPLKRIEIRI 107  
DB 55 LTRLSLAYLPVKVPSOAFRGNEVVKIEISQDSLERIEANAFDNLNLSLIQMTKN 114  
QY 108 LLYINPEAFONLPSRLYLISMTGKILPAVHKIQSLQ-KVLLDQDNIHIVAARNSP 166  
DB 115 LHTEPGAPNLPRLKYLISCTGRTLPDVKISSSEFNFILEICDNLHITTPGNAFO 174  
QY 167 LGHESVGLHLSKNGIEIHCNCFNGQDELKNSDNNLEELPNDVFGAGPVILDIS 226  
DB 175 GANNESITLKYNGFEVQSHAFNGTIVLSLEKENTYLERKHSAGPAGTGS 234  
QY 227 RTKVSPLHGLENLKILBARSTYRLKLPNDKFTYLMKASLTYPHCCAFNLKROIS 286  
DB 235 STKLOALPSHGLESIOTLIATSSYSLATLPSKEKFTSLVATLTPSHCCAFNVPK 292  
QY 287 ELHPICNLSILRODIDMTQIGDQVSLDDDEPSYSGSDMNYEFDYLCNEVVDVTC 346  
DB 293 -----DTPAIPAESGOSCMYDYG-FLPKTPRCA 321  
QY 347 PKDAPNCPEDINGNIRLVLPISLAIATGNTTVLVLTSTYKLTVPFRFLMCLNAPA 406  
DB 322 PEPDAPNCPEDINGDVLRLVLIHILAIPLGRLVLTSTYKLTVPFRFLMCLNAPA 381  
QY 407 DLCTGYLLIASVDIHTSKOYHNADQGTGACDAGPFTVPASELSVTTLTATLER 466  
DB 382 DFCNGLYLLIASVDSQGTQYHNADQGTGACDAGPFTVPASELSVTTLTATLER 441  
QY 467 WHITTHAMOLECKVOLRHAASVYVLTGTFAPAAALPFGISSYMKVSIKLPMDIDPLS 526  
DB 442 WHITTAHLDKRLRLHAIPIMLGOMLESTLIATMTPLVGVSNMKVSIKLPMDIETPS 501  
QY 527 QLYMALLVLNLPVFCGCTTHIYTVRNPTIVSSSDTKIAKRMATLIFTDFLCHAP 586  
DB 502 QAYVILVLPVFCGCTTHIYTVRNPTIVSSSDTKIAKRMATLIFTDFLCHAP 561  
QY 587 ISFALSASUKVPLTVSKAKILLVLPYINSCAMPFLYAIPTKPRDPFIILSKPGCY 646  
DB 562 ISFALSASUKVPLTVSKAKILLVLPYINSCAMPFLYAIPTKPRDPFIILSKPGCY 621  
QY 647 EMOAOIYRTETSSATHPHARKSCSSAPRVNYSVLPVPLNH 688  
DB 622 KURAEYLRKDKSAVTSNTY---KNGFTGSGKPSOSTLKLPAH 661

RESULT 13  
US-09-804-626-6



```
; Sequence 6, Application US/09804626
; Patent No. US20020128190A1
; GENERAL INFORMATION:
; APPLICANT: Lusbader, Joyce
; TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF
; FILE REFERENCE: 0575/62259/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/804,626
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-804-626-6

Query Match      49.4%; Score 1776; DB 10; Length 699;
Best Local Similarity 55.4%; Pred. No. 1.le-137;
Matches 349; Conservative 108; Mismatches 147; Indels 26; Gaps 6;

QY 55 LTKL-----RVTPKGSFAGFDLEKIEISONDVLEIADVFSNLPKLHEIRKANN 107
DB 51 LTRLAYLPVKVIPSOAFLNEVIEKIEISQIDSLERIEANAFDNLNLSEILLQNTKN 110
QY 108 LLYINPEAFONLPSRLYLISNTGKIKHLPVAKI--QSLQKVLDDTDODNINIHIARNFSM 166
DB 111 LRYTEPGAFINLPRLKYLISICNTGIRKPPDVTKVFSSNSFLEICDNLHTTIPGNAFP 170
QY 167 GLSPESVILWLSKNGIEBHNCAPNGTQDELINLSDNNLDELNDVPQASGPVILDIS 226
DB 171 GNNESVTLKLYNGFEVQSHAFNGTTLTSLKENVHLEKMHNGARGTGPKYLDIS 230
QY 227 RTKVSHPHNGLENLKLBARSTRKLPNDLPVTLMEASLTPSHCCAFANLKROIS 286
DB 231 STKLOALPSYGLSIRQLRTATSSYSLKPLSRETFFVNLLEATLTPSHCCAFRLN----- 285
QY 287 ELHPICNKSLRQDIDDMTOIGDQVRSLIDDEPSYK--GSDMMYNEFDYDLGNEVDV 343
DB 286 ---PTKEQNFHSISENFKOCSTYRKVNKNTLYSSMLAESELGWDIEYGFCLPKTP- 341
QY 344 TCSKPKDAPNCPEDIMGYNIIRLVIFISILAITGNTTVLVLTTSOYKLTVPFRLMCLN 403
DB 342 RCAPEPDAPNCPEDIMGYDFLRVLILINILAINGMTVFLVLTSTRYKLTVPFRLMCLN 401
QY 404 AFADLCIGIYLLLTASVDIHTKSQYHNAIDWQAGCAGDAAGFTTVFASLSVYTLTAT 463
DB 402 SFADFCMGLYLLLTASVDQTKQYINHAIDWQAGCAGTGTAGFTTVFASLSVYTLTAT 461
QY 464 LERWHTITHAMOLECKVOLRAASVMVLGWTAFANAALFFIGTSSYMKVSLCPLMDIDS 523
DB 462 LERWHTIYAHLOKLERHAILIMJGWLFFSSLIAMLPVLGVSNMKVSLCPLMDVET 521
QY 524 PLSQLYMALLVNLVLAFFVIGCYTHIYLVARNPTIVSSSDTKIAKRMATLIFTDFLC 583
DB 522 TLSQVYILTLINVAFFIICACVYKIYFAVRNPELMATKTDKIAKMALLIFTDFTC 581
QY 584 MAPISFFAISLSKPLVLTYSKAKILLVLPINSCANPFLYAIPTKFNRRDFFLLSKF 643
DB 582 MAPISFFAISAFKPLVLTYSKAKILLVLPINSCANPFLYAIPTKFNRRDFFLLSKF 641
QY 644 GYEMOAOIYRTETSSATHFNHARKSHCSS 673
DB 642 GCCRRARELYRRK-----DFSAYTSNCKN 665

RESULT 14
US-10-045-624B-2
; Sequence 2, Application US/10045624B
; Publication No. US20030009778A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.

; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING THYROID
; FILE REFERENCE: R-666
; CURRENT APPLICATION NUMBER: US/10/045,624B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 10/045,624
; FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-045-624B-2

Query Match      46.0%; Score 1653.5; DB 9; Length 764;
Best Local Similarity 48.9%; Pred. No. 1.5e-127;
Matches 346; Conservative 106; Mismatches 194; Indels 61; Gaps 11;

QY 3 LLLVSLLAFLGT--GSGCHHWLCHCSNRVFLCQDSKVT-----EIPDTLPRAIELRVL 55
DB 7 LLLVLLALLSLRSGKECAPPCHEQHE-----DDFRVTKELHRIPS-LPSTOTLKLIE 61
QY 56 TKLRVIPKGSFAGFDLEKIEISONDVLEIADVFSNLPKLHEIRIEKANNLLVINPEA 115
DB 62 THLKTIPSLAFSSLPNISRIYLSIDATLQRIEPHSFYNLKRWTHIEINRSLTYIDPDA 121
QY 116 FONLPRLYLISNTGKIKHLPVAKIQLQ--KVLDDIODNINIHIARNFSMGLSFESI 174
DB 122 LTELPLKFLGIFNTGLRIFFDPLTKIYSTDITDFFILEITDNPVMTSPVENAFGLCNETLT 181
QY 175 LWSLNGLEEHTNCAFNGTQDELNLSNNLEELPNDFOGA--SGPVILDISRTKVNLS 233
DB 182 LKLYNNGFTSVOGHAFINCTKLDVYLNKNKYLTATDNDAGFVGVSPTLLDVSSTVATL 241
QY 234 PNHGLLENLKLARSTRYRLKPLNLDKFTVLMASLTYPVSHCCAFANLKROISELHPI-C 292
DB 242 PSKGLHLEKLIADKDTWTLKPLSLSLHLTRADLSYPSHCCAFKOKKIRGILESMLC 301
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RESULT 15
US-09-804-626-4
; Sequence 4, Application US/09804626
; Patent No. US20020128190A1
; GENERAL INFORMATION:
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APPLICANT: Lobel, Leslie  
APPLICANT: Mersereau, Georges  
TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF  
TITLE OF INVENTION: CONADOPTROPIN RECEPTOR  
FILE REFERENCE: 0575/62259/3PW/GHS  
CURRENT APPLICATION NUMBER: US/09/804,626  
CURRENT FILING DATE: 2001-03-09  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 4  
LENGTH: 516  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-09-804-626-4

Query Match 41.9%; Score 1505.5; DB 10; Length 516;  
Best Local Similarity 85.5%; Pred. No. 1.3e-115;  
Matches 289; Conservative 22; Mismatches 26; Indels 1; Gaps 1;

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Qy 88 ADVFSLPKLHEIRIEKANNLLYINPEAFONLPFLRYLLISNTGKIKHLPVHKIQLQKV 147  
Db 228 ADVFSLPKLHEIRIEKANNLLYITPEAFONLPFLRYLLISNTGKIKHLPVHKIQLQKV 287

Qy 148 LLDIQDNINIHIVARNFGLSFESVILMLSKNGIEIHNKAFNGTQDDELNLSONNLE 207  
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Qy 327 MWTNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNIL 364  
Db 468 MWTNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNIL 505

Search completed: June 16, 2003, 13:52:47  
Job time : 173.089 secs

GenCore version 5.1.6  
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2003, 13:26:01 : Search time 26.8296 Seconds  
(without alignments)  
2479.543 Million cell updates/sec

Title: US-09-877-804-6  
Perfect score: 3594  
Sequence: 1 MALLVSLAPLTGSGCHH.....SAPRVNYSVLVPLNHSN 692

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3594	100.0	692	2 A34548	foliitropin recept
2	3250.5	89.5	695	1 ORHUT	foliitropin recept
3	3208.5	89.3	695	1 YN888	foliitropin recept
4	3208.5	89.3	695	2 JC3493	follicle stimulat
5	3199.5	89.0	695	2 JC3493	foliitropin recept
6	3140	87.4	694	2 JC3237	foliitropin recept
7	3118	86.8	694	2 JC3201	foliitropin recept
8	2503	69.6	696	2 JC7361	foliitropin recept
9	1807.5	50.3	696	2 A41344	lutropin-receptor
10	1799	50.1	700	2 A42395	lutropin-choriogon
11	1797	50.0	700	2 I77463	lutropin-choriogon
12	1797	50.0	700	2 A49744	lutropin-choriogon
13	1776	49.4	699	1 ORHUT	thyrotropin recept
14	1673.5	46.6	764	2 A40077	thyrotropin recept
15	1660	46.2	764	2 ORHUR	thyrotropin recept
16	1653.5	46.0	764	2 I48882	thyrotropin recept
17	1636.5	45.3	764	2 JC5643	thyroid stimulat
18	1636.5	45.1	764	2 A35966	thyroid stimulat
19	1632	45.1	764	2 JC7389	thyroid stimulat
20	1507	44.4	814	2 JC7389	thyroid stimulat
21	864	24.0	935	2 JC2033	protein-coupled
22	809	22.5	889	2 T20123	protein-coupled
23	644	17.9	907	2 JG0193	G protein-coupled
24	636	17.7	907	2 JG0193	orphan G protein-c
25	587.5	16.3	339	2 B41344	lutropin-choriogon
26	587.5	16.3	339	2 D41344	lutropin-choriogon
27	587.5	16.3	331	2 C41344	lutropin-choriogon
28	578	16.1	342	2 I77461	lutropin-choriogon
29	522.5	14.5	1115	2 S40241	G protein-coupled

ALIGNMENTS

RESULT 1

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C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 13-Aug-1999  
C:Accession: A34548; A41729  
R:Sprengel, R.; Braun, T.; Nikolic, K.; Segaloff, D.L.; Seeburg, P.H.  
Mol. Endocrinol. 4, 525-530, 1990  
A:Title: The testicular receptor for follicle stimulating hormone: structure and func  
A:Reference number: A34548; MUID:91125358; PMID:2126341  
A:Accession: A34548  
A:Molecule type: mRNA  
A:Residues: 1-692 <SPR>  
A:Cross-references: GB:J08442; MUI:9204183; PDB:AAA1175.1; PID:g204184  
R:Heckert, L.L.; Daley, I.J.; Griswold, M.D.  
Mol. Endocrinol. 6, 70-80, 1992  
A:Title:Structure: Organization of the follicle-stimulating hormone receptor gene.  
A:Reference number: A41729; MUID:92149579; PMID:1738373  
A:Accession: A41729  
A>Status: preliminary  
A:Molecule type: DNA  
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A:Cross-references: GB:381198; MUI:9245344; PDB:AA21415.1; PID:g245345  
A:Note: sequence inconsistent with the nucleotide translation  
R:Davis, D.; Liu, X.; Segaloff, D.L.  
Mol. Endocrinol. 9, 159-170, 1995  
A:Title: Identification of the sites of N-linked glycosylation on the follicle-stimul  
A:Reference number: A37562; MUI:9529749; PMID:7776966  
A:Contents: annotation; glycosylation sites  
C:Keywords: receptor that mediates the biochemical effects of follicle-stimulating hormone; glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat; glycoprotein; hormone receptor; signal sequence; status predicted <SIG>  
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P:6632-6656/Domain: transmembrane status predicted <TM258>  
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P:6732-6756/Domain: transmembrane status predicted <TM262>  
P:6757-6781/Domain: transmembrane status predicted <TM263>  
P:6782-6806/Domain: transmembrane status predicted <TM264>  
P:6807-6831/Domain: transmembrane status predicted <TM265>  
P:6832-6856/Domain: transmembrane status predicted <TM266>  
P:6857-6881/Domain: transmembrane status predicted <TM267>  
P:6882-6906/Domain: transmembrane status predicted <TM268>  
P:6907-6931/Domain: transmembrane status predicted <TM269>  
P:6932-6956/Domain: transmembrane status predicted <TM270>  
P:6957-6981/Domain: transmembrane status predicted <TM271>  
P:6982-7006/Domain: transmembrane status predicted <TM272>  
P:7007-7031/Domain: transmembrane status predicted <TM273>  
P:7032-7056/Domain: transmembrane status predicted <TM274>  
P:7057-7081/Domain: transmembrane status predicted <TM275>  
P:7082-7106/Domain: transmembrane status predicted <TM276>  
P:7107-7131/Domain: transmembrane status predicted <TM277>  
P:7132-7156/Domain: transmembrane status predicted <TM278>  
P:7157-7181/Domain: transmembrane status predicted <TM279>  
P:7182-7206/Domain: transmembrane status predicted <TM280>  
P:7207-7231/Domain: transmembrane status predicted <TM281>  
P:7232-7256/Domain: transmembrane status predicted <TM282>  
P:7257-7281/Domain: transmembrane status predicted <TM283>  
P:7282-7306/Domain: transmembrane status predicted <TM284>  
P:7307-7331/Domain: transmembrane status predicted <TM285>  
P:7332-7356/Domain: transmembrane status predicted <TM2

F:554/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
F:595/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 100.0% Score 3594; DB 2; Length 692; -  
Best Local Similarity 100.0%; Pred. No. 5.6e-242;  
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MALLVSLAFLGSGCHWLCHCSNRVFLCQDSKVTETPTDLPRAIELRVLTKLRV 60
DB 1 MALLVSLAFLGSGCHWLCHCSNRVFLCQDSKVTETPTDLPRAIELRVLTKLRV 60
QY 61 IPKGSFAGFGLERIEISQNDVLEIADVFESNLPKLHEIRIEKANNLLIYINPAFONLP 120
DB 61 IPKGSFAGFGLERIEISQNDVLEIADVFESNLPKLHEIRIEKANNLLIYINPAFONLP 120
QY 121 SLRYLLSNTGIIKHLPAVHKIQSLQKVLDDIQDNNIHIIVARNISFVGLSFEVILWLSKN 180
DB 121 SLRYLLSNTGIIKHLPAVHKIQSLQKVLDDIQDNNIHIIVARNISFVGLSFEVILWLSKN 180
QY 181 GIEEIHNCAPNGTQDELNLSDNNLELNDVFGAGSPVILDSRTKVSLSLPHNGLEN 240
DB 181 GIEEIHNCAPNGTQDELNLSDNNLELNDVFGAGSPVILDSRTKVSLSLPHNGLEN 240
QY 241 LKLLRASTYRLKLLPNLDKFTVLTMEASLTYPSCCAFAFLKROISELHPICNKSILROD 300
DB 241 LKLLRASTYRLKLLPNLDKFTVLTMEASLTYPSCCAFAFLKROISELHPICNKSILROD 300
QY 301 IDDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPDAPNCEIDMG 360
DB 301 IDDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPDAPNCEIDMG 360
QY 361 YNILLRLWFTSILAITGNTVLLVLTTSQYKLTVPFLMCLNAPADLCIGIYILLTASV 420
DB 361 YNILLRLWFTSILAITGNTVLLVLTTSQYKLTVPFLMCLNAPADLCIGIYILLTASV 420
QY 421 DIHTKSOYHNTAIDWQTGAGDAAGFFVTFVASELSVYLTATILRWHITTHAMOLECKV 480
DB 421 DIHTKSOYHNTAIDWQTGAGDAAGFFVTFVASELSVYLTATILRWHITTHAMOLECKV 480
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DB 481 QLRHAASVNVLGWTFAPAAALPFIPIGSISSMKVSIKLPMDISPLSQLYVNVLLVLA 540
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DB 541 FVWICGCTHYLTVRNPTIYSSSDTKIARMTATLFTDFLCWAPISFFAISASLKVPL 600
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DB 601 ITVSKAKILLVLYPINSANPFLYAIFTKNFRDRDFILLSKFCYEMQAIYRTETSSA 660
QY 661 THNFHARKSHCSSAPRVNTSVYVLPNLHSSON 692
DB 661 THNFHARKSHCSSAPRVNTSVYVLPNLHSSON 692

```

## RESULT 2

## QHUFU

folliotropin receptor precursor - human  
N:Alternate names: follicle stimulating hormone receptor (FSHR)  
N:Contains: folliotropin receptor precursor long splice form; folliotropin receptor precursor  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1991 #sequence\_revision 06-Sep-1996 #text\_change 22-Jun-1999  
C:Accession: 157661; 156448; PC1147; S30560; 157672; JN0122  
R:Gromoll, J.; Dankbar, B.; Gudermann, T.  
Mol. Cell. Endocrinol. 102, 93-102, 1994  
A:Title: Characterization of the 5' flanking region of the human follicle-stimulating hormone receptor  
A:Reference number: 157661; MUID:95011044; PMID:7926278  
A:Accession: 157661  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-51 <GRO>  
A:Cross-references: GB:S73199; NID:g685036; PIDN:AAB32071.1; PID:g685037

R:Gromoll, J.; Ried, T.; Holtgreve-Grez, H.; Nieschlag, E.; Gudermann, T.  
J. Mol. Endocrinol. 12, 265-271, 1994  
A:Title: Localization of the human FSH receptor to chromosome 2 p21 using a genomic p  
A:Reference number: 156448; MUID:95000244; PMID:7916967  
A:Accession: 156448  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 286-695 <GRO>  
A:Cross-references: GB:S73526; NID:g688069; PIDN:AAB32225.1; PID:g688070  
R:Gromoll, J.; Gudermann, T.; Nieschlag, E.  
Biochem. Biophys. Res. Commun. 188, 1077-1083, 1992  
A:Title: Molecular cloning of a truncated isoform of the human follicle stimulating h  
A:Reference number: PC1147; MUID:93075197; PMID:1359889  
A:Accession: PC1147  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-223,286-294,'P',296-342 <GR3>  
A:Cross-references: EMBL:X68044; NID:g31473; PIDN:CAA48179.1; PID:g31474  
A:Experimental source: testis  
R:Gromoll, J.  
submitted to the EMBL Data Library, August 1992  
A:Reference number: S30560  
A:Accession: S30560  
A:Molecule type: mRNA  
A:Residues: 1-12,'R',14-223,286-294,'P',296-342 <GR4>  
A:Cross-references: EMBL:X68044; NID:g31473; PIDN:CAA48179.1; PID:g31474  
R:Kelton, C.A.; Cheng, S.V.; Nugent, N.P.; Schweickhardt, R.L.; Rosenthal, J.L.; Over  
Mol. Cell. Endocrinol. 89, 141-151, 1992  
A:Title: The cloning of the human follicle stimulating hormone receptor and its expe  
A:Reference number: 157672; MUID:93246012; PMID:1301382  
A:Accession: 157672  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-679,'N',681-695 <REL>  
A:Cross-references: GB:S59900; NID:g300072; PIDN:AAB26480.1; PID:g300073  
R:Minegishi, T.; Nakamura, K.; Takakura, Y.; Ibukki, Y.; Igarashi, M.  
Biochem. Biophys. Res. Commun. 175, 1125-1130, 1991  
A:Title: Cloning and sequencing of human FSH receptor cDNA.  
A:Reference number: JN0122; MUID:91222171; PMID:1709010  
A:Accession: JN0122  
A:Molecule type: mRNA  
A:Residues: 1-111,'T',113-196,'AV',199-306,'A',308-695 <MIN>  
A:Cross-references: EMBL:M65085; NID:g182770; PIDN:AAAS2477.1; PID:g182771  
C:Genetics:  
A:Gene: GDB:FSHR  
A:Cross-references: GDB:127510; OMIM:136435  
A:Map position: 2p21-2p16  
A:Introns: 223/3  
A:Note: the exact position of the intron cannot be determined from the experimental d  
C:Function:  
A:Description: receptor that mediates the biochemical effects of follitropin  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repea  
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone r  
F:1-695/Product: follitropin receptor precursor, long splice form #status predicted <  
F:1-223,286-695/Product: follitropin receptor precursor, short splice form #status pr  
F:1-15/Domain: signal sequence #status predicted &ltSIG>  
F:16-695/Product: follitropin receptor #status predicted &ltMAT>  
F:16-366/Domain: extracellular hormone binding #status predicted &ltEHB>  
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F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology &ltLRR2>  
F:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology &ltLRR3>  
F:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology &ltLRR4>  
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology &ltLRR5>  
F:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology &ltLRR6>  
F:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology &ltLRR7>  
F:367-387/Domain: transmembrane #status predicted &ltTM1>  
F:398-421/Domain: transmembrane #status predicted &ltTM2>  
F:444-465/Domain: transmembrane #status predicted &ltTM3>  
F:486-508/Domain: transmembrane #status predicted &ltTM4>  
F:529-550/Domain: transmembrane #status predicted &ltTM5>  
F:574-597/Domain: transmembrane #status predicted &ltTM6>  
F:609-630/Domain: transmembrane #status predicted &ltTM7>  
F:191,199,293,318/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:556/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
F:596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
Query Match 89.9%; Score 3230.5; DB 1; Length 695;  
Best Local Similarity 89.4%; Pred. No. 1e-216;  
Matches 621; Conservative 32; Mismatches 39; Indels 3; Gaps 2;

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DB 1 MALLVSLAPFATGSGCHHLCNRVFLCDQSKVTEIPTDLPNRIELRFLVTKLRV 60
QY 61 IPKSGAGFGOLEKIEISQNDVLEIADVSNLPLKHEIRIKANMLYINPEAFONLP 120
DB 61 IQKSGAGFGOLEKIEISQNDVLEIADVSNLPLKHEIRIKANMLYINPEAFONLP 120
QY 121 SLYLLISWTGILHPLVAVKIOSQVLOKLVLODQNNIHIIVARNSPGLSPESVILMLSKN 180
DB 121 NLYLLISWTGILHPLVAVKIOSQVLOKLVLODQNNIHIIVARNSPGLSPESVILMLSKN 180
QY 181 GTEIHNCAFNGTQDLDELNSNNLLELPNDVFGAGSPVILDTSRKTVHSLPNHGLEN 240
DB 181 GIOEIHNCFAFNGTQDLDELNSNNLLELPNDVFGAGSPVILDTSRKTVHSLPNHGLEN 240
QY 241 LKKLRARSTYRLKLPNDKFTVTLMEASLUTYPSHCCAFANLKRQISELHPICNKSILRQD 300
DB 241 LKKLRARSTYRLKLPNDKFTVTLMEASLUTYPSHCCAFANLKRQISELHPICNKSILRQD 300
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QY 420 VOIHTKSOYHNALDMQTGACDGAAGFTVFASLSVYTLTATLTERHHTITHAMOLECK 479
DB 420 VOIHTKSOYHNALDMQTGACDGAAGFTVFASLSVYTLTATLTERHHTITHAMOLECK 479
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DB 480 VOLRHAASVWLVGTFAAALPFIPIGISTYKYSICLPMIDISPLSQLYMALLVNLV 539
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DB 600 LITVSKAKILLVLPINSCANPLFYALPTKFRDRDFILLSKFCGYEMQAQIYRTETSS 659
QY 660 ATNHPHARKSCSSAPRYTN--NSYLVPLNHSQON 692
DB 661 TVNHPHARKSCSSAPRYTN--NSYLVPLNHSQON 695
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## RESULT 3

JN0898  
foliitropin receptor - crab-eating macaque  
N:Alternate names: follicle-stimulating hormone receptor (FSHR)  
C:Species: Macaca fascicularis (crab-eating macaque)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change/10-Sep-1999  
C:Accession: JN0898; S36452  
R:Gronow, J.; Dankbar, B.; Sharma, R.S.; Nieschlag, E.  
Biochem. Biophys. Res. Commun. 196; 1068-1072; 1993  
A:Reference: 1068-1072; 1993  
A:Reference: 1068-1072; 1993  
A:Reference: 1068-1072; 1993  
A:Accession: JN0898; PMID:7504463  
A:Molecule type: mRNA  
A:Residues: 1-695 <GRO>  
A:Cross-references: ENBL:X74454; NID:q396801; PIDN:CAA52463.1; PID:q396802  
A:Note: the authors translated the codon AGT for residue 488 as Arg  
C:Function:

A:Description: receptor that mediates the biochemical effects of follitropin  
C:Supernatant: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
C:Keywords: 1 protein coupled receptor; glycoprotein; hormone receptor; phosphoprotein  
F:117/Domain: signal sequence #status predicted <SIG>  
F:18-695/Product: follitropin receptor #status predicted <PPH>  
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:367-387/Domain: transmembrane #status predicted <TM1>  
F:399-421/Domain: transmembrane #status predicted <TM2>  
F:444-465/Domain: transmembrane #status predicted <TM3>  
F:486-508/Domain: transmembrane #status predicted <TM4>  
F:529-550/Domain: transmembrane #status predicted <TM5>  
F:569-630/Domain: transmembrane #status predicted <TM6>  
F:131-199/Domain: transmembrane #status predicted <TM7>  
F:555/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
F:596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 89.8%; Score 3226.5; DB 1; Length 695;  
Best Local Similarity 89.4%; Pred. No. 2e-216;  
Matches 621; Conservative 30; Mismatches 41; Indels 3; Gaps 2;

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DB 1 MALLVSLAPFATGSGCHHLCNRVFLCDQSKVTEIPTDLPNRIELRFLVTKLRV 60
QY 61 IPKSGAGFGOLEKIEISQNDVLEIADVSNLPLKHEIRIKANMLYINPEAFONLP 120
DB 61 IQKSGAGFGOLEKIEISQNDVLEIADVSNLPLKHEIRIKANMLYINPEAFONLP 120
QY 121 SLYLLISWTGILHPLVAVKIOSQVLOKLVLODQNNIHIIVARNSPGLSPESVILMLSKN 180
DB 121 NLYLLISWTGILHPLVAVKIOSQVLOKLVLODQNNIHIIVARNSPGLSPESVILMLSKN 180
QY 181 GTEIHNCAFNGTQDLDELNSNNLLELPNDVFGAGSPVILDTSRKTVHSLPNHGLEN 240
DB 181 GIOEIHNCFAFNGTQDLDELNSNNLLELPNDVFGAGSPVILDTSRKTVHSLPNHGLEN 240
QY 241 LKKLRARSTYRLKLPNDKFTVTLMEASLUTYPSHCCAFANLKRQISELHPICNKSILRQD 300
DB 241 LKKLRARSTYRLKLPNDKFTVTLMEASLUTYPSHCCAFANLKRQISELHPICNKSILRQD 300
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DB 420 VOIHTKSOYHNALDMQTGACDGAAGFTVFASLSVYTLTATLTERHHTITHAMOLECK 479
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DB 600 LITVSKAKILLVLPINSCANPLFYALPTKFRDRDFILLSKFCGYEMQAQIYRTETSS 659
QY 660 ATNHPHARKSCSSAPRYTN--NSYLVPLNHSQON 692
DB 661 TVNHPHARKSCSSAPRYTN--NSYLVPLNHSQON 695
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## RESULT 4

145896  
follicle stimulating hormone receptor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 15-Oct-1996 #sequence\_revision 15-Oct-1996 #text\_change 21-Jan-2000  
C:Accession: J45896  
R:Houde, A.; Lambert, A.; Saumande, J.; Silversides, D.W.; Lussier, J.G.  
Mol. Reprod. Dev. 39, 127-135, 1994  
A:Title: Structure of the bovine follicle-stimulating hormone receptor complementary DNA  
A:Reference number: 145896; MUID:95127199; PMID:7826612  
A:Accession: J45896  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-695 <HOU>  
A:Cross-references: GB:L22319; NID:g404671; PIDN:AAC37324.1; PID:g404672  
C:Gene: FSHR  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
Query Match 89.3%; Score 3208.5; DB 2; Length 695;  
Best Local Similarity 87.8%; Pred. NO. 3.5e-215;  
Matches 610; Conservative 46; Mismatches 36; Indels 3; Gaps 2;  
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Db 1 MALLVALLAFLSGGCHHLCNSGVFLCQSKVTEIPSDLPDRAVELRFLVTLKRV 60  
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Db 61 IPKGSFAGFGDLEKIEISQNDVLEIADVFSNPKLHEIRIEKANNLLYIDPAFQNL 120  
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Db 241 LKKLRARSTYRLKLPNDKFTVMEASLTYPSCCAFANLKRQISELHPICNKSILRQ 300  
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Db 301 VDDMTQARGQRVSLAEDDEPSYAKGFDYSEFDYDLNVEVDVTCSPKPAFNPCEIM 360  
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Db 361 GDDILRLVIFSLITAITGNTVLTSLVLTTSQKLVTPRFLMCLNLAFAADLCIGIYLLTAS 420  
Qy 420 VDIHTKSOYHNYAIDWQTGACDAGFFTVFASLSVYTLTAITLERWHTITHAMOLECK 479  
Db 421 VDVHTKSOYHNYAIDWQTGACDAGFFTVFASLSVYTLTAITLERWHTITHAMOLECK 480  
Qy 480 VOLRHAASVMVLTGWTFAFAALPFIPTGSSYMKVSIICLPMDIDSPLSQLYVALLVNLV 539  
Db 481 VOLRHAASIMLVGWTFAFAVALPFIPTGSSYMKVSIICLPMDIDSPLSQLYVALLVNLV 540  
Qy 540 APVVICGCTHYLTIVRNPITVSSSDTKIAKRMATLIFTDFLCNAPISFAISASLKP 599  
Db 541 APVVICGCTHYLTIVRNPITVSSSDTKIAKRMATLIFTDFLCNAPISFAISASLKP 600  
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Db 601 LITVSKAILLVLPINSCANPFLYAITKFNFRDFFILLSKFCYEQMQAIYRTSS 660  
Qy 660 ATHNPHARKSHCSAPRVN - SYVLVPLNHISSON 692  
Db 661 TANNPHRNGHCAPPAPRVNNGSNYTLIPLRLAKN 695

## RESULT 5

JC1493  
follicotropin receptor - sheep  
N:Alternate names: follicle stimulating hormone receptor  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C:Accession: JC1493; I47080  
R:Khan, H.; Yarney, T.A.; Sairam, M.R.  
Biochem. Biophys. Res. Commun. 190, 888-894, 1993  
A:Title: Cloning of alternatively spliced mRNA transcripts coding for variants of ovine  
A:Reference number: JC1493; MUID:93176195; PMID:8439338  
A:Accession: JC1493  
A:Molecule type: mRNA  
A:Residues: 1-695 <KHA>  
A:Experimental source: testis  
R:Yarney, T.A.; Sairam, M.R.; Khan, H.; Ravindranath, N.; Payne, S.; Seidah, N.G.  
Mol. Cell. Endocrinol. 93, 219-226, 1993  
A:Title: Molecular cloning and expression of the ovine testicular follicle stimulating  
A:Reference number: I47080; MUID:93351750; PMID:8394255.  
A:Accession: I47080  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-695 <YAR>  
A:Cross-references: GB:L07302; NID:g165884; PIDN:AAA31525.1; PID:g165885  
C:Genetics:  
A:Gene: FSH-R  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
F:191,199/Binding site: carbohydrate (Asn) (covalent) status predicted  
Query Match 89.0%; Score 3199.5; DB 2; Length 695;  
Best Local Similarity 87.2%; Pred. NO. 1.5e-214;  
Matches 606; Conservative 48; Mismatches 38; Indels 3; Gaps 2;  
Qy 1 MALLVSLAFLGTGSGCHHLCNSRVFLCQSKVTEIPTDLPRNAIEFLVTLKRV 60  
Db 1 MALFLVALLAFLSGGCHHLCNSGVFLCQSKVTEIPSDLPDRAVELRFLVTLKRV 60  
Qy 61 IPKGSFAGFGDLEKIEISQNDVLEIADVFSNPKLHEIRIEKANNLLYINPEAFQNL 120  
Db 61 IPEGAFSGFGDLEKIEISQNDVLEIADVFSNPKLHEIRIEKANNLLYIDPAFQNL 120  
Qy 121 SLRYLLISNTGKHLPAVHKIQSLQKVLDDQDNINIHIVARNSPMGLSFESVILWSKN 180  
Db 121 NLRYLLISNTGKHLPAVHKIQSLQKVLDDQDNINIHIVARNSPMGLSFESVILWSKN 180  
Qy 181 GIEETHNCAFNGTDLDELNDNNLELPNDVFOGASGPVLLDLSRTKVVHSLPNHGLN 240  
Db 181 GIEETHNCAFNGTDLDELNDNNLELPNDVFOGASGPVLLDLSRTKVVHSLPNHGLN 240  
Qy 241 LKKLRARSTYRLKLPNDKFTVMEASLTYPSCCAFANLKRQISELHPICNKSILRQD 300  
Db 241 LKKLRARSTYRLKLPNDKFTVMEASLTYPSCCAFANLKRQISELHPICNKSILRQ 300  
Qy 301 IDDMTQIGDQVSLI - DDEPSYSGSDMYNEFDYDLNVEVDVTCSPKPAFNPCEIM 359  
Db 301 VDDMTQARGQRVSLAEDDEPSYAKGFDYSEFDYDLNVEVDVTCSPKPAFNPCEIM 360  
Qy 360 GYNILRLVIFSLITAITGNTVLTSLVLTTSQKLVTPRFLMCLNLAFAADLCIGIYLLTAS 419  
Db 361 GYDILRLVIFSLITAITGNTVLTSLVLTTSQKLVTPRFLMCLNLAFAADLCIGIYLLTAS 420  
Qy 420 VDIHTKSOYHNYAIDWQTGACDAGFFTVFASLSVYTLTAITLERWHTITHAMOLECK 479  
Db 421 VDVHTKSOYHNYAIDWQTGACDAGFFTVFASLSVYTLTAITLERWHTITHAMOLECK 480  
Qy 480 VOLRHAASVMVLTGWTFAFAALPFIPTGSSYMKVSIICLPMDIDSPLSQLYVALLVNLV 539  
Db 481 VVHRHAASIMLVGWTFAFAVALPFIPTGSSYMKVSIICLPMDIDSPLSQLYVALLVNLV 540

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OY 540 AFVVICGCTHYIYLVNPTIVSSSDTKIAKMATLIFTDFELCMAPISFAISASLAVP 599
Db 541 AFVVICGCTHYIYLVNPTIVSSSDTKIAKMATLIFTDFELCMAPISFAISASLAVP 600
OY 600 LITVSKAILLVLPINSCANPLVAIFTKNRPDFFILLSKFCYEMOQIYRTETSS 659
Db 601 LITVSKAILLVLPINSCANPLVAIFTKNRPDFFILLSKFCYEMOQIYRTETSS 660
OY 660 ATNHPHARKSHCSAPRVN--SYVLVPLNHSSON 692
Db 661 TANHPRNGHCPAPRVNCSNTYLPLRLAKN 695

RESULT 6
JC2237
folliculotropin receptor, testis - horse
N:Alternate names: eFSHR
C:Species: Equus caballus (domestic horse)
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 13-Aug-1999
C:Accession: JC2237; JC2370
R:Robert, P.; Ansell, S.; Christophe, S.; Benifla, J.L.; Ballet, D.; Roman, A.; Bideret
Biochem. Biophys. Res. Commun. 201, 201-207, 1994
A:Title: Cloning and sequencing of the equine testicular folliculotropin receptor.
A:Reference number: JC2237; MUID:94256980; PMID:8198575
A:Accession: JC2237
A:Molecule type: mRNA
A:Residues: 1-694 <R0B>
A:Cross-references: GB:S70150; MUI:9546896; PIDN:AB30854.1; PID:9546897
A:Experimental source: testis
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
P:56-70/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
P:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
P:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
P:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
P:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
P:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
P:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
P:366-386/Domain: transmembrane #status predicted <TM1>
P:398-420/Domain: transmembrane #status predicted <TM2>
P:443-464/Domain: transmembrane #status predicted <TM3>
P:485-507/Domain: transmembrane #status predicted <TM4>
P:528-549/Domain: transmembrane #status predicted <TM5>
P:573-596/Domain: transmembrane #status predicted <TM6>
P:608-629/Domain: transmembrane #status predicted <TM7>
P:191-193,206,239/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.4%; Score 3140; DB 2; Length 694;
Best Local Similarity 87.6%; Pred. No. 26-210;
Matches 609; Conservative 35; Mismatches 47; Indels 4; Gaps 3;
OY 1 MALLVSLAFLATGSGCHHWCNRYFLCOESKVTETPLDPRNAELRYFLTKRV 60
Db 1 MALLVSLAFLATGSGCHHWCNRYFLCOESKVTETPLDPRNAELRYFLTKRV 60
OY 61 IPKGSFAGFGLKLETSQNDVLEADVFNPLKREIRKANNLLYINPEAFONLP 120
Db 61 IPKGSFAGFGLKLETSQNDVLEADVFNPLKREIRKANNLLYINPEAFONLP 120
OY 121 SLRTLLISPTGKIELPAVHKIQSLQKLVLDIQNINITHIVARNSPMGLSFESVILWLSKN 180
Db 121 SLRTLLISPTGKIELPAVHKIQSLQKLVLDIQNINITHIVARNSPMGLSFESVILWLSKN 180
OY 181 GIEETHNCAFNQTDDELNLSDNNLELNDVDFGASGPVILDISETVSLPUGLEN 240
Db 181 GIEETHNCAFNQTDDELNLSDNNLELNDVDFGASGPVILDISETVSLPUGLEN 240
OY 241 LKRLARSTYLAALPNLDFYTLKMAESTYPSHCAPANLKRQISELIPTCNKSLROD 300
Db 241 LKRLARSTYLAALPNLDFYTLKMAESTYPSHCAPANLKRQISELIPTCNKSLROD 300
OY 301 IDMTQIGQORVSLT--DDEPSTYSGSDNNTREFDYDLNEDVYVTCSPKDPAPNCEIM 359
Db 301 IDMTQIGQORVSLT--DDEPSTYSGSDNNTREFDYDLNEDVYVTCSPKDPAPNCEIM 359
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Db 301 V-DNQARGERSVLAEDDESSYPKGFDMHSEFYDLCNEVDVYVTCSPKDPAPNCEIM 359
OY 360 GYNILRVLMFISLITATCTVTYLVLTYSOKLTVPRFLACNLAFADLCIGIYLLIAS 419
Db 360 GYNILRVLMFISLITATCTVTYLVLTYSOKLTVPRFLACNLAFADLCIGIYLLIAS 419
OY 420 VDIHTKSOYHNTAIDMGTGACDAGFTTFVASELSVYTLTAITLERHHTITHAMOLECK 479
Db 420 VDIHTKSOYHNTAIDMGTGACDAGFTTFVASELSVYTLTAITLERHHTITHAMOLECK 479
OY 480 VOLRHAASVYVLMGTFAAALPFIPIGSISSVMKVSICLPHDIDSPISQLYMALVNLVL 539
Db 480 VOLRHAASVYVLMGTFAAALPFIPIGSISSVMKVSICLPHDIDSPISQLYMALVNLVL 539
OY 540 AFVVICGCTHYIYLVNPTIVSSSDTKIAKMATLIFTDFELCMAPISFAISASLAVP 599
Db 540 AFVVICGCTHYIYLVNPTIVSSSDTKIAKMATLIFTDFELCMAPISFAISASLAVP 599
OY 600 LITVSKAILLVLPINSCANPLVAIFTKNRPDFFILLSKFCYEMOQIYRTETSS 659
Db 600 LITVSKAILLVLPINSCANPLVAIFTKNRPDFFILLSKFCYEMOQIYRTETSS 659
OY 660 ATNHPHARKSHCSAPRVN--SYVLVPLNHSSON 692
Db 660 TANHPRNGHCPAPRVNCSNTYLPLRLAKN 695

RESULT 7
JC4301
folliculotropin receptor - pig
N:Alternate names: follicle-stimulating hormone receptor
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 21-Jan-2000
C:Accession: JC4301
R:Remy, J.; 257-260, 1995
A:Title: The porcine folliculotropin receptor: cDNA cloning, functional expression and chr
ematogenesis in male and oogenesis in female.
A:Reference number: JC4301; MUID:96011644; PMID:7590277
A:Accession: JC4301
A:Molecule type: mRNA
A:Residues: 1-694 <R0B>
A:Cross-references: GB:L31966
A:Experimental source: ovarian granulosa cells
C:Comment: This receptor belongs to the family of the G-protein coupled receptors. It
C:Genetics:
A:Gene: fshr
A:Map position: 3 q2.2-q2.3
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repoe
P:56-70/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
P:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
P:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
P:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
P:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
P:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
P:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
P:366-386/Domain: transmembrane #status predicted <TM1>
P:398-420/Domain: transmembrane #status predicted <TM2>
P:443-464/Domain: transmembrane #status predicted <TM3>
P:485-507/Domain: transmembrane #status predicted <TM4>
P:528-549/Domain: transmembrane #status predicted <TM5>
P:573-596/Domain: transmembrane #status predicted <TM6>
P:608-629/Domain: transmembrane #status predicted <TM7>

Query Match 86.8%; Score 3118; DB 2; Length 694;
Best Local Similarity 86.0%; Pred. No. 6.9e-209;
Matches 598; Conservative 40; Mismatches 53; Indels 4; Gaps 3;
OY 1 MALLVSLAFLATGSGCHHWCNRYFLCOESKVTETPLDPRNAELRYFLTKRV 60
Db 1 MALLVSLAFLATGSGCHHWCNRYFLCOESKVTETPLDPRNAELRYFLTKRV 60
OY 61 IPKGSFAGFGLKLETSQNDVLEADVFNPLKREIRKANNLLYINPEAFONLP 120
Db 61 IPKGSFAGFGLKLETSQNDVLEADVFNPLKREIRKANNLLYINPEAFONLP 120
OY 121 SLRTLLISPTGKIELPAVHKIQSLQKLVLDIQNINITHIVARNSPMGLSFESVILWLSKN 180
Db 121 SLRTLLISPTGKIELPAVHKIQSLQKLVLDIQNINITHIVARNSPMGLSFESVILWLSKN 180
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Db 120 NLRVLLISNTGCVKLPVAVKIOSLQKVLDDIQDNIHTVERNSFMGLSFESMILWLSKN 179  
Qy 181 GIEEIHNCFAFGTQDDELNDNNLELNDVDFOGAGPVLIDISRTKVKHSLNPHGLE 240  
Db 180 GIREIHNCFAFGTQDDELNDNNLELNDVDFOGAGPVLIDISRTKVKHSLNPHGLE 239  
Qy 241 LKKLRARSTYRLKLPNDKLVTLMEASLTYPSCCAAFANLKRQISELHPTCNKSLRQD 300  
Db 240 LKKLRARSTYRLKLPNDKLVTLMEASLTYPSCCAAFANLKRQISELHPTCNKSLRQD 299  
Qy 301 IDDMTQIGDQSVLIDD-EPYSGKSGDMYNEFDYDLCNEVVDVTCSPKDPAFNPCE 359  
Db 300 VDMTQARGQSVLAEDGESSLAKFEEDTMYSEFYDLCNEVVDVTCSPKDPAFNPCE 359  
Qy 360 GYNILRVLIWISILAITGNTVTLVLTTSQYKLTVPFRLMCNLAFAADLCIGIYLL 419  
Db 360 GHDILRVLIWISILAITGNTVTLVLTTSQYKLTVPFRLMCNLAFAADLCIGIYLL 419  
Qy 420 VDIHTKSOYHNYAIDMOTGAGCDAAGFTVFASLSVYTLTAITLERHWHITAMOLE 479  
Db 420 IDIHTKSOYHNYAIDMOTGAGCDAAGFTVFASLSVYTLTAITLERHWHITAMOLE 479  
Qy 480 VOLRHAASVMVLGWTFAFAALFFPIFGISSYMKVSCICLPMDDISPLSOLYVLLVNL 539  
Db 480 QVVRHAASIMLYGWIFAFVAFVLPFIPIFGISSYMKVSCICLPMDDISPLSOLYVLLVNL 539  
Qy 540 APVWICGCTHYIYLVNPTIVSSSSDRTKIARMAITLFTDLCNAPISFFAISASL 599  
Db 540 AFWVWICGCTHYIYLVNPTIVSSSSDRTKIARMAITLFTDLCNAPISFFAISASL 599  
Qy 600 LITVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFGCYEQAQIYRTENS 659  
Db 600 LITVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFGCYEQAQIYRTENS 659  
Qy 660 ATHNPHARKSHCSSAPRVN--SYVLVPLNHSQN 692  
Db 660 TAHNIHPRNGHCPAPRITNSSSYTLIPLSLAQN 694

## RESULT 8

JC7361  
follicitropin receptor precursor - new  
N:Alternate names: follicle-stimulating hormone receptor  
C:Species: Cynops pyrrhogaster (newt)  
C:Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 31-Dec-2000  
R:Nakayama, Y.; Yamamoto, T.; Oba, Y.; Nagahama, Y.; Abe, S.  
Biochem. Biophys. Res. Commun. 275, 121-128, 2000  
A:Title: Molecular cloning, functional characterization, and gene expression of a follicle-stimulating hormone receptor from the newt, *Cynops pyrrhogaster*  
A:Reference number: JC7361  
A:Contents: Testis  
A:Accession: JC7361  
A:Molecule type: mRNA  
A:Residues: 1-696 <NAK>  
A:Cross-references: DDBJ:AB005587  
C:Comment: This protein, containing seven transmembrane domains and a large glycosylated in and thyroid stimulating hormone. This receptor has a common signal transduction pathway in and thyroid stimulating hormone.  
C:Genetics:  
A:Gene: fsh-r  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat H  
C:Keywords: disulfide bond; glycolysis; glycoprotein; hormone receptor; testis; transmembrane  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-696/Product: follicle-stimulating hormone receptor #status predicted <MAT>  
F:18-359/Domain: extracellular #status predicted <EXT>  
F:370-389/Domain: transmembrane #status predicted <TM1>  
F:402-424/Domain: transmembrane #status predicted <TM2>  
F:447-468/Domain: transmembrane #status predicted <TM3>  
F:489-511/Domain: transmembrane #status predicted <TM4>  
F:532-553/Domain: transmembrane #status predicted <TM5>  
F:577-600/Domain: transmembrane #status predicted <TM6>  
F:612-633/Domain: transmembrane #status predicted <TM7>  
F:46,190,198,267,292/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:445-520/Disulfide bonds: #status predicted

Query Match 69.6%; Score 2503; DB 2; Length 696;  
Best Local Similarity 70.2%; Pred. No. 3.9e-166;  
Matches 488; Conservative 86; Mismatches 113; Indels 8; Gaps 5;

Qy 1 MALLVSLAFLGTGSGCHWLCNHNRFVLCQDSKVTETDPLPRNRIELRFLVTLKRV 60  
Db 1 MSLAFLCLLLAVLSSFGCHP--VCLNRVFTQESHVQVQIPRDIIPRNSITELRFLVTKV 59  
Qy 61 IPKSGFAGFGLDLEKIEISQNDVLEIVADVSNLPKLEHRIEKANLLYINPEAFONLP 120  
Db 60 IPKAFSGFDEVENIEISQNDVLEIVADVSNLPKLEHRIEKANLLYINPEAFONLP 119  
Qy 121 SLRVLLISNTGKILPAVKIOSLQKVLDDIQDNIHTVERNSFMGLSFESVILWLSKN 180  
Db 120 SLRVLLISNTGKILPAVKIOSLQKVLDDIQDNIHTVERNSFMGLSFESVILWLSKN 179  
Qy 181 GIEEIHNCFAFGTQDDELNDNNLELNDVDFOGAGPVLIDISRTKVKHSLNPHGLE 240  
Db 180 GIEEIHNCFAFGTQDDELNDNNLELNDVDFOGAGPVLIDISRTKVKHSLNPHGLE 239  
Qy 241 LKKLRARSTYRLKLPNDKLVTLMEASLTYPSCCAAFANLKRQISELHPTCNKSLRQD 300  
Db 240 LKKLRARSTYRLKLPNDKLVTLMEASLTYPSCCAAFANLKRQISELHPTCNKSLRQD 299  
Qy 301 IDDMTQIGDQSVLIDD-EPYSGKSGDMYNEFDYDLCNEVVDVTCSPKDPAFNPCE 355  
Db 300 VDMTQARGQSVLAEDGESSLAKFEEDTMYSEFYDLCNEVVDVTCSPKDPAFNPCE 359  
Qy 360 GYNILRVLIWISILAITGNTVTLVLTTSQYKLTVPFRLMCNLAFAADLCIGIYLL 415  
Db 360 GHDILRVLIWISILAITGNTVTLVLTTSQYKLTVPFRLMCNLAFAADLCIGIYLL 419  
Qy 416 LITVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFGCYEQAQIYRTENS 475  
Db 420 LITVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFGCYEQAQIYRTENS 479  
Qy 476 LECKVQLRHAASVMVLGWTFAFAALFFPIFGISSYMKVSCICLPMDDISPLSOLYVLLVNL 535  
Db 480 LDRKVRHATAMVVGWIFAFVAFVLPFIPIFGISSYMKVSCICLPMDDISPLSOLYVLLVNL 539  
Qy 536 LNVLPVWICGCTHYIYLVNPTIVSSSSDRTKIARMAITLFTDLCNAPISFFAISAS 595  
Db 540 LNVLPVWICGCTHYIYLVNPTIVSSSSDRTKIARMAITLFTDLCNAPISFFAISAS 599  
Qy 596 LKVPILTVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFGCYEQAQIYRT 655  
Db 600 LKVPILTVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFGCYEQAQIYRT 659  
Qy 656 ETSSATHNPHARKSHCSSAPRVN--SYVLVPLNHSQN 688  
Db 660 ETSSATHNPHARKSHCSSAPRVN--SYVLVPLNHSQN 694

## RESULT 9

A41344  
lutropin-choriogonadotropin receptor precursor (splice form A) - pig  
N:Alternate names: luteinizing hormone-choriogonadotropin receptor  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 21-Jan-2000  
C:Accession: A41344  
R:Loosfelt, H.; Mistrati, M.; Atger, M.; Salesse, R.; Vu Hai-Luu Thi, M.T.; Jolivet, Science 245, 525-528, 1989  
A:Title: Cloning and sequencing of porcine LH-hCG receptor cDNA: variants lacking the extracellular domain  
A:Accession: A41344  
A:Molecule type: mRNA  
A:Residues: 1-696 <LOO>  
A:Cross-references: NID:g164528; PIDN:AAA31062.1; PID:g164529  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
C:Keywords: alternative splicing; G-protein-coupled receptor; glycoprotein; membrane  
F:1-27/Domain: signal sequence #status predicted <SIG>





A:Residues: 1-700 <RES>  
A:Cross-references: GB:S40803; MID:g252163; PIDN:AAB22680.1; PID:g252164  
C:Genetics:  
A:Introns: 58/2; 82/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat F.153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
Query Match 50.0%; Score 1797; DB 2; Length 700;  
Best Local Similarity 56.5%; Pred. No. 4.8e-117;  
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;  
QY 45 PRNATLRLPVLTKL--RVIPKSPAGFGDLEKIEISQNDVLEIVADVPSNLPKLHEIRI 102  
DB 51 PRAGL-ARLSLTYLPVKVIPSQAFRLNEVVKIEISQSDSLERIEANFDNLNLSLLI 109  
QY 103 EKANNLLYNPAFONLPSRLYLLISNTGKHLPAVHKIOSLO-KVLLDIDONINHIYA 161  
DB 110 QNTKNLLIYEPGAFNLPRLKYLSTCNTGIRLPDVTKISSSEFPNLEICDNLHITTP 169  
QY 162 RNSFMGLSPESVILNLSKNGIEEIHNCAPNGTQDDELNLSNNLEELPNDFVQSGAPV 221  
DB 170 GNAFGMNNESVTLKLYGNPREVQSHAFNGTTLISLEKENIYLEKMHSGAFQATGFS 229  
QY 222 ILDISRTKVHSLPNHGLENLKRLARSTYRLKKNLKNLDFVTLMEASLTYPSSHCCAFANL 281  
DB 230 ILDISRTKVHSLPNHGLENLKRLARSTYRLKKNLKNLDFVTLMEASLTYPSSHCCAFANL 281  
QY 282 KROISELHPICKNSILRODIDDMTOIGDQVSLIDDEPSYG---KGSDMYNEFDYDLGN 338  
DB 290 PKK-----EQNFSEIFENFSKQCESTVRKADNETLYSAIFEEENELSGWDYDYGFS 341  
QY 339 EYVDVTSCKPDAFNPCEIDMGYNILRLWIFISILAITGNTVLVLTTSYKLTVPFR 398  
DB 342 PRT-LQCAPEPDAFNPCEIDMGYAFRLWLINILAILFNLTLVLLTSYKLTVPFR 400  
QY 399 LMCNLAPADLCIGYLLIASVDIHTKSOYHAYIDMOTGACDAGFTFVASELSVYT 458  
DB 401 LMCNLSFADFCMLGLLLATLSDVSTKQGYNHADIMOTGSCGAGFTFVASELSVYT 460  
QY 459 LTAITLERWHTTTHAMOLECKVOLRAASVMVLGTEFAFAALFLPFGISSYMKVSIQCLP 518  
DB 461 LVVILERWHTTYAVQLDQKRLRHAPIMLGGMLFSLTIATMPLVLGINSYMKVSIQCLP 520  
QY 519 MDIDSPSLQYVALLVNLVAFVVICGTHYILTVRNPVTIVSSSDTKIAKRMATLIF 578  
DB 521 MDVESTLSQVILSILLNVAVFVICACYIRIYFAVQNPCLTAPKDTKIAKMAILLIF 580  
QY 579 TDFLCNAPISFAISASLKVPLITVSKAILLVLPYIPNSCANPFLYIFTNFRDFFI 638  
DB 581 TDFTCNAPISFAISAAFKVPLITVTSKILLVLFYPVNSCANPFLYIFTNFRDFFI 640  
QY 639 LLSKFCYEQMAQIYRTTSSATHNFAHRSKSS 673  
DB 641 LLSRFCCCKRAELRYRK-----EFSATYSNCKN 669  
RESULT 12  
A49744  
lutropin-choriogonadotropin receptor precursor - rat  
N:Alternate names: lutalinizing hormone-choriogonadotropin receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 03-May-1994 #sequence\_revision 13-Sep-1998 #text\_change 13-Aug-1999  
C:Accession: A49744; A40545; A41343; A61453; A32460  
R:Koo, Y.B.; Ji, I.; Slaughter, R.G.; Ji, T.H.  
Endocrinology 128, 2297-2308, 1991  
A:Title: Structure of the lutalinizing hormone receptor gene and multiple exons of the cDNA  
A:Reference number: A49744; MUID:91209270; PMID:2019252  
A:Accession: A49744  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-700 <KOO>  
A:Cross-references: GB:M6917  
A:Note: authors translated the codon CAA for residue 307 as Glu, AAC for residue 355 as

R:Tsal-Morris, C.H.; Buczko, E.; Wang, W.; Xie, X.Z.; Dufau, M.L.  
J. Biol. Chem. 266, 11355-11359, 1991  
A:Title: Structural organization of the rat lutalinizing hormone (LH) receptor gene.  
A:Reference number: A40545; MUID:91250455; PMID:2040640  
A:Accession: A40545  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-320 <TSA>  
A:Cross-references: GB:M63918; GB:M63919; GB:M63920; GB:M63921; GB:M63922; GB:M63923  
R:McFarland, K.C.; Sprengel, R.; Phillips, H.S.; Koehler, M.; Rosemblyt, N.; Nikolic  
Science 245, 494-499, 1989  
A:Title: Lutropin-choriogonadotropin receptor: an unusual member of the G protein-coupled receptor family.  
A:Reference number: A41343; MUID:89332512; PMID:2502842  
A:Accession: A41343  
A:Molecule type: mRNA  
A:Residues: 1-700 <MCF>  
A:Cross-references: GB:M26199; MID:g205178; PIDN:AAA41528.1; PID:g205179  
R:Dufau, M.L.; Minegishi, T.; Buczko, E.S.; Delgado, C.J.; Zhang, R.  
J. Steroid Biochem. 33, 715-720, 1989  
A:Title: Characterization and structure of ovarian and testicular LH/hCG receptors.  
A:Reference number: A61453; MUID:90097014; PMID:2601325  
A:Accession: A61453  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-33, 'X', 35-37, 'X', 39, 'X', 41-44 <DUF>  
R:Roche, P.C.; Ryan, R.J.  
J. Biol. Chem. 264, 4636-4641, 1989  
A:Title: Purification, characterization, and amino-terminal sequence of rat ovarian LH/hCG receptor.  
A:Reference number: A32460; MUID:89174723; PMID:2925659  
A:Accession: A32460  
A:Molecule type: protein  
A:Residues: 27-32, 'LX', 35-37 <ROC>  
C:Genetics:  
A:Introns: 58/2; 82/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat F.153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
F.54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F.78-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F.103-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F.128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F.153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F.180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F.202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F.368-389/Domain: transmembrane #status predicted <TM1>  
F.400-422/Domain: transmembrane #status predicted <TM2>  
F.444-466/Domain: transmembrane #status predicted <TM3>  
F.489-511/Domain: transmembrane #status predicted <TM4>  
F.530-551/Domain: transmembrane #status predicted <TM5>  
F.575-598/Domain: transmembrane #status predicted <TM6>  
F.610-631/Domain: transmembrane #status predicted <TM7>  
F.103, 178, 199, 295, 303, 317/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F.647, 648/Binding site: palmitate (Cys) (covalent) #status predicted  
F.681/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted



Db 522 TLSQVYLTLLNVAFFACIYKIKYFAVRNPELMATNKTAKKMAILFTDTC 581  
 QY 584 MAPISFAISAKVPLITYSKAILLYFPYPPINSCANPPLAIFATKFNRRDFILLSKF 643  
 Db 582 MAPISFAISAAKVPPLITYSKAILLYFPYPPINSCANPPLAIFATKFNRRDFILLSKF 641  
 QY 644 GCYEMOQAIYRTTSSATHNFAHAKSCSS 673  
 Db 642 GCCKRAELRYRK-----DFSAYTSCKN 665

## RESULT 14

A40077  
 thyrotropin receptor precursor - dog  
 N:Alternate names: thyroid-stimulating hormone receptor; TSH receptor  
 C:Species: Canis lupus familiaris (dog)  
 C>Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 13-Aug-1999  
 C:Accession: A40077; S06933  
 R:Parmentier, M.; Libert, F.; Maenhaut, C.; Lefort, A.; Gerard, C.; Perret, J.; Van Sand  
 Science 246, 1620-1622, 1989  
 A:Title: Molecular cloning of the thyrotropin receptor.  
 A:Reference number: A40077; MUID:90084524; PMID:2556796  
 A:Accession: A40077  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-764 <P>  
 A:CROSS-references: GB:M29957; NID:g164098; PIDN:AAA30901.1; PID:g164099  
 R:Parmentier, M.; Libert, F.; Maenhaut, C.; Lefort, A.; Gerard, C.; Perret, J.; van Sand  
 Nucleic Acids Res. 17, 10493, 1989  
 A:Title: Nucleotide sequence of the dog thyrotropin receptor cDNA.  
 A:Reference number: S06933; MUID:9009886; PMID:2602159  
 A:Accession: S06933  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-764 <P>  
 A:CROSS-references: EMBL:X17146; NID:g849; PIDN:CAA35026.1; PID:g850  
 C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
 F:1-20/Domain: G protein-coupled receptor; glycoprotein; transmembrane protein  
 F:21-764/Product: thyrotropin receptor #status predicted <SIG>  
 F:53-76/Domain: leucine-rich alpha-2-glycoprotein repeat predicted <MAT>  
 F:77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:152-176/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F:179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
 F:201-225/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

Query Match 46.6%; Score 1673.5; DB 2; Length 764;

Best Local Similarity 47.1%; Pred. No. 2.le-108;

Matches 351; Conservative 116; Mismatches 217; Indels 61; Gaps 11;

QY 4 LNVSLAFLGTGGCHHWLCHCSN----RVFLCDSKVTEIPDLPNATELFLVTLKLR 59  
 Db 11 LLLALPRSLG-GRGCPSPCECHQEDFRV-TCKD--IHRPT-LPPSTOTLKFETOLK 65  
 QY 60 VIPKSGPAGGDLKTEISONDVLEADVFNPLKHLRIEKANLLYINPEAFQNL 119  
 Db 66 TIPSRAFNPLNRIYLSIDATLQRLSHSFNLSKMTHEIRNTRSLTSIDPDALKEL 125  
 QY 120 PSRLYLISNTGKHLPAVHKIOSLQK-VLLDQDNIHIVARNFMSGLSFEFVILWLS 178  
 Db 126 PLLKFLGIFTGLGVDPVTKYVSTOVFFLEITDNPYMASIPANAFGLCNETTLKLY 185  
 QY 179 KNGIEETHNCAFNGTDLDELNDNNLEELPNDVFOGA-SGPVILDISRTKVSHPNHC 237  
 Db 186 NNGFTSQGHAFNGTKLDVYLNKNKYLSAIDKDAFGVYSGPTLLDVSYSVTALPSKG 245  
 QY 238 LENLKLRASTYELKLLPLNLDKFLVMEASLYPSHCCAFANLKRQISELHPI-CNKSI 296  
 Db 246 LEHLKELIARTWTLLKKLPLSLSLHLTRADLSYPHCCAFKQKIRGILESLMCNESS 305

QY 297 LRQ-----DIDDMTOIGDORVSLTIDBPSYCKGSDMMY----- 329  
 Db 306 IRSLRORSVNTLNGPFDQEEYELGDSHAGYKDNSQFQDTDSNHYVFEFQDEILG 365  
 QY 330 -----NEFDYDLCEVVDVTCSPKPDAPNCPEDMGYNILRVLIWFIS 372  
 Db 366 FGQELKNPQEEETLQAFDSHYDYTVCGNEDMVCCTPKSDEPNCPEDMGYKFLRVWFVS 425  
 QY 373 ILAITCNTVVLVLTTSQYKLTVPRLMCLNLAFCIGIYLLLIASVDITKSOYHNYA 432  
 Db 426 LLALLGNVFLVLLTSHYKLTVPRLMCLNLAFCIGIYLLLIASVDITKSOYHNYA 485  
 QY 433 IDWOTGAGCDAAGFFTVFASLSVYTLTALTLEWHITTHAMOLECKVOLRHAASVNLG 492  
 Db 486 IDWOTGPGCNTAGFTTVFASLSVYTLTALTLEWHITTHAMOLECKVOLRHAASVNLG 545  
 QY 493 WTPFAAAALFFPIFGISSYMKVSIICLPMDIDSPISQLYVALLVNLVAFVVICGCTHIY 552  
 Db 546 WVCCELLALLPLVGISSYAKVSIICLPMDIETPLALAYIILVLLINIVAFIIVCSYKVIY 605  
 QY 553 LTVRNPTIVSSSDTKIARMAITLITDFLCMAPISEFFAISLSKVLPLITVSKAKILLVL 612  
 Db 606 ITVRNPNQNGDKDKTKIARMAVLIETDFCMAPISFYALSALMKNKPLITVTSKILLVL 665  
 QY 613 FYDINSCANPELYAIETKNFRDRFFILLSKFCGYEMOQAIYRTTSSATHNF-----HAR 667  
 Db 666 FYDINSCANPELYAIETKNFRDRFFILLSKFCGYEMOQAIYRTTSSATHNF-----HAR 725  
 QY 668 KSHCSAPRVNTSVYVLPVNLHSSON 692  
 Db 726 RDMQSLPNMQDEYELLENLHSLTPN 750

## RESULT 15

## QRHURH

thyrotropin receptor precursor - human  
 N:Alternate names: thyroid stimulatory hormone receptor (TSHR)  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Jan-1993 #sequence\_revision 01-Mar-1996 #text\_change 22-Jun-1999  
 C:Accession: A33789; A33786; A34052; A36120; S38280  
 R:Libert, F.; Lefort, A.; Gerard, C.; Parmentier, M.; Perret, J.; Ludgate, M.; Dumor  
 Biochem. Biophys. Res. Commun. 165, 1250-1255, 1989  
 A:Reference number: A33789; MUID:90121232; PMID:2610690  
 A:Accession: A33789  
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-86; 'L', 88-764 <LIT>  
 R:Nagayama, Y.; Kaufman, K.D.; Seto, P.; Rapoport, B.  
 Biochem. Biophys. Res. Commun. 165, 1184-1190, 1989  
 A:Title: Molecular cloning, sequence and functional expression of the cDNA for the h  
 A:Reference number: A33786; MUID:90121223; PMID:2558651  
 A:Accession: A33786  
 A:Molecule type: mRNA  
 A:Residues: 1-600; 'H', 602-764 <NAG>  
 A:CROSS-references: GB:M31774; NID:g340003; PIDN:AAA36783.1; PID:g340004  
 R:Mirzahi, M.; Loosfelt, H.; Atger, M.; Sar, S.; Guiochon-Mantel, A.; Milgrom, E.  
 Biochem. Biophys. Res. Commun. 166, 394-403, 1990  
 A:Title: Cloning, sequencing and expression of human TSH receptor.  
 A:Reference number: A34052; MUID:90147730; PMID:23021212  
 A:Accession: A34052  
 A:Molecule type: mRNA  
 A:Residues: 1-726; 'E', 728-743; 'K', 745-764 <MIS>  
 A:CROSS-references: GB:M32215; NID:g307524; PIDN:AAA61236.1; PID:g307525  
 A:Note: 13-Pro, 260-Pro, 414-His, 500-Leu, 634-Leu, and 744-Asn were also f  
 R:Frazier, A.L.; Robbins, L.S.; Stork, P.J.; Sprengel, R.; Segaloff, D.L.; Cone, R.D  
 Mol. Endocrinol. 4, 1264-1276, 1990  
 A:Title: Isolation of TSH and LH/CG receptor cDNAs from human thyroid: regulation by  
 A:Reference number: A36120; MUID:91155962; PMID:2293030  
 A:Accession: A36120  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-129; 'S', 131; 'AFS', 135-195; 'D', 197; 'F', 199-256; 'S', 258-263; 'A', 265-305,

0y	3	LLIYSLAFICGTCGSHHMLCHCSN-----RVFLCDSKVTETPDPNPAELRVLTKL 58
0y	9	: : : : :     : : : : :     : : : : :     : : : : :     : : : : :
0b	10	VLLDLDPRDLG-GAGCSSPCECQIEDPAAV--TCG----TQIYPS-LPSTQILKIEHL 64
0y	59	RVTGSPAGCGDKELKELSONDLEVTADVPSNLKPKHERTEKANNLLIYNPEAFON 118
0y	65	RTIPSHAFPMLEPNISRIYYSIDVTLQQLGSHSFYNLSKTYHETIRNLTNYLIDDPALKE 124
0b	119	LPSLRYLITSGTKHLPVAVHKIQSIGQ--KVLVDIODINIHIIVARNSPGMLSPESVILML 177
0y	125	: : : : :     : : : : :     : : : : :     : : : : :     : : : : :
0b	178	LPPLAFAGTPTGLKAMPOLTKTYVDFIIEITDTPMYTSPYVNAFGICNRYETLKL 184
0y	179	SKNGIEETHHCYACNGTODELANSDNNLLELPNDVPOGA--SGPVILDISRTKVIHSPNH 236
0y	185	YNGSTFVQVAFNRKIDVAYLNKKYLLVITDKDAQVSGPSLSDVSTWPTSLR 244
0y	237	GLENLKILRARSTYALKPLNDKPYPTLMEASITVPSSHCAPANKLRSLEHPT--CNKS 295
0y	245	GLERLKLILARMTYTLAKPLSLSPILHTRADLSYPSSHCAPFNKKIRGILLESIMKNES 304
0b	296	TL-----RQIDDMT-----QIGDQARVLID-----DEPSY 321
0y	305	SMQSLQRKESVNALNSPLHQEYENIGDSITGVYKFKQDTHNHHAYVFFSEDEEII 364
0b	322	KGSDN-----MYNEPDTLCNVDVTCSPKPDAPNCEIDIMYILRWLWFT 371
0y	365	CPQELARQWZEITLQAPDSNDHYITCGDSEAWCFPSDEPNCEIDIMYILRWLWFT 424
0b	372	SILATNGMYPLVLLTYSOKLYVPFKLKNLAFADLCIGYITLLTASVDHKTQSYNH 431
0y		: : : : :     : : : : :     : : : : :     : : : : :     : : : : :

1	3594	100.0	692	1	F8HR_RAT
2	3420	95.2	692	1	F8HR_MOUSE
3	3235.5	90.0	695	1	F8HR_HUMAN
4	3226.3	89.8	695	1	F8HR_MACACA
5	3206.5	89.3	695	1	F8HR_BOVINE
6	3180.5	87.7	695	1	F8HR_PIG
7	3133.5	87.4	695	1	F8HR_MOUSE
8	3114.0	87.4	694	1	F8HR_HUMAN
9	3076.5	85.6	687	1	F8HR_EQUUS
10	2605.5	72.5	693	1	F8HR_CHICK
11	1807.5	50.3	701	1	L8HR_PIG
12	1807.5	50.3	701	1	L8HR_BOVINE
13	1799	50.1	700	1	L8HR_MOUSE
14	1797	50.0	700	1	L8HR_RAT
15	1776	49.4	699	1	L8HR_HUMAN
16	1766.5	49.2	676	1	L8HR_CALAJA
17	1673.5	46.6	764	1	T8HR_CANFA
18	1655	46.0	764	1	T8HR_HUMAN
19	1653.5	46.0	764	1	T8HR_MOUSE
20	1642.5	45.7	763	1	T8HR_BOVINE
21	1636.5	45.4	764	1	T8HR_SHEEP
22	1632.5	45.4	764	1	T8HR_RAT
23	1589.5	44.2	538	1	L8HR_CHICK
24	1589.5	44.2	538	1	L8HR_MOUSE
25	1256.5	27.0	807	1	LGR5_HUMAN
26	684	17.9	807	1	LGR5_MOUSE
27	636	17.7	807	1	LGR5_HUMAN
28	596.5	16.3	951	1	LGR4_RAT
29	571	15.9	951	1	LGR4_RAT
30	522.5	14.5	1115	1	GPCR_LYMNST
31	517.5	14.4	828	1	LGR6_HUMAN
32	483.5	13.5	757	1	LGR7_HUMAN
33	472.5	13.1	737	1	LGR8_MOUSE

SMART: SM00013; LRRNT: 1.  
 DR PROSITE: PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 DR PROSITE: PS0262; G-PROTEIN RECP\_F2\_1; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 Phosphorylation; Repeat; Leucine-rich repeat.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 692 FOLLICLE STIMULATING HORMONE RECEPTOR.  
 FT DOMAIN 18 365 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 366 386 1 (POTENTIAL).  
 FT DOMAIN 387 397 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 398 420 2 (POTENTIAL).  
 FT DOMAIN 421 442 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 443 464 3 (POTENTIAL).  
 FT DOMAIN 465 484 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 485 507 4 (POTENTIAL).  
 FT DOMAIN 508 527 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 528 549 5 (POTENTIAL).  
 FT DOMAIN 550 572 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 573 596 6 (POTENTIAL).  
 FT DOMAIN 597 607 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 608 629 7 (POTENTIAL).  
 FT DOMAIN 630 692 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 44 68 LRR 1.  
 FT REPEAT 69 93 LRR 2.  
 FT REPEAT 119 143 LRR 3.  
 FT REPEAT 170 192 LRR 4.  
 FT REPEAT 193 216 LRR 5.  
 FT REPEAT 218 240 LRR 6.  
 FT DISULFID 441 516 BY SIMILARITY.  
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 692 AA; 77681 MW; 267EA78C7CFD8EC6 CRC64;  
 Query Match 100.0%; Score 3594; DB 1; Length 692;  
 Best Local Similarity 100.0%; Pred. No. 2e-222;  
 Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MALLVSLALFLGTGSGCHHNLCHSNNRVFLCQSKVTEIPTDLPNRAIELRFLVTKURV 60  
 DB 1 MALLVSLALFLGTGSGCHHNLCHSNNRVFLCQSKVTEIPTDLPNRAIELRFLVTKURV 60  
 OY 61 IPKGSFAGFGLKEIETSONDVLEIADVSNLPKLHEIRKANNLLYINPEAFQNP 120  
 DB 61 IPKGSFAGFGLKEIETSONDVLEIADVSNLPKLHEIRKANNLLYINPEAFQNP 120  
 OY 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIODNINIHVARNFPMGLSFESVILWLSKN 180  
 DB 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIODNINIHVARNFPMGLSFESVILWLSKN 180  
 OY 181 GIEETHNCAFNGTQDLDELNLSDNNLELPNDVFGASGPVILDSRTKVSHPNGLN 240  
 DB 181 GIEETHNCAFNGTQDLDELNLSDNNLELPNDVFGASGPVILDSRTKVSHPNGLN 240  
 OY 241 LKLRARSTYRLKLPNDKFTLMEASLTTPSHCCAFANLKRQISELHPICNKSILROD 300  
 DB 241 LKLRARSTYRLKLPNDKFTLMEASLTTPSHCCAFANLKRQISELHPICNKSILROD 300  
 OY 301 IDDMTQIGDQVSLDDPSYSGKSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMG 360  
 DB 301 IDDMTQIGDQVSLDDPSYSGKSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMG 360  
 OY 361 YNILRVLWFSILAITGNTVVLVLTTSQYKLVTPVFLMNLAFADLCIGIYLLIASV 420  
 DB 361 YNILRVLWFSILAITGNTVVLVLTTSQYKLVTPVFLMNLAFADLCIGIYLLIASV 420  
 OY 421 DIHTKSQYHNVAIDQTCAGDAGFFTVFASVLSVYTLTTLERWHTITHAMOLECKV 480  
 DB 421 DIHTKSQYHNVAIDQTCAGDAGFFTVFASVLSVYTLTTLERWHTITHAMOLECKV 480  
 OY 481 QLRHAASVNLGWTFAFAAALFPFISGYMKVSIKLPMDIDSPLSQLYVALLVNLVLA 540  
 DB 481 QLRHAASVNLGWTFAFAAALFPFISGYMKVSIKLPMDIDSPLSQLYVALLVNLVLA 540

OY 541 FVVICGCTHYIYLVNPTIVSSSDTKIAKRMATLIPTDFLCNAPISFFAISLKVPL 600  
 DB 541 FVVICGCTHYIYLVNPTIVSSSDTKIAKRMATLIPTDFLCNAPISFFAISLKVPL 600  
 OY 601 ITVSKAKILLVLFYPIINSCANPELYAIFTKNFRDFFILLSKFGCYEMQAIYRTETSSA 660  
 DB 601 ITVSKAKILLVLFYPIINSCANPELYAIFTKNFRDFFILLSKFGCYEMQAIYRTETSSA 660  
 OY 661 THNFHARKSHCSSAPRVNTSYVLPLNHSQN 692  
 DB 661 THNFHARKSHCSSAPRVNTSYVLPLNHSQN 692

## RESULT 2

FSHR\_MOUSE  
 ID FSHR\_MOUSE STANDARD; PRT: 692 AA.  
 AC P35378; O9QW8; O9DAC2;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Follicotropin receptor).  
 DE FSHR.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv; TISSUE=Testis;  
 RA Tena-Sempere M., Manna P.R., Huhtaniemi I.T.;  
 RT "Molecular cloning of the mouse follicle stimulating hormone receptor  
 RT complementary deoxyribonucleic acid: functional expression of  
 RT alternatively spliced variants and receptor inactivation by a C566T  
 RT transition in exon 7 of the coding sequence.";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakura I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,  
 RA Yuzhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE OF 1-51 FROM N.A.  
 RX MEDLINE=93093308; PubMed=1459341;  
 RA Huhtaniemi I.T., Eskola V., Pakarinen P., Matikainen T.,  
 RA Sprengel R.;  
 RT "The murine luteinizing hormone and follicle-stimulating hormone  
 RT receptor genes: transcription initiation sites, putative promoter  
 RT sequences and promoter activity.";  
 RL Mol. Cell. Endocrinol. 88:55-66(1992).  
 CC -!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY  
 CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
 CC ADENYLATE CYCLASE.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC PSH/ASH/TSB SUBFAMILY  
CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
CC  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC EMBL: AF095642; AAC67559.1; --  
CC EMBL: AK016635; BAB30351.1; --  
CC EMBL: S49632; AAB24401.1; --  
CC EMBL: M87570; AAK37641.1; --  
CC XGD: M87570; AAK37641.1; --  
CC InterPro: IPR000026; GPCR\_Rhodopsin.  
CC InterPro: IPR001611; LRR\_Nterm.  
CC InterPro: IPR000372; LRR\_Nterm.  
CC Pfam: PF00001; Lrr\_1; 1.  
CC Pfam: PF05560; Lrr\_3.  
CC Pfam: PF01462; LRRNT; 1.  
CC PRINTS: PR00237; GPCR\_Rhodopsin.  
CC SMART: SM00013; LRRNT; 1.  
CC PROSITE: PS00337; G-PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE: PS00362; G-PROTEIN\_RECEP\_F1\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
CC Phosphorylation; Repeat; Leucine-rich repeat.  
CC SIGNAL 1 17 POTENTIAL.  
CC CHAIN 18 692  
CC TRANSMEN 365 382  
CC TRANSMEN 387 397  
CC TRANSMEN 398 420  
CC TRANSMEN 421 442  
CC TRANSMEN 443 464  
CC TRANSMEN 465 484  
CC TRANSMEN 485 507  
CC TRANSMEN 508 527  
CC TRANSMEN 528 549  
CC TRANSMEN 550 572  
CC TRANSMEN 573 596  
CC TRANSMEN 597 607  
CC TRANSMEN 608 629  
CC TRANSMEN 630 692  
CC REPEAT 4 68  
CC REPEAT 119 143  
CC REPEAT 170 192  
CC REPEAT 193 216  
CC REPEAT 218 240  
CC DISULFID 441 516 BY SIMILARITY.  
CC CARBOHYD. 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD. 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD. 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CONFLICT 436 436 O -> K (IN REF. 2).  
CC SEQUENCE 692 AA; 485729180563A44 CRC64;  
Query Match 95.2%; Score 3420; DB 1; Length 692;  
Best Local Similarity 94.2%; Pred. No. 2.6e-211;  
Matches 632; Conservative 21; Mismatches 19; Indels 0; Gaps 0;  
Cc 1 MALLVSLAFLPTGSGCHWLCNCHSRVFLCDSKVTEIPDLPRLNATELRVFLKRV 60  
Db 1 MALLVSLAFLPTGSGCHWLCNCHSRVFLCDSKVTEIPDLPRLNATELRVFLKRV 60  
Oy 61 IPKGSFGADLEKLEISQNDVLEADVPSNLPKLEIRKERNKLLINPEAFONLP 120  
Db 61 IPKGSFGADLEKLEISQNDVLEADVPSNLPKLEIRKERNKLLINPEAFONLP 120  
Oy 121 SLRYLLISNTGKHLPAVKIQLQVLLDIQDNIHIIARNSPFGLSFESVILWLSKN 180

Db 121 SLRYLLISNTGKHLPAVKIQLQVLLDIQDNIHIIARNSPFGLSFESVILWLSKN 180  
Oy 181 GIEEIHNCANCTQDELMLSDNNWLEELNDVFOGASGPIVDISRTKYSLPNIWLEN 240  
Db 181 GIEEIHNCANCTQDELMLSDNNWLEELNDVFOGASGPIVDISRTKYSLPNIWLEN 240  
Oy 241 LKLRARSTYRLKLPDLKFTVLMFASLTYPHSCCAFANLKRQISELHPICNKSILROD 300  
Db 241 LKLRARSTYRLKLPDLKFTVLMFASLTYPHSCCAFANLKRQISELHPICNKSILROD 300  
Oy 301 IDDMTOIGDQPSVLIIDEPSTGKSGDMYNEFDYDLCNEVDYVTCSPKPDANPCEDIMG 360  
Db 301 IDDMTOIGDQPSVLIIDEPSTGKSGDMYNEFDYDLCNEVDYVTCSPKPDANPCEDIMG 360  
Oy 361 YNLRLVLPNFISILAITGNTTVLVLTTSQYKLTVPFLMCLNLAFAADLCIGITLLLIJASV 420  
Db 361 YNLRLVLPNFISILAITGNTTVLVLTTSQYKLTVPFLMCLNLAFAADLCIGITLLLIJASV 420  
Oy 421 DIHTSOYHNYAIIDMOTGAGCDAGFFTFVASELSVYTLTALTLEHWHITTHAMQLECKV 480  
Db 421 DIHTSOYHNYAIIDMOTGAGCDAGFFTFVASELSVYTLTALTLEHWHITTHAMQLECKV 480  
Oy 481 QLRHAASVYLVGMFTFAAALPFIIGISSTMYKVSICLPMIDPSLPSLYVALLVNLALA 540  
Db 481 QLRHAASVYLVGMFTFAAALPFIIGISSTMYKVSICLPMIDPSLPSLYVALLVNLALA 540  
Oy 541 FVYICGCVTHIYLVTRNPTIVSSSDTKIARKMATLIFTDFLCMAPIFFAISAISKVPL 600  
Db 541 FVYICGCVTHIYLVTRNPTIVSSSDTKIARKMATLIFTDFLCMAPIFFAISAISKVPL 600  
Oy 601 ITYSKAKILLVLFYPIINSCANPFLYAITFKNFRDFFILLSKFCGYEQMAQIYRTETSSA 660  
Db 601 ITYSKAKILLVLFYPIINSCANPFLYAITFKNFRDFFILLSKFCGYEQMAQIYRTETSSA 660  
Oy 661 THNFHARKNCSSAPRVTHSVYLVPLNLSQSN 692  
Db 661 THNFHARKNCSSAPRVTHSVYLVPLNLSQSN 692  
RESULT 3  
FSHR\_HUMAN  
ID FSHR\_HUMAN STANDARD: PRT: 695 AA.  
AC P23945;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Follicle stimulating hormone receptor precursor (FSH-R) (Poultropin  
DE receptor).  
GN FSHR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=9122171; PubMed=1709010;  
RA Minegishi T., Nakamura K., Takakura Y., Ibuki Y., Igarashi M.;  
RT "Cloning and sequencing of human FSH receptor cDNA";  
RL Biochem. Biophys. Res. Commun. 175:1125-1130(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=93246012; PubMed=1301382;  
RA Melton C.A., Cheng S.Y., Nugent N.P., Schweichhardt R.L.,  
RA Chappel S.C., Overton S.A., Wanda G.D., Kuzaja J.B., Luchette C.A.,  
RA "The cloning of the human follicle stimulating hormone receptor and  
RT its expression in COS-7, CHO, and Y-1 cells";  
RL Mol. Cell. Endocrinol. 89:141-151(1992).  
RN [3]  
RP SEQUENCE FROM N.A.



RA Tilly L.T., Alhara T., Nishimori K., Jai X.-C., Billig H.,  
RA Kowalski K.I., Perlas E.A., Hsueh A.J.;  
RL Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 1-342 FROM N.A.  
RC TISSUE-Testis;  
RX MEDLINE-93075197; PubMed-1359889;  
RA Gromoll J., Gudermann T., Nieschlag E.;  
RT "Molecular cloning of a truncated isoform of the human follicle  
RT stimulating hormone receptor.";  
RL Biochem. Biophys. Res. Commun. 188:1077-1083(1992).  
RN [5]  
RX SEQUENCE OF 1-51 FROM N.A.  
RY MEDLINE-95011044; PubMed-7926278;  
RA Gromoll J., Dankbar B., Gudermann T.;  
RT "Characterization of the 5' flanking region of the human follicle-  
RT stimulating hormone receptor gene.";  
RL Mol. Cell. Endocrinol. 102:93-102(1994).  
RN [6]  
RX 3D-STRUCTURE MODELING OF 49-228.  
RY MEDLINE-96363672; PubMed-8747461;  
RA Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H.,  
RA Hendrickson W.A., el Tayar N.;  
RT "Structural predictions for the ligand-binding region of glycoprotein  
RT hormone receptors and the nature of hormone-receptor interactions.";  
RL Structure 3:1341-1353(1995).  
CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY  
CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
CC ADENYLATE CYCLASE.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: SERTOLI CELLS AND OVARIAN GRANULOSA CELLS.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC FSH/LSH/TSH SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 5 LEUCINE-RICH REPEATS (LRR).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M65085; AAA52477.1; -  
DR EMBL; S59900; AAB26480.1; -  
DR EMBL; M95489; AAB32478.1; -  
DR EMBL; X68044; CAA48179.1; -  
DR EMBL; S73199; AAB32071.1; -  
DR PIR; JN0122; JN0122.  
DR PDB; 1XUN; 15-MAY-97.  
DR Genew; HGNC:3969; FSHR.  
DR MIM; 136435; -  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR Pfam; PF00560; LRR; 3.  
DR Pfam; PF01462; LRRNT; 1.  
DR SMART; SM00013; LRRNT; 1.  
DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS00262; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing;  
KW 3D-structure.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.  
FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 367 387 1 (POTENTIAL).  
FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 399 421 2 (POTENTIAL).  
FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).

TRANSMEM	444	465	3 (POTENTIAL).
FT DOMAIN	466	485	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	486	508	4 (POTENTIAL).
FT DOMAIN	509	528	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	529	550	5 (POTENTIAL).
FT DOMAIN	551	573	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	574	597	6 (POTENTIAL).
FT DOMAIN	598	608	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	609	630	7 (POTENTIAL).
FT DOMAIN	631	695	CYTOPLASMIC (POTENTIAL).
FT REPEAT	69	93	LRR 1.
FT REPEAT	119	143	LRR 2.
FT REPEAT	170	192	LRR 3.
FT REPEAT	193	216	LRR 4.
FT REPEAT	218	240	LRR 5.
FT DISULFID	442	517	BY SIMILARITY.
FT CARBOHYD	191	191	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	199	199	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	293	293	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	318	318	N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC	224	285	MISSING (IN SHORT ISOFORM).
FT VARSPLIC	342	695	MISSING (IN SHORT ISOFORM).
FT CONFLICT	13	13	S -> R (IN REF. 4).
FT CONFLICT	112	112	N -> T (IN REF. 1).
FT CONFLICT	197	198	EL -> AV (IN REF. 1).
FT CONFLICT	295	295	S -> P (IN REF. 4).
FT CONFLICT	307	307	T -> A (IN REF. 1).
FT CONFLICT	680	680	N -> S (IN REF. 1).
SEQ SEQUENCE	695 AA; 78294 MM; 723B8E71F76D2C5 CRC64;		

Query Match 90.0%; Score 3235.5; DB 1; Length 695;  
Best Local Similarity 89.5%; Pred. No. 1.6e-199;  
Matches 622; Conservative 31; Mismatches 39; Indels 3; Caps 2;

QY	1	MALLVSLLAFLGTGSGCHHMLCHCSNRVFLCQDSKVTETPTDLPNAIELRFLVKLRV	60
DB <td>1<td>MALLVSLLAFLSLGSGCHHMLCHCSNRVFLCQESKVTETPTDLPNAIELRFLVKLRV<td>60</td></td></td>	1 <td>MALLVSLLAFLSLGSGCHHMLCHCSNRVFLCQESKVTETPTDLPNAIELRFLVKLRV<td>60</td></td>	MALLVSLLAFLSLGSGCHHMLCHCSNRVFLCQESKVTETPTDLPNAIELRFLVKLRV <td>60</td>	60
QY <td>61<td>IPKGFAGDGLKLEKIEISQNDVLEADVFNLPKLHEIRKANNLLYINPEAFONLP<td>120</td></td></td>	61 <td>IPKGFAGDGLKLEKIEISQNDVLEADVFNLPKLHEIRKANNLLYINPEAFONLP<td>120</td></td>	IPKGFAGDGLKLEKIEISQNDVLEADVFNLPKLHEIRKANNLLYINPEAFONLP <td>120</td>	120
DB <td>61<td>IQKGFAGDGLKLEKIEISQNDVLEADVFNLPKLHEIRKANNLLYINPEAFONLP<td>120</td></td></td>	61 <td>IQKGFAGDGLKLEKIEISQNDVLEADVFNLPKLHEIRKANNLLYINPEAFONLP<td>120</td></td>	IQKGFAGDGLKLEKIEISQNDVLEADVFNLPKLHEIRKANNLLYINPEAFONLP <td>120</td>	120
QY <td>121<td>SLRYLLISNTGKHLPAVHKIOSLOKVLIDIODNINIHIVARNFSGFESVILWLSKN<td>180</td></td></td>	121 <td>SLRYLLISNTGKHLPAVHKIOSLOKVLIDIODNINIHIVARNFSGFESVILWLSKN<td>180</td></td>	SLRYLLISNTGKHLPAVHKIOSLOKVLIDIODNINIHIVARNFSGFESVILWLSKN <td>180</td>	180
DB <td>121<td>NQYLLISNTGKHLPAVHKIOSLOKVLIDIODNINIHIVARNFSGFESVILWLSKN<td>180</td></td></td>	121 <td>NQYLLISNTGKHLPAVHKIOSLOKVLIDIODNINIHIVARNFSGFESVILWLSKN<td>180</td></td>	NQYLLISNTGKHLPAVHKIOSLOKVLIDIODNINIHIVARNFSGFESVILWLSKN <td>180</td>	180
QY <td>181<td>GIEETHNCAFNGTQDDELNLSDNNNLEELPNDVFOGASGPVILDISRTKVHSLPNHLEN<td>240</td></td></td>	181 <td>GIEETHNCAFNGTQDDELNLSDNNNLEELPNDVFOGASGPVILDISRTKVHSLPNHLEN<td>240</td></td>	GIEETHNCAFNGTQDDELNLSDNNNLEELPNDVFOGASGPVILDISRTKVHSLPNHLEN <td>240</td>	240
DB <td>181<td>GIQETHNCAFNGTQDDELNLSDNNNLEELPNDVFOGASGPVILDISRTKVHSLPNHLEN<td>240</td></td></td>	181 <td>GIQETHNCAFNGTQDDELNLSDNNNLEELPNDVFOGASGPVILDISRTKVHSLPNHLEN<td>240</td></td>	GIQETHNCAFNGTQDDELNLSDNNNLEELPNDVFOGASGPVILDISRTKVHSLPNHLEN <td>240</td>	240
QY <td>241<td>LKKLRARSTYRLKLPNLDKFTVLMASLTYSHCACAFANLKRQISELHPICKNLSLRQD<td>300</td></td></td>	241 <td>LKKLRARSTYRLKLPNLDKFTVLMASLTYSHCACAFANLKRQISELHPICKNLSLRQD<td>300</td></td>	LKKLRARSTYRLKLPNLDKFTVLMASLTYSHCACAFANLKRQISELHPICKNLSLRQD <td>300</td>	300
DB <td>241<td>LKKLRARSTYRLKLPNLDKFTVLMASLTYSHCACAFANLKRQISELHPICKNLSLRQD<td>300</td></td></td>	241 <td>LKKLRARSTYRLKLPNLDKFTVLMASLTYSHCACAFANLKRQISELHPICKNLSLRQD<td>300</td></td>	LKKLRARSTYRLKLPNLDKFTVLMASLTYSHCACAFANLKRQISELHPICKNLSLRQD <td>300</td>	300
QY <td>301<td>IDDMTOIGDQVRSLIDD-EPSTYKSGSDMMYNEFDYDLCNEVDVDTCSKPDAENPCEDIM<td>359</td></td></td>	301 <td>IDDMTOIGDQVRSLIDD-EPSTYKSGSDMMYNEFDYDLCNEVDVDTCSKPDAENPCEDIM<td>359</td></td>	IDDMTOIGDQVRSLIDD-EPSTYKSGSDMMYNEFDYDLCNEVDVDTCSKPDAENPCEDIM <td>359</td>	359
DB <td>301<td>VDYMTQTRGORSLSAEDNESSYRGDMYTFEDYDLCNEVDVDTCSKPDAENPCEDIM<td>360</td></td></td>	301 <td>VDYMTQTRGORSLSAEDNESSYRGDMYTFEDYDLCNEVDVDTCSKPDAENPCEDIM<td>360</td></td>	VDYMTQTRGORSLSAEDNESSYRGDMYTFEDYDLCNEVDVDTCSKPDAENPCEDIM <td>360</td>	360
QY <td>360<td>GYNILRVLIWFISILAITGNTTVLVVLTTSQYKLTVPFLMCLNLAFCICIGIYLLIAS<td>419</td></td></td>	360 <td>GYNILRVLIWFISILAITGNTTVLVVLTTSQYKLTVPFLMCLNLAFCICIGIYLLIAS<td>419</td></td>	GYNILRVLIWFISILAITGNTTVLVVLTTSQYKLTVPFLMCLNLAFCICIGIYLLIAS <td>419</td>	419
DB <td>361<td>GYNILRVLIWFISILAITGNTTVLVVLTTSQYKLTVPFLMCLNLAFCICIGIYLLIAS<td>420</td></td></td>	361 <td>GYNILRVLIWFISILAITGNTTVLVVLTTSQYKLTVPFLMCLNLAFCICIGIYLLIAS<td>420</td></td>	GYNILRVLIWFISILAITGNTTVLVVLTTSQYKLTVPFLMCLNLAFCICIGIYLLIAS <td>420</td>	420
QY <td>420<td>VDIHTKSOYHNVAIDMOTGAGCDAAGFTTFVASELSVYTLTALTRERWHTITHAMOLECK<td>479</td></td></td>	420 <td>VDIHTKSOYHNVAIDMOTGAGCDAAGFTTFVASELSVYTLTALTRERWHTITHAMOLECK<td>479</td></td>	VDIHTKSOYHNVAIDMOTGAGCDAAGFTTFVASELSVYTLTALTRERWHTITHAMOLECK <td>479</td>	479
DB <td>421<td>VDIHTKSOYHNVAIDMOTGAGCDAAGFTTFVASELSVYTLTALTRERWHTITHAMOLECK<td>480</td></td></td>	421 <td>VDIHTKSOYHNVAIDMOTGAGCDAAGFTTFVASELSVYTLTALTRERWHTITHAMOLECK<td>480</td></td>	VDIHTKSOYHNVAIDMOTGAGCDAAGFTTFVASELSVYTLTALTRERWHTITHAMOLECK <td>480</td>	480
QY <td>480<td>VOLRHAASVYVLGWTFAFAALFFIFGSISSYKMKVSTCLPMDIDSPISQVYVALLVNL<td>539</td></td></td>	480 <td>VOLRHAASVYVLGWTFAFAALFFIFGSISSYKMKVSTCLPMDIDSPISQVYVALLVNL<td>539</td></td>	VOLRHAASVYVLGWTFAFAALFFIFGSISSYKMKVSTCLPMDIDSPISQVYVALLVNL <td>539</td>	539
DB <td>481<td>VOLRHAASVYVLGWTFAFAALFFIFGSISSYKMKVSTCLPMDIDSPISQVYVALLVNL<td>540</td></td></td>	481 <td>VOLRHAASVYVLGWTFAFAALFFIFGSISSYKMKVSTCLPMDIDSPISQVYVALLVNL<td>540</td></td>	VOLRHAASVYVLGWTFAFAALFFIFGSISSYKMKVSTCLPMDIDSPISQVYVALLVNL <td>540</td>	540
QY <td>540<td>AFVVICGCTHYIYLTVRNPTIVSSSDTKIARMMATLIETDFLCMAPIFFFAISASIKVP<td>599</td></td></td>	540 <td>AFVVICGCTHYIYLTVRNPTIVSSSDTKIARMMATLIETDFLCMAPIFFFAISASIKVP<td>599</td></td>	AFVVICGCTHYIYLTVRNPTIVSSSDTKIARMMATLIETDFLCMAPIFFFAISASIKVP <td>599</td>	599
DB <td>541<td>AFVVICGCTHYIYLTVRNPTIVSSSDTKIARMMATLIETDFLCMAPIFFFAISASIKVP<td>600</td></td></td>	541 <td>AFVVICGCTHYIYLTVRNPTIVSSSDTKIARMMATLIETDFLCMAPIFFFAISASIKVP<td>600</td></td>	AFVVICGCTHYIYLTVRNPTIVSSSDTKIARMMATLIETDFLCMAPIFFFAISASIKVP <td>600</td>	600

OY 600 LITVSKAKILLVLPYNSCANPFLVATKPRDFILLKPGCYEQAOQIYRTSS 659  
 DB 601 LITVSKAKILLVLPYNSCANPFLVATKPRDFILLKPGCYEQAOQIYRTSS 660  
 OY 660 ATNFHARKSHCCSAPRTN--SYVLVPLHSSON 692  
 DB 661 TWNTHPRNCSSAPRTNGSYVLVPLSLAQN 695

RESULT 4  
 FSHR\_MACFA STANDARD; PRT: 695 AA.  
 AC P32212;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 18-OCT-1993 (Rel. 27, Last sequence update)  
 DT 18-OCT-2001 (Rel. 40, Last annotation update)  
 DE Follitropin stimulating hormone receptor precursor (FSH-R) (follitropin receptor).  
 GN FSHR.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryote; Mammalia; Chordata; Ctenalia; Vertebrata; Euarchontom; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopitheciinae; Macaca.  
 OC NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA MEDLINE=94071854; PubMed=7504463;  
 RA Gromoll J., Dankbar B., Sharma R.S., Nieschlag E.;  
 RT Molecular cloning of the testicular follicle stimulating hormone receptor of the non human primate Macaca fascicularis and identification of multiple transcripts in the testis.\*;  
 RT Biochem. Biophys. Res. Commun. 196:1066-1072(1993).  
 CC -1- THIS RECEPTOR IS A FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. FSH/LSH/FSH SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
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 CC EMBL: Y74454; CAA52463.1;  
 CC PIR: S36432; S36433;  
 CC PIR: JN0898; JN0898.  
 CC HSSP: P23945; 1XDN.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR Pfam: PF00560; LRR; 3.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR SMART: SM00013; LRRNT; 1.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE: PS00262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat.  
 FT CHAIN 1 695  
 FT DOMAIN 18 366 POTENTIAL  
 FT DOMAIN 367 387 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 388 398 1 (POTENTIAL).  
 FT DOMAIN 399 421 2 (POTENTIAL).  
 FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 444 465 3 (POTENTIAL).  
 FT TRANSMEM 444 465

FT DOMAIN 466 485  
 FT TRANSMEM 486 508 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 509 528 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 529 550 5 (POTENTIAL).  
 FT DOMAIN 551 573 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 574 596 7 (POTENTIAL).  
 FT DOMAIN 597 619 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 620 630 7 (POTENTIAL).  
 FT DOMAIN 631 695 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 44 68 LRR 1;  
 FT REPEAT 69 93 LRR 2;  
 FT REPEAT 119 143 LRR 3;  
 FT REPEAT 170 192 LRR 4;  
 FT REPEAT 218 216 LRR 5;  
 FT REPEAT 240 240 LRR 6;  
 FT DISULFID 442 517 BY SIMILARITY.  
 FT CARBOHYD 191 191 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 199 199 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 318 318 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 695 AA; 78343 MW; 0D60A233729B5250 CRC64;  
 Query Watch 89.84; Score 3226.5; DB 1; Length 695;  
 Best Local Similarity 89.44; Pred No 66-199;  
 Matches 621; Conservative 30; Mismatches 41; Indels 3; Gaps 2;  
 OY 1 MALLVSLFLAFLGTGGCHHWCNRRVFLCQDSKVTEIPDLPRNAELRVLTKLRV 60  
 DB 1 MALLVSLFLAFLGTGGCHHWCNRRVFLCQDSKVTEIPDLPRNAELRVLTKLRV 60  
 OY 61 IPKGSFAGGDLKIEISONDVLEIADVFNLPKLIHEIRKANNLLYINPEAFONLP 120  
 DB 61 IPKGSFAGGDLKIEISONDVLEIADVFNLPKLIHEIRKANNLLYINPEAFONLP 120  
 OY 61 IOKGAFSGGDLKIEISONDVLEIADVFNLPKLIHEIRKANNLLYINPEAFONLP 120  
 DB 61 IOKGAFSGGDLKIEISONDVLEIADVFNLPKLIHEIRKANNLLYINPEAFONLP 120  
 OY 121 SURLYISNFGKHLPAVHKIOSLQVLLDIODNINHIVARNSPMGLSFESVYILMSKN 180  
 DB 121 SURLYISNFGKHLPAVHKIOSLQVLLDIODNINHIVARNSPMGLSFESVYILMSKN 180  
 OY 181 GTEETHCANGTQDELINSDNNLELENDVFGAGSGVLDISPTKVSHPNKGLEN 240  
 DB 181 GTEETHCANGTQDELINSDNNLELENDVFGAGSGVLDISPTKVSHPNKGLEN 240  
 OY 181 GIOETHCANGTQDELINSDNNLELENDVFGAGSGVLDISPTKVSHPNKGLEN 240  
 DB 181 GIOETHCANGTQDELINSDNNLELENDVFGAGSGVLDISPTKVSHPNKGLEN 240  
 OY 241 LKLRARSTYRLKLPNLPKFLPMAASLTYPHCCAFANLKRQISELHPICNKSILROD 300  
 DB 241 LKLRARSTYRLKLPNLPKFLPMAASLTYPHCCAFANLKRQISELHPICNKSILROD 300  
 OY 241 LKLRARSTYRLKLPNLPKFLPMAASLTYPHCCAFANLKRQISELHPICNKSILROD 300  
 DB 241 LKLRARSTYRLKLPNLPKFLPMAASLTYPHCCAFANLKRQISELHPICNKSILROD 300  
 OY 301 IDMTQIGQQRVSLIDD-EPYSGKSDMNTNEFDYDLCNEVDYVTCSPKPAFNPCEIM 359  
 DB 301 IDMTQIGQQRVSLIDD-EPYSGKSDMNTNEFDYDLCNEVDYVTCSPKPAFNPCEIM 359  
 OY 301 VDMYOTRGORSLSLAEDNESSYRGFDYTAEDYDLCNEVDYVTCSPKPAFNPCEIM 360  
 DB 301 VDMYOTRGORSLSLAEDNESSYRGFDYTAEDYDLCNEVDYVTCSPKPAFNPCEIM 360  
 OY 360 GYNILRVLIWFTISILAITNTVTVVLTQYKLVTPRTMCNLAFAOLCIGIYLLILAS 419  
 DB 360 GYNILRVLIWFTISILAITNTVTVVLTQYKLVTPRTMCNLAFAOLCIGIYLLILAS 419  
 OY 361 GYNILRVLIWFTISILAITNTVTVVLTQYKLVTPRTMCNLAFAOLCIGIYLLILAS 420  
 DB 361 GYNILRVLIWFTISILAITNTVTVVLTQYKLVTPRTMCNLAFAOLCIGIYLLILAS 420  
 OY 420 VDIHTKSOYHVAIDMOTGACGDAAGFTVFASLSVTLTAITLERWHITHANQLOCK 479  
 DB 420 VDIHTKSOYHVAIDMOTGACGDAAGFTVFASLSVTLTAITLERWHITHANQLOCK 479  
 OY 421 VDIHTKSOYHVAIDMOTGACGDAAGFTVFASLSVTLTAITLERWHITHANQLOCK 480  
 DB 421 VDIHTKSOYHVAIDMOTGACGDAAGFTVFASLSVTLTAITLERWHITHANQLOCK 480  
 OY 480 VOLRHAASVAVLGMTFAFAALPFIIGISSYMKVSCICLPMDIDSPLSOLYVNSLLVNLV 539  
 DB 480 VOLRHAASVAVLGMTFAFAALPFIIGISSYMKVSCICLPMDIDSPLSOLYVNSLLVNLV 539  
 OY 481 VHVRAASVAVLGMTFAFAALPFIIGISSYMKVSCICLPMDIDSPLSOLYVNSLLVNLV 540  
 DB 481 VHVRAASVAVLGMTFAFAALPFIIGISSYMKVSCICLPMDIDSPLSOLYVNSLLVNLV 540  
 OY 540 AFVVICGYTHLYTVRNPTTVSSSDTKAKRMATLIFTDFLCMAPISEFAISAKVP 599  
 DB 540 AFVVICGYTHLYTVRNPTTVSSSDTKAKRMATLIFTDFLCMAPISEFAISAKVP 599  
 OY 541 AFVVICGYTHLYTVRNPTTVSSSDTKAKRMATLIFTDFLCMAPISEFAISAKVP 600  
 DB 541 AFVVICGYTHLYTVRNPTTVSSSDTKAKRMATLIFTDFLCMAPISEFAISAKVP 600  
 OY 600 LITVSKAKILLVLPYNSCANPFLVATKPRDFILLKPGCYEQAOQIYRTSS 659  
 DB 601 LITVSKAKILLVLPYNSCANPFLVATKPRDFILLKPGCYEQAOQIYRTSS 660  
 OY 660 ATNFHARKSHCCSAPRTN--SYVLVPLHSSON 692  
 DB 661 TWNTHPRNCSSAPRTNGSYVLVPLSLAQN 695

RESULT 5  
FSHR\_BOVIN STANDARD; PRT; 695 AA.

AC P35376; 1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).  
DE RECEPTOR.  
GN FSHR.

OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]

SEQUENCE FROM N.A.  
RC STRAIN-Holstein; TISSUE-Ovary, and Testis;  
RX MEDLINE=95127199; PubMed=7826612;  
RA Houde A., Lambert A., Saumande J., Silversides D.W., Lussier J.G.;  
RT "Structure of the bovine follicle-stimulating hormone receptor complementary DNA and expression in bovine tissues";  
RL Mol. Reprod. Dev. 39:127-135(1994).  
CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. FSH/LSH/TSH SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
CC -----  
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CC -----  
CC EMBL: L23219; AAC37324.1;  
CC HSP; P33945; 1XUN.  
CC InterPro: IPR000276; GPCR\_Rhodpsn.  
CC InterPro: IPR001611; LRR.  
CC InterPro: IPR00372; LRR\_Nterm.  
CC Pfam: PF00001; 7tm\_1; 1.  
CC Pfam: PF00560; LRR; 4.  
CC Pfam: PF01462; LRRNT; 1.  
CC SMART: SM00013; LRRNT; 1.  
CC PROSITE: PS00237; G-PROTEIN\_RECPT\_F1\_1;  
CC PROSITE: PS0262; G-PROTEIN\_RECPT\_F1\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat.  
KW SIGNAL  
FT CHAIN 1  
FT 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.  
FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).  
FT TRANSHEM 367 387 1 (POTENTIAL).  
FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).  
FT TRANSHEM 399 421 2 (POTENTIAL).  
FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).  
FT TRANSHEM 444 465 3 (POTENTIAL).  
FT DOMAIN 466 485 CYTOPLASMIC (POTENTIAL).  
FT TRANSHEM 486 508 4 (POTENTIAL).  
FT DOMAIN 509 528 EXTRACELLULAR (POTENTIAL).  
FT TRANSHEM 529 550 5 (POTENTIAL).  
FT DOMAIN 551 573 CYTOPLASMIC (POTENTIAL).  
FT TRANSHEM 574 597 6 (POTENTIAL).  
FT DOMAIN 598 608 EXTRACELLULAR (POTENTIAL).  
FT TRANSHEM 609 630 7 (POTENTIAL).  
FT DOMAIN 631 695 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 44 68 LRR 1.  
FT REPEAT 69 LRR 2.

FT REPEAT 119 143 LRR 3.  
FT REPEAT 170 192 LRR 4.  
FT REPEAT 193 216 LRR 5.  
FT REPEAT 218 240 LRR 6.  
FT DISULFID 442 517 BY SIMILARITY.  
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 695 AA; 78084 MW; 18F9DFEFC046380D CRC64;

Query Match 89.3%; Score 3208.5; DB 1; Length 695;  
Best Local Similarity 87.8%; Pred. No. 8.5e-198;  
Matches 610; Conservative 46; Mismatches 36; Indels 3; Gaps 2;

QY 1 MALLVSLAFLGTGSGCHHMLCHCNRVFLCDSKVTEIPTDLPRNAIELRVLTCLR 60  
DB 1 MALLVALLAFLSLGSGCHHRLCHCSNGVFLCQESKVTEIPSDLPDAVELRFLVTLR 60

QY 61 IPKSGPAGGDLKIEIISONDVLEIVADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120  
DB 61 IPGAFSGGDLKIEIISONDVLEIVADVFSNLPKLHEIRIEKANNLLYIDPDAFONLP 120

QY 121 SLRYLLISNTGIKHLPAVHKIQSLQKVLIDQININIHIVARNFMSGLSPESVTLWSKN 180  
DB 121 NLRYLLISNTGIKHLPAVHKIQSLQKVLIDQININIHIVARNFMSGLSPESVTLWSKN 180

QY 181 GIEEINCAFNQGLDELNLSDNNLEELPNDVFOGASGPVILDISRTKVSHPNHGLEN 240  
DB 181 GIOEINCAFNQGLDELNLSDNNLEELPNDVFOGASGPVILDISRTKVSHPNHGLEN 240

QY 241 LKLRARSYRKLLNPKLNFVTLMEASLTYPSCAFANLKRQISLHPICNKSILRQD 300  
DB 241 LKLRARSYRKLLNPKLNFVTLMEASLTYPSCAFANLKRQISLHPICNKSILRQD 300

QY 301 IDDMTQIGQQRVSLI--DDEPSYKGDMMYNEFDYDLNEVDVTCSPKDAFNPCEDIM 359  
DB 301 VDDMTQARGQVSLAEDEDEPSYKGDMMYNEFDYDLNEVDVTCSPKDAFNPCEDIM 359

QY 360 GYNILRVLWFTSILAITGNTTVLVLTTSQYKLVTPRFLMCLNLAFLADLCIGYLLIAS 419  
DB 361 GDDILRVLWFTSILAITGNTTVLVLTTSQYKLVTPRFLMCLNLAFLADLCIGYLLIAS 420

QY 420 VDIHTKSOYHNVAIDMOTGAGCDAAGFFVFASLSVYTLTALTLEWHITTHAMOLECK 479  
DB 421 VDVHTKTEYHNVAIDMOTGAGCDAAGFFVFASLSVYTLTALTLEWHITTHAMOLECK 480

QY 480 VQLRHAASVYVLGWTFAFAAALPFIPIGSIYMKVSIKLPMDIDSPISQLYVMALLVNLV 539  
DB 481 VQLRHAASVYVLGWTFAFAAALPFIPIGSIYMKVSIKLPMDIDSPISQLYVMALLVNLV 540

QY 540 AFVVICGCTHYLTVRNPTIVSSSDTKIAKNMALTIFDFLCMAPISFALISLKV 599  
DB 541 AFVVICGCTHYLTVRNPTIVSSSDTKIAKNMALTIFDFLCMAPISFALISLKV 600

QY 600 LITVSKAKILLVLYFPINSCANPFLVAIFTKNRRDFFILLSKFCGYEQAOIYRTSS 659  
DB 601 LITVSKAKILLVLYFPINSCANPFLVAIFTKNRRDFFILLSKFCGYEQAOIYRTSS 660

QY 660 ATHNPHARKSHCSSAPRVNT--SYVLVPLNHSQSN 692  
DB 661 TAHNPHRNGCHCPPAPRVNTGNSNYTLIPLRLAKN 695

RESULT 6  
FSHR\_SHEEP  
ID FSHR\_SHEEP STANDARD; PRT; 695 AA.  
AC P35379; Q28573; Q28574; Q9TSI9;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).  
GN FSHR.

OS Ovis aries (Sheep).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Caprinae; Ovis.  
 CC NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R1).  
 RC TISSUE-Testis;  
 RX MEDLINE=93351750; PubMed=9394255;  
 RA Farney T.A., Sairam M.R., Khan H., Ravindranath N., Payne S.,  
 RA Seiden N.G.;  
 RT Molecular cloning and expression of the ovine testicular follicle  
 RT stimulating hormone receptor.;  
 RL [2]. Cell. Endocrinol. 9:219-226(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS FSH-R4 AND FSH-R3).  
 RC STRAIN=Dorset-Leicester-Suffolk 1; TISSUE-Testis;  
 RX MEDLINE=93176195; PubMed=8439338;  
 RA Khan H., Farney T.A., Sairam M.R.;  
 RT "Cloning of alternatively spliced mRNA transcripts coding for variants  
 RT of ovine testicular follicle-stimulating hormone receptor lacking the G protein  
 RT coupling domains.";  
 RL Biochem. Biophys. Res. Commun. 190:888-894(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R2), AND CHARACTERIZATION.  
 RC STRAIN=Dorset-Leicester-Suffolk 1; TISSUE-Testis;  
 RX MEDLINE=98031015; PubMed=9364440;  
 RA Farney T.A., Jiang L., Khan H., MacDonald E.A., Laird D.W.,  
 RA Sairam M.R.;  
 RT Molecular cloning, structure, and expression of a testicular  
 RT follicle-stimulating hormone receptor with selective alteration in the carboxy terminus  
 RT that affects signaling.;  
 RL Mol. Reprod. Dev. 48:458-470(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R3), AND CHARACTERIZATION.  
 RC STRAIN=Dorset-Leicester-Suffolk 1; TISSUE-Ovary;  
 RX MEDLINE=2031225; PubMed=10527886;  
 RA Babu P.S., Jiang L., Sairam M.R., Touyz R.M., Sairam M.R.;  
 RT "Structural features and expression of an alternatively spliced growth  
 RT factor type I receptor for follicle-stimulating hormone in the developing  
 RT ovary.";  
 RL Mol. Cell Biol. Res. Commun. 2:21-27(1999).  
 RN [6]  
 RP SEQUENCE OF 1-51 FROM N.A.  
 RX MEDLINE=98031017; PubMed=9364442;  
 RA Khan H., Sairam M.R., Sairam M.R.;  
 RT "Cloning of the ovine follicle-stimulating hormone receptor gene.";  
 RL Mol. Reprod. Dev. 48:480-487(1997).  
 CC -1- FUNCTION: Receptor for follicle stimulating hormone. The activity  
 CC of Isoform FSH-R1 is mediated by G proteins which activate  
 CC adenylyl cyclase. Isoforms FSH-R2 and FSH-R3 also bind FSH, but  
 CC this does not result in activation of adenylyl cyclase. Isoform  
 CC FSH-R3 may be involved in calcium signaling.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane  
 CC (isoforms FSH-R1 and FSH-R2); Cell surface (isoform FSH-R3).  
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; FSH-R1 (shown here), FSH-R2,  
 CC FSH-R3 and FSH-R4; are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Isoform FSH-R3 is expressed in ovary and  
 CC testis but not in kidney.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor superfamily.  
 CC FSH/LSH/FSH SUPERFAMILY  
 CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 CC EMBL; L07302; AAA31525.1;

DR EMBL: L12766; AAA31523.1;  
 DR EMBL: L12766; AAA31524.1;  
 DR EMBL: L36115; AAA31525.1;  
 DR EMBL: A311735; CA810495.1;  
 DR EMBL: AF050438; AAC61749.1;  
 DR PIR: JCI493; JCI493;  
 DR HSSP: P23945; 1XUN;  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR003172; LRR\_Nterm.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR Pfam: PF00560; LRR; 4.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR SMART: SM00013; LRRNT; 1.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE: PS00462; G-PROTEIN\_RECEP\_FL\_2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 DR 9-protein family; Receptor; Leucine-rich repeat; Alternative splicing.  
 DR SIGNAL 1 695  
 FT CHAIN 18 695  
 FT DOMAIN 18 366  
 FT TRANSMEM 367 387  
 FT DOMAIN 388 398  
 FT TRANSMEM 399 421  
 FT DOMAIN 422 443  
 FT TRANSMEM 444 465  
 FT DOMAIN 466 485  
 FT TRANSMEM 486 508  
 FT DOMAIN 509 528  
 FT TRANSMEM 529 550  
 FT DOMAIN 551 573  
 FT TRANSMEM 574 597  
 FT DOMAIN 598 608  
 FT TRANSMEM 609 630  
 FT DOMAIN 631 658  
 FT REPEAT 69 93  
 FT REPEAT 119 143  
 FT REPEAT 170 192  
 FT REPEAT 193 216  
 FT REPEAT 218 240  
 FT REPEAT 242 266  
 FT DISULFID 442 517  
 FT CARBOHYD 191 191  
 FT CARBOHYD 199 199  
 FT CARBOHYD 293 293  
 FT VARSPLIC 126 133  
 FT VARSPLIC 135 695  
 FT VARSPLIC 224 239  
 FT VARSPLIC 260 695  
 FT VARSPLIC 643 670  
 FT VARSPLIC 671 695  
 SQ SEQUENCE 695 AA; 78237 MW; PBF75089D8C0D4B CRC64;  
 Query Match 89.04; Score 3199.5; DB 1; Length 695;  
 Best Local Similarity 87.24; Pred. No. 3.2e-197;  
 Matches 606; Conservative 48; Mismatches 38; Indels 3; Gaps 2;  
 Oy 1 MALLVSLAPLGTGSCCHWCHCSNRVLCDSKVTEPTDLPNATELRFVLKRV 60  
 Db 1 WALPVLAPLALGSCCHWCHCSNRVLCDSKVTEPTDLPNATELRFVLKRV 60  
 Oy 61 TPKGSFAGDLEKLEISONDVLEVTADYFSLPKLEHETKANNLLYINPEATQNP 120  
 Db 61 TPKGSFAGDLEKLEISONDVLEVTADYFSLPKLEHETKANNLLYINPEATQNP 120  
 Oy 121 SYRVLLISNTGKHPAVKHQISQKVLDDQDNINHIYARNFSLFESVILWSKN 180  
 Db 121 NRYVLLISNTGKHPAVKHQISQKVLDDQDNINHIYARNFSLFESVILWSKN 180

181 GIEETHNCAFNCTQDELNLSDNNLEELPNDVFGASGVPVILDISRTKRVSHLNHLEN 240  
181 GIOEIHNCANFGTQDELNLSDNNLEELPNDVFGASGVPVILDISRTKRVSHLNHLEN 240  
241 LKKLRARSYRLKLPDLKFTLMPASITYSYHCCAFANLKRQISELHPICNKSILROD 300  
241 LKKLRARSYRLKLPDLKFTLMPASITYSYHCCAFANLKRQISELHPICNKSILROD 300  
301 IDDMTOIGQORVSLI--DDPSYSGKSGDMYNEFDYDLCNEVVDVTCSPKPDAPNCCEDIM 359  
301 VDMTQARQORISLAEDDEPSAKGDMYSEFDYDLCNEVVDVTCSPKPDAPNCCEDIM 360  
360 GYNILRVLIWFTSILAITNTVTVLVTTSQYKLTVPRELMCNLAFADLCIGIYLLLIAS 419  
361 GVDILRVLIWFTSILAITNTVTVLVTTSQYKLTVPRELMCNLAFADLCIGIYLLLIAS 420  
420 VDIHTKSOYHNDAIDQWOTGAGDAAGFFTVFASLSVYVLTALTLEWHITTHAMOLECK 479  
421 VDVHTKSOYHNDAIDQWOTGAGDAAGFFTVFASLSVYVLTALTLEWHITTHAMOLECK 480  
480 VOLRHAASVWLVGTFFAFAALFPPIFGISSYKVSICLPMIDISPLSQVWVALLVNL 539  
481 VVHRHAASVWLVGTFFAFAALFPPIFGISSYKVSICLPMIDISPLSQVWVALLVNL 540  
540 AFVWICGCTHYLTVRNPTIVSSSDTKIAKRMATLFTDFLCMAPISFFAISASLKVP 599  
541 AFVWICGCTHYLTVRNPTIVSSSDTKIAKRMATLFTDFLCMAPISFFAISASLKVP 600  
600 LITVSKAKILLVLYPINSANPFLYAIKTRFRDRFFILLSKFGCYEHOAQIYRSTSS 659  
601 LITVSKAKILLVLYPINSANPFLYAIKTRFRDRFFILLSKFGCYEHOAQIYRSTSS 660  
660 ATHNPHARKSHCSSAPRVN--SYVLVPLNHSSON 692  
661 TAHNPHARKSHCSSAPRVN--SYVLVPLNHSSON 695

## RESULT 7

FSHR\_PIG STANDARD; PRT; 695 AA.  
AC P49059; 077514;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).  
GN FSHR.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Ovary;  
RX MEDLINE=96011644; PubMed=7590277;  
RA Remy J.J., Lahbib-Mansais Y., Verle M., Bozon V., Couture L.,  
RA Pajot E., Grebert D., Salesse R.;  
RT "The porcine follitropin receptor: cDNA cloning, functional  
expression and chromosomal localization of the gene."  
RL Gene 163:257-261(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Ovary;  
RA Wang Y.F., Meyer K.B., Schmidt K., Wan S.J., Degen S.J.F.,  
RA la Barbara A.R.;  
RT "Porcine follicle-stimulating hormone receptor."  
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
CC -I- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY  
CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
CC ADENYLATE CYCLASE.  
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC FSH/LSH/TSH SUBFAMILY.

-I- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
CC  
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CC  
CC EMBL; L31966; AAA86933.1;  
CC EMBL; AF025377; AAC24981.1;  
CC HSSP; P23945; 1XUN.  
CC InterPro: IPR000276; GPCR\_Rhodpsn.  
CC InterPro: IPR001611; LRR.  
CC InterPro: IPR000372; LRR\_Nterm.  
CC Pfam; PF00001; 7tm\_1; 1.  
CC Pfam; PF00560; LRR; 2.  
CC Pfam; PF01462; LRRNT; 1.  
CC SMART; SM00013; LRRNT; 1.  
CC PROSITE; PS00337; G\_PROTEIN\_RECP\_FL\_1; 1.  
CC PROSITE; PS00362; G\_PROTEIN\_RECP\_FL\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Phosphorylation; Repeat; Leucine-rich repeat.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.  
FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 367 387 1 (POTENTIAL).  
FT DOMAIN 368 398 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 399 421 2 (POTENTIAL).  
FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 444 465 3 (POTENTIAL).  
FT DOMAIN 466 485 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 486 508 4 (POTENTIAL).  
FT DOMAIN 509 528 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 529 550 5 (POTENTIAL).  
FT DOMAIN 551 573 6 (POTENTIAL).  
FT TRANSMEM 574 597 7 (POTENTIAL).  
FT DOMAIN 598 608 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 609 630 7 (POTENTIAL).  
FT DOMAIN 631 695 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 44 68 LRR 1.  
FT REPEAT 69 93 LRR 2.  
FT REPEAT 119 143 LRR 3.  
FT REPEAT 170 192 LRR 4.  
FT REPEAT 193 216 LRR 5.  
FT REPEAT 218 240 LRR 6.  
FT DISULFID 442 517 BY SIMILARITY.  
FT CARBOHYD 191 191 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 199 199 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CONFLICT 2 2 S -> A (IN REF. 1).  
FT CONFLICT 13 13 T -> S (IN REF. 1).  
FT CONFLICT 60 60 V -> A (IN REF. 1).  
FT CONFLICT 166 166 V -> M (IN REF. 1).  
FT CONFLICT 215 215 Q -> H (IN REF. 1).  
FT CONFLICT 247 247 K -> R (IN REF. 1).  
FT CONFLICT 257 257 S -> T (IN REF. 1).  
FT CONFLICT 334 334 D -> N (IN REF. 1).  
FT CONFLICT 349 349 E -> K (IN REF. 1).  
FT CONFLICT 352 352 T -> A (IN REF. 1).  
FT CONFLICT 383 383 V -> E (IN REF. 1).  
FT CONFLICT 407 407 A -> T (IN REF. 1).  
FT CONFLICT 421 421 V -> I (IN REF. 1).  
FT CONFLICT 427 427 T -> S (IN REF. 1).  
FT CONFLICT 435 435 D -> N (IN REF. 1).  
FT CONFLICT 483 483 L -> V (IN REF. 1).  
FT CONFLICT 550 550 T -> I (IN REF. 1).  
FT CONFLICT 586 586 A -> V (IN REF. 1).  
FT CONFLICT 607 607 S -> L (IN REF. 1).  
FT CONFLICT 691 691 R -> H (IN REF. 1).  
SQ SEQUENCE 695 AA; 78172 MW; E9EBED929C79C450 CRC64;

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Query Match      87.7% Score 3153.5; DB 1; Length 695;
Best Local Similarity 86.6% Pred. No. 2,8e-194;
Matches 602; Conservative 44; Mismatches 46; Indels 3; Gaps 2;

OY 1 MALLVSLAFITGSGCHHWCNHRVFLQDSKVTETPTDLPNNAIELRFLVTLKRV 60
DB 1 MALLVSLAFITGSGCHHWCNHRVFLQDSKVTETPTDLPNNAIELRFLVTLKRV 60
OY 61 IPKGSFAGFDELEKIBISONDVLEADVFNPLKLIHEIRIEKANLLYINPEAFONLP 120
DB 61 IPKGSFAGFDELEKIBISONDVLEADVFNPLKLIHEIRIEKANLLYINPEAFONLP 120
OY 121 SLRYLLISNTGKULPAVHKVLOSQVLDIODNINHIVARNSFGLSFEVILNLSN 180
DB 121 SLRYLLISNTGKULPAVHKVLOSQVLDIODNINHIVARNSFGLSFEVILNLSN 180
OY 181 GTEEHINCAFNCTOLDLNLSDNNLELPELVDFQASGPVILDISRTKVSILPHNGLEN 240
DB 181 GTEEHINCAFNCTOLDLNLSDNNLELPELVDFQASGPVILDISRTKVSILPHNGLEN 240
OY 241 LAKLRASRYRLKLPNDKFPVTLMBASLTYSHCACAFANLKRQISELHPICNKSILROD 300
DB 241 LAKLRASRYRLKLPNDKFPVTLMBASLTYSHCACAFANLKRQISELHPICNKSILROD 300
OY 301 IDMTQIGDQVSLID-EPYSGKSDMYNEFDYDLCNEVYDVTCSPKPAFNPCEDM 359
DB 301 IDMTQIGDQVSLID-EPYSGKSDMYNEFDYDLCNEVYDVTCSPKPAFNPCEDM 359
OY 360 GYMLVLELVNFIISLAICTGTVLVLTQSYKUTVPRPLCNLAPADLCIGIYLLILAS 419
DB 360 GYMLVLELVNFIISLAICTGTVLVLTQSYKUTVPRPLCNLAPADLCIGIYLLILAS 419
OY 420 VDIHTKSOYHNTADMGTCAGDAGPPTVFASELSVYTLTATLKRHTITHANQLECK 479
DB 420 VDIHTKSOYHNTADMGTCAGDAGPPTVFASELSVYTLTATLKRHTITHANQLECK 479
OY 480 VOLRHAASVYVLGTFAPAAALPFIPIGSISSYKVSICLPMIDPSLSQLYVVALVNLV 539
DB 480 VOLRHAASVYVLGTFAPAAALPFIPIGSISSYKVSICLPMIDPSLSQLYVVALVNLV 539
OY 540 APVYICGCTHYLYLVNPTIVSSSDTKIAKRNATLIFTDFCHAPISFFAISASUKVP 599
DB 540 APVYICGCTHYLYLVNPTIVSSSDTKIAKRNATLIFTDFCHAPISFFAISASUKVP 599
OY 600 LITVSEAKILLVLPINSCANPLFAITKFNRPDPFILLSKFGCYEQAOIYRTTSS 659
DB 600 LITVSEAKILLVLPINSCANPLFAITKFNRPDPFILLSKFGCYEQAOIYRTTSS 659
OY 660 ATHNFHARKSHCSAPRVN--SYLVPLNHSQSN 692
DB 660 ATHNFHARKSHCSAPRVN--SYLVPLNHSQSN 692

RESULT 8
FSHR_HORSE STANDARD; PRT: 694 AA.
ID FSHR_HORSE STANDARD; PRT: 694 AA.
OC 0477991, 1996 (Rel. 33, Created)
OC 01-FEB-1996 (Rel. 33, Last sequence update)
OC 16-OCT-2003 (Rel. 40, Last annotation update)
DE Pollicle stimulating hormone precursor (FSH-R) (Follicle tropin receptor)...
GN FSHR.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=94256980; PubMed=8198575;
RA Robert P., Amselein S., Christophe S., Benifla J.L., Bellot D.,
  Koman A., Bidart J.M.;
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*Cloning and sequencing of the equine testicular follitropin
receptor. Biophys. Res. Commun. 201:201-207(1994).
-1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
ADENYLATE CYCLASE. AMONG ALL MAMMALIAN FSH RECEPTORS, ON THE HORSE
RECEPTOR DOES NOT BIND LH/CHORIONIC GONADOTROPHIN (CG).
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH/LSH SUBFAMILY.
-1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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or send an email to listproc@ebi.ac.uk)
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DB EMBL: S70150; AAB30854.1;
DB HSSP: P23945; 1XUN.
DB InterPro: IPR000276; GPCR_Rhodopn.
DB InterPro: IPR001611; LRR.
DB InterPro: IPR000372; LRR_Nterm.
DB Pfam: PF00001; 7tm_1; 1.
DB Pfam: PF00560; LRR; 3.
DB Pfam: PF01462; LRRNT; 1.
DB PRINTS: PR00237; GPCR_RHODOPS.
DB SMART: SM0013; LRRNT; 1.
DB PROSITE: PS00237; G-PROTEIN_RECP_F1; 1.
DB PROSITE: PS00262; G-PROTEIN_RECP_F2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
  Phosphorylation; Repeat; Leucine-rich repeat.
FT CHAIN 18 694
FT DOMAIN 18 365
FT TRANSMEM 366 386
FT DOMAIN 387 397
FT TRANSMEM 398 420
FT DOMAIN 421 442
FT TRANSMEM 443 464
FT DOMAIN 465 484
FT TRANSMEM 485 507
FT DOMAIN 508 527
FT TRANSMEM 528 549
FT DOMAIN 550 570
FT TRANSMEM 571 597
FT DOMAIN 598 629
FT TRANSMEM 630 694
FT REPEAT 44 68
FT REPEAT 69 93
FT REPEAT 119 143
FT REPEAT 168 192
FT REPEAT 193 216
FT REPEAT 218 240
FT DISULFID 441 516
FT CARBOHYD 191 191
FT CARBOHYD 199 199
FT CARBOHYD 268 268
FT CARBOHYD 293 293
SQ SEQUENCE 694 AA; 78004 MW; E2F077C5E8CBAC54 CRC64;
Query Match      87.4% Score 3140; DB 1; Length 694;
Best Local Similarity 87.4% Pred. No. 2e-193;
Matches 609; Conservative 35; Mismatches 47; Indels 4; Gaps 3;

OY 1 MALLVSLAFITGSGCHHWCNHRVFLQDSKVTETPTDLPNNAIELRFLVTLKRV 60
DB 1 MALLVSLAFITGSGCHHWCNHRVFLQDSKVTETPTDLPNNAIELRFLVTLKRV 60
OY 61 IPKGSFAGFDELEKIBISONDVLEADVFNPLKLIHEIRIEKANLLYINPEAFONLP 120
```

Db 61 IPKAFSGDLEKIEISQNDVLEVEANFVSNLPKHEIRKANNLLYIDHDAFQNP 120  
Qy 121 SLRYLLISNTGKIKHLPVAVKIQSLQKVLDDIQONINIHIVARNFSGLSFESVILWLSKN 180  
Db 121 NLYVLLISNTGKIKHLPVAVKIQSLQKVLDDIQONINIHIVARNFSGLSFESVILWLSKN 180  
Qy 181 GIEIHNCAFNGTQDLELNDLNNLELNDVFOGASGVPVLDISRTKVKHSLPNHGLEN 240  
Db 181 GIEIHNCAFNGTQDLELNDLNNLELNDVFOGASGVPVLDISRTKVKHSLPNHGLEN 240  
Qy 241 LKLRARSTYRLKPLNLDLNFVLTMEASLTYPSCCAFANLKRQISLHPICHNKSILRQD 300  
Db 241 LKLRARSTYRLKPLNLDLNFVLTMEASLTYPSCCAFANLKRQISLHPICHNKSILRQD 300  
Qy 301 IDMTQIGDQVSLI--DDEPSYKSGSDMYNEFDYDLCNEVDVDTCSKPKDAFNPCEIDM 359  
Db 301 V-DMTQARGERSVLAEDDESSYPKGFOMYSEFEYDLCNEVDVDTCSKPKDAFNPCEIDM 359  
Qy 360 GYNLRLVIFISILATGNTVLTWLTTSOYKLTVPFELMCNLFADLCIGIYLLIAS 419  
Db 360 GYNLRLVIFISILATGNTVLTWLTTSOYKLTVPFELMCNLFADLCIGIYLLIAS 419  
Qy 420 VDIHTKSOYHNYAIDMTGACDGAAGFTVFASLSVYTLTALRWHHTITHAMOLECK 479  
Db 420 VDIHTKSOYHNYAIDMTGACDGAAGFTVFASLSVYTLTALRWHHTITHAMOLECK 479  
Qy 480 VOLRHAASVVLGWTFAAALPFIIGISSYMKVSYICLPMIDISPLSOLYVALLVNLV 539  
Db 480 VOLRHAASVVLGWTFAAALPFIIGISSYMKVSYICLPMIDISPLSOLYVALLVNLV 539  
Qy 540 AFVVICCYTHIYLTVRNPTVSSSDTKAKRMATLIFTDFLCMAPISEFAISAKVP 599  
Db 540 AFVVICCYTHIYLTVRNPTVSSSDTKAKRMATLIFTDFLCMAPISEFAISAKVP 599  
Qy 600 LITVSKAKILVLEVPINSCANPELYAIFTNFRDRFILLKFCGYEMQAQYRTTSS 659  
Db 600 LITVSKAKILVLEVPINSCANPELYAIFTNFRDRFILLKFCGYEMQAQYRTTSS 659  
Qy 660 ATHNFHARKSCSAPRVN--SYVLPVPLNHSN 692  
Db 660 TAHISHPRNGHCPTPTPRVINGANCTVPLSLAQN 694

## RESULT 9

FSHR\_EQUAS STANDARD; PRT; 687 AA.  
AC Q95179;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).  
OS Equus asinus (Donkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_taxid=9793;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=97338913; PubMed=9195473;  
RA Richard F., Martinat N., Remy J.-J., Salesse R., Combarnous Y.;  
RT "Cloning, sequencing and in vitro functional expression of recombinant donkey follicle-stimulating hormone receptor: a new insight into the binding specificity of gonadotrophin receptors.";  
RL J. Mol. Endocrinol. 18:193-202(1997).  
CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. FSH/LSH/TSH SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
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CC  
CC EMBL; U73659; RAB18245.1;  
DR HSP; P23945; IXUN.  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR Pfam: PF00560; LRR; 3.  
DR Pfam: PF01462; LRRNT; 1.  
DR PRINTS: PR00237; GPCRHHODPSN.  
DR SMART: SM00013; LRRNT; 1.  
DR PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
DR PROSITE: PS00262; G-PROTEIN\_RECEP\_FL\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 687 FOLLICLE STIMULATING HORMONE RECEPTOR.  
FT DOMAIN 18 358 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 359 379 1 (POTENTIAL).  
FT DOMAIN 380 390 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 391 413 2 (POTENTIAL).  
FT DOMAIN 414 435 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 436 457 3 (POTENTIAL).  
FT DOMAIN 458 477 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 478 500 4 (POTENTIAL).  
FT DOMAIN 501 520 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 521 542 5 (POTENTIAL).  
FT DOMAIN 543 565 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 566 589 6 (POTENTIAL).  
FT DOMAIN 590 600 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 601 622 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 623 687 7 (POTENTIAL).  
FT REPEAT 69 93 LRR 1.  
FT REPEAT 119 143 LRR 2.  
FT REPEAT 170 192 LRR 3.  
FT REPEAT 193 216 LRR 4.  
FT REPEAT 218 240 LRR 5.  
FT DISULFID 434 509 BY SIMILARITY.  
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 687 AA; 76937 MW; FC3AF0B55531DA9A CRC64;  
Query Match 85.6%; Score 3076.5; DB 1; Length 687;  
Best Local Similarity 86.0%; Pred. No. 2.3e-189;  
Matches 597; Conservative 38; Mismatches 50; Indels 9; Gaps 3;  
Qy 1 MALLVSLAFGLTGSGCHHWHLCNSNRVFCQDSKVTEIPTDLPRNAIELRVLTCLR 60  
Db 1 MALLVSLAFGLTGSGCHHWHLCNSNRVFCQDSKVTEIPTDLPRNAIELRVLTCLR 60  
Qy 61 IPKSGAFSGDLEKIEISQNDVLEVEANFVSNLPKHEIRKANNLLYINPEAFQNP 120  
Db 61 IPKSGAFSGDLEKIEISQNDVLEVEANFVSNLPKHEIRKANNLLYIDHDAFQNP 120  
Qy 121 SLRYLLISNTGKIKHLPVAVKIQSLQKVLDDIQONINIHIVARNFSGLSFESVILWLSKN 180  
Db 121 NLYVLLISNTGKIKHLPVAVKIQSLQKVLDDIQONINIHIVARNFSGLSFESVILWLSKN 180  
Qy 181 GIEIHNCAFNGTQDLELNDLNNLELNDVFOGASGVPVLDISRTKVKHSLPNHGLEN 240  
Db 181 GIEIHNCAFNGTQDLELNDLNNLELNDVFOGASGVPVLDISRTKVKHSLPNHGLEN 240





Db 121 SURYLLISNTGSLFPLVVKHVSFOKVLVDQDNTHIRTIERNTFMGLSSSESVILRLKN 180  
QY 181 GIEEIHNCFAFNGTQDELNDNNLEELPNDVFOGASGPVILDSRTKTVHSLPNHGLEN 240  
Db 181 GIOEIKHAFNGTCLDELNDNNLEELPNDVFOGASGPVILDSRTKTVHSLPNHGLEF 240  
QY 241 LKKLRARSTYRLKKLPNDKFTVLMKASLTYPHSHCCAFANLKRQISELHPICNKSILROD 300  
Db 241 IKKLRARSTYRLKKLPNDKFTVLMKASLTYPHSHCCAFANLKRQISELHPICNKSILROD 300  
QY 301 IDDMTOIGQORVSLIDDEPS-VGKSDMYNFEFDYLCNEVVDVTCSPKPDFAFNPCEDIM 359  
Db 301 LGEOTGKRHRHRAAEDYISHYGRFPGVNEFDYGLCNEVVDVTCSPKPDFAFNPCEDIM 360  
QY 360 GYNILRLVFWISILAITNTVTVLTVTSQVKTVPFRLMCLNAPADLCIGYLLLIAS 419  
Db 361 GYNVRLVFWISILAITNTVTVLTVTSQVKTVPFRLMCLNAPADLCIGYLLLIAS 420  
QY 420 VDIHTKSYHNAIDMOTGAGCDAAGFFTFVASELSVYTLTITLIRWHITTHAMOLECK 479  
Db 421 VDIHTKSYHNAIDMOTGAGCDAAGFFTFVASELSVYTLTITLIRWHITTHAMOLECK 480  
QY 480 VOLRHAASVWLGWTFAPAAALPPIGSISSYKWSICLPMDSPLSQLYVWALLVNLV 539  
Db 481 VLRHAAVIMVFGWTFAPAAALPPIGSISSYKWSICLPMDSPLSQLYVWALLVNLV 540  
QY 540 AFVIGCGYTHYLVTRNPTVSSSDTKIAKMATLIETDFLCMAPIFFFAISASLKP 599  
Db 541 AFVIGCGYTHYLVTRNPTVSSSDTKIAKMATLIETDFLCMAPIFFFAISASLKP 600  
QY 600 LITVSKAILLVLYPINSCLPFLYAIETKFRDFFILLKFGCEYMAQIYRTETSS 659  
Db 601 LITVSKAILLVLYPINSCLPFLYAIETKFRDFFILLKFGCEYMAQIYRTETSS 660  
QY 660 ATHNFAKSHCSSAPRVNLS--YVLVPLNH 688  
Db 661 SAHNFTNRNGHYPTASKNSDGTIYSLVPLNH 691

RESULT 11  
LSHR\_PIG STANDARD: PRT: 696 AA.  
AC P16582;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lutropin-chorionadotropic hormone receptor precursor (LH/CG-R)  
GN LHCR.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89332517; PubMed=2502844;  
RA Loosfelt H., Misrahi M., Atger M., Salesse R., Thi M.T.V.H.-L.,  
RA Jolivet A., Guiochon-Mantel A., Sar S., Jallat B., Garnier J.,  
RA Milgrom E.;  
RT Cloning and sequencing of porcine LH-hCG receptor cDNA: variants  
RT lacking transmembrane domain.\*;  
RL Science 245:525-528(1989).  
CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIONADOTROPIC HORMONE.  
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
CC ACTIVATE ADENYLATE CYCLASE.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), B, C AND D; ARE  
CC PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC FSH/LSH/TSH SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL: M29525; AAA31062.1; -  
DR EMBL: M29526; AAA31063.1; -  
DR EMBL: M29527; AAA31064.1; -  
DR EMBL: M29528; AAA31065.1; -  
DR PIR: A41344; A41344.  
DR PIR: B41344; B41344.  
DR PIR: C41344; C41344.  
DR PIR: D41344; D41344.  
DR HSSP: P22888; IL07.  
DR InterPro: IPR00276; GPCR\_Rhodpsn.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR003372; LRR\_Nterm.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR Pfam: PF00560; LRR; 2.  
DR SMART: SM00013; LRRNT; 1.  
DR PROSITE: PS00237; G\_PROTEIN\_RECP\_FL1; 1.  
DR PROSITE: PS0262; G\_PROTEIN\_RECP\_FL2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing.  
FT SIGNAL 1 27 POTENTIAL.  
FT CHAIN 28 696 LUTROPIN-CHORIONADOTROPIC HORMONE  
FT RECEPTOR.  
FT DOMAIN 28 358 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 359 386 1 (POTENTIAL).  
FT DOMAIN 387 395 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 396 418 2 (POTENTIAL).  
FT DOMAIN 419 439 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 440 462 3 (POTENTIAL).  
FT DOMAIN 463 482 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 483 505 4 (POTENTIAL).  
FT DOMAIN 506 525 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 526 547 5 (POTENTIAL).  
FT DOMAIN 548 570 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 571 594 6 (POTENTIAL).  
FT DOMAIN 595 605 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 606 626 7 (POTENTIAL).  
FT DOMAIN 627 696 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 48 71 LRR 1.  
FT REPEAT 122 147 LRR 2.  
FT REPEAT 149 171 LRR 3.  
FT REPEAT 172 196 LRR 4.  
FT REPEAT 198 220 LRR 5.  
FT REPEAT 221 244 LRR 6.  
FT DISULFID 439 514 BY SIMILARITY.  
FT CARBOHYD 99 99 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 291 291 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARSPLIC 317 329 YSAIFAELSLSW -> LLHGALPATHCLS (IN  
FT ISOFORM B).  
FT VARSPLIC 330 696 MISSING (IN ISOFORM B).  
FT VARSPLIC 317 331 YSAIFAELSLSW -> SKSRADYQQRHKDC (IN  
FT ISOFORM C).  
FT VARSPLIC 332 696 MISSING (IN ISOFORM C).  
FT VARSPLIC 317 628 MISSING (IN ISOFORM D).  
SQ SEQUENCE 696 AA; 78092 MW; 593DEFIC25F982FE CRC64;

Query Match 50.3%; Score 1807.5; DB 1; Length 696;  
Best Local Similarity 55.1%; Pred. No. 2.8e-108;  
Matches 373; Conservative 103; Mismatches 154; Indels 47; Gaps 13;  
QY 1 MALLLV-----SLAFLGTGSGCHWLCHCNVFLCQDSKVTEPTDLPRAIAELRFV 54  
Db 12 LALLLVPPPLPQTLL-----GAPCPE---PCS-----CRPDGALRCFG--PRAGLS-RLS 55



Db 55 RLSLTPLPKVIPSQAFRLNEVKIEISQSDLSLEKIEANAFDNLNLSEILQNTKLV 114  
Oy 110 YINPEAFONLPSVLLSNTGKIKHLPVAVHQISLO-KVLLDIOONTNHIHVARNSMGL 168  
Db 115 HIECAFNLPRKLTSCNTGKIKHLPVAVHQISLO-KVLLDIOONTNHIHVARNSMGL 174  
Oy 169 SFESVILWLSNGIEEHNCAFNQTLDELNSNNLELPDVFQCGASGPFVILDSRT 228  
Db 175 NNESTILKLYNGFEEIOSHAFNGTLLSLEKENARLEKMHKNDARFGATGSPILDSST 234  
Oy 229 KVHSLPNHGLNKLKRLARSYRKLKPNLNDKFTVLMASITYSHCCAFANLKRQISEL 288  
Db 235 KLOALPTGLSIOITLATSYSKLPKPSREKFTNLLDNLATLTPSHCCAFANL 287  
Oy 289 HPICKNSILRODIDMTGIGQVSLIDDESYG---KGSMDMYNEFDYDLCNEVDVTC 345  
Db 288 -PTNEQNFSSIFKNSKOCSTARRPNNETLYSAFAESLSESGWDYDYGFCFLPKT-LQC 345  
Oy 346 SPKPDAPNCPEDIMGYNILRLVILFISILAITGNTTVLVLTTSQYKLTVPFRLMCLAF 405  
Db 346 AEPDAPNCPEDIMGYNILRLVILFISILAITGNTTVLVLTTSQYKLTVPFRLMCLAF 405  
Oy 406 ADLCIGIYLLIASVDIHTKSOYHNAYIDWOTGAGCDAAAGFTVPASELSVYTLTATLE 465  
Db 406 ADFCMGLYLLIASVDIHTKSOYHNAYIDWOTGAGCDAAAGFTVPASELSVYTLTATLE 465  
Oy 466 RWHITTHAMOLECKVOLRHAASVNVLGWTFAPFAALFPFGLSSYMKYSICLPMDIDSPL 525  
Db 466 RWHITTHAMOLECKVOLRHAASVNVLGWTFAPFAALFPFGLSSYMKYSICLPMDIDSPL 525  
Oy 526 SOLYVMAILLVNLVAFVVICGTHYILTVRNPTIVSSSDTKIAKRNATLIFTDFCLMA 585  
Db 526 SOLYVMAILLVNLVAFVVICGTHYILTVRNPTIVSSSDTKIAKRNATLIFTDFCLMA 585  
Oy 586 PISFPAISAKLVPLITSKAKILLVLPYNSCANPELYAIFTNFRDRFILLSKRGCC 645  
Db 586 PISFPAISAKLVPLITSKAKILLVLPYNSCANPELYAIFTNFRDRFILLSKRGCC 645  
Oy 646 YEMOAOIYRTSSATHNFHARKSHCSS 673  
Db 646 KYRAELIRK-----DFSAYISCKN 667

RESULT 13  
ID LSHR\_MOUSE STANDARD; PRT: 700 AA.  
AC P30730;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)  
DE (LSH-R) (Luteinizing hormone receptor).  
GN LHCR OR LHR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92165799; PubMed=1311310;  
RA Gudermann T., Birnbaumer M., Birnbaumer L.;  
RT "Evidence for dual coupling of the murine luteinizing hormone  
RT receptor to adenylyl cyclase and phosphoinositide breakdown and Ca2+  
RT mobilization. Studies with the cloned murine luteinizing hormone  
RT receptor expressed in L cells.";  
RL J. Biol. Chem. 267:4479-4488(1992).  
RN [2]  
RP SEQUENCE OF 1-58 FROM N.A.  
RX MEDLINE=93093308; PubMed=1459341;  
RA Huhtaniemi I.T., Eskola V., Pakarinen P., Matikainen T., Sprengel R.;  
RT "The murine luteinizing hormone and follicle-stimulating hormone  
RT receptor genes: transcription initiation sites, putative promoter

sequences and promoter activity.";  
RL Mol. Cell. Endocrinol. 88:55-66(1992).  
CC -!- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.  
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
CC ACTIVATE ADENYLATE CYCLASE.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC FSH/LSH/TSH SUBFAMILY.  
CC -!- SIMILARITY: CONTAINS 4 LEUCINE-RICH REPEATS (LRR).  
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CC  
CC EMBL: S49753; AAB24402.1; -  
CC EMBL: M81310; AAA39432.1; -  
CC EMBL: M87571; AAA39433.1; -  
CC PIR: A42395; A42395.  
CC HSP: P22888; ILUT.  
CC MGD: MGI:96783; Lhcgr.  
CC InterPro: IPR000276; GPCR\_Rhodpsn.  
CC InterPro: IPR001611; LRR.  
CC InterPro: IPR000372; LRR\_Nterm.  
CC Pfam: PF00001; 7tm\_1; 1.  
CC Pfam: PF00560; LRR; 1.  
CC SMART: SM00013; LRRNT; 1.  
CC PROSITE: PS00337; G-PROTEIN\_RECF1\_1; 1.  
CC PROSITE: PS00262; G-PROTEIN\_RECF1\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Phosphorylation; Repeat; Leucine-rich repeat.  
FT SIGNAL 1 26  
FT CHAIN 27 700  
FT LUTROPIN-CHORIOGONADOTROPIC HORMONE  
FT RECEPTOR.  
FT DOMAIN 27 362  
FT TRANSMEM 363 390  
FT DOMAIN 391 399  
FT TRANSMEM 400 422  
FT DOMAIN 423 443  
FT TRANSMEM 444 466  
FT DOMAIN 467 486  
FT TRANSMEM 487 509  
FT DOMAIN 510 529  
FT TRANSMEM 530 551  
FT DOMAIN 552 574  
FT TRANSMEM 575 598  
FT DOMAIN 599 609  
FT TRANSMEM 610 631  
FT DOMAIN 632 700  
FT REPEAT 52 75  
FT REPEAT 126 150  
FT REPEAT 176 200  
FT REPEAT 225 248  
FT DISULFID 443 518  
FT CARBOHYD 103 103  
FT CARBOHYD 178 178  
FT CARBOHYD 199 199  
FT CARBOHYD 295 295  
FT CARBOHYD 303 303  
FT CARBOHYD 317 317  
SQ SEQUENCE 700 AA; 78214 MW; 8A6840A011E1E014 CRC64;  
Query Match 50.1%; Score 1799; DB 1; Length 700;  
Best Local Similarity 55.1%; Pred. No. 1e-107;  
Matches 362; Conservative 108; Mismatches 153; Indels 34; Caps 9;  
Oy 45 PRNATELREVLTKL--RVIPKGSFAGFGDLEKIEISQSDLSLEKIEANAFDNLNLSEIL 102  
Db 51 PRAGL-ARLSLTPLPKVIPSQAFRLNEVKIEISQSDLSLEKIEANAFDNLNLSEIL 109

OY 103 EKANNLITINPFAONLPSLYLLISNGIKULPAVYKIQSLQ-KVLLDQTDQNHINIVA 161  
DB 110 ONTKNLLYIEPCATNLPKALYSTGTRIGRLDPSKLSSEFNFEILECNDLITTP 169  
OY 162 RNSPGLSIPESVILKSKNGTEEHNCANGTOLDLNLSONNNLEELPNDVFOGASCPY 221  
DB 170 GNAPOGMNNESTLLKLYNGPEVOSHAFNGTLLSLKELNIVLEKMSGTFOGATPS 229  
OY 222 ILDIRTKVHSLPHNGLEKLLKRLARSTYRLKLPNDKFTVLMWASLYTPSHCCAFANL 281  
DB 230 ILVDSSTKQALPGLSGLSIOTLATSSYSLATPLSRKFTSLVATLYTPSHCCAFANL 289  
OY 282 KROISELHPICNKSILRODDDMTOIGDQVSLDDDEPSYG---KGSOMMYNEFDYDLCN 338  
DB 290 PKR-----SQPSPSIFENFSKQCESTVEANNETLYSAIFENELSGMDYDFCS 341  
OY 339 EYVDVTCSPKPDANPCDINGYHNLVILWIFSLATGNTVTVLVITSTQKTVPRP 398  
DB 342 PKT-LOCTPEPDANPCDINGYHNLVILWILNLAIFONLVTVLVITSTQKTVPRP 400  
OY 399 LACNLAFADLCIGYLLLASVDYHTKSOYHVAIDMOTGACDAGFEFTVPASELSVYT 458  
DB 401 LACNLAFADPCMGYLLLASVDYHTKSOYHVAIDMOTGACDAGFEFTVPASELSVYT 460  
OY 459 LTAITLERHTITHAMOLECIVOLRHAASVWLVGTFAPFAALPFIPIGSSYMKVSIQPL 518  
DB 461 LTVITLERHTITVAOLDOQLRLRHATIPMLGGWIFSTLMAATLPLVGVSSYMKVSIQPL 520  
OY 519 MDIDSPLSQLYVALLVNLVAFVYCCCTHYLYTVRNPTIVSSSDTKIARMTALIF 578  
DB 521 MDVSTLSQVYITSLILNLVAFVYCACTRYIYFVONPELTAPOKOTKIARKMALIF 580  
OY 579 TDFLCAPISFPAISALVPLTVSKAKLLVLYPINSANPFLIATFKNPRDFPI 638  
DB 581 TDFTCAPISFPAISALVPLTVSKAKLLVLYPINSANPFLIATFKNPRDFPI 640  
OY 639 LLSKPGCYENAOIYRTSSA-----TINPARKS-----HCS--SAPRV 677  
DB 641 LLSRPGCKHRAELRYRKEPSACTFNSANGFPSSKPSOAMKLISIVHCQPTPRV 697  
  
RESULT 14  
LSHR\_RAT  
ID AC P16235: P70646; 063807; 063808; 063809; PRT: 700 AA.  
DT 01-APR-1990 (Rel. 14, Created)  
DI 02-APR-1990 (Rel. 14, Last sequence update)  
DE LSH-R (Lutropin-choriogonadotropin hormone receptor precursor (LH/CG-R)  
GN LSH-R (Luteinizing hormone receptor).  
OS Rattus norvegicus (Rat).  
OC Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89332512; PubMed=2502842;  
RA Rosenblatt N., Nikolics K., Segaloff D.L., Seeburg P.H.,  
RT "Lutropin-choriogonadotropin receptor: an unusual member of the G  
protein-coupled receptor family.",  
RL Mol. Cell. Endocrinol. 245:494-499(1999).  
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
RX STRAIN-Sprague-Dawley; Tissue-Ovary;  
RC MEDLINE=93347604; PubMed=13533463;  
RA AasLanki J.T., Pietila E.M., Lakkakorpi J.T., Rajaniemi H.J.,  
RT "Expression of the LH/CG receptor gene in rat ovarian tissue is  
regulated by an extensive alternative splicing of the primary  
transcript.",  
RL Mol. Cell. Endocrinol. 84:127-135(1992).  
RN [3]  
  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91209270; PubMed=2019252;  
RA Roo Y.B., Slaughter R.G., Ji T.H.,  
RT "Structure of the luteinizing hormone receptor gene and multiple  
exons of the coding sequence.",  
RL Endocrinology 128:2297-2308(1991).  
RN [4]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=91006819; PubMed=1976554;  
RA Bernard M.P., Myers R.V., Moyle W.R.,  
RT "Cloning of rat lutropin (LH) receptor analogs lacking the soybean  
lectin domain.",  
RL Mol. Cell. Endocrinol. 71:R19-R23(1990).  
RN [5]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=91126285; PubMed=2281186;  
RA Segaloff D.L., Sprengel R., Nikolics K., Ascoli M.,  
RT "Structure of the lutropin/choriogonadotropin receptor.",  
RL Recent Prog. Horm. Res. 46:261-303(1990).  
RN [6]  
RP SEQUENCE OF 295-700 FROM N.A.  
RX MEDLINE=91060531; PubMed=2174034;  
RA Tsai-Morris C.H., Buckle E., Wang W., Dufau M.L.,  
RT "Intronic nature of the rat luteinizing hormone receptor gene defines  
a soluble receptor subtypes with hormone binding activity.",  
RL J. Biol. Chem. 265:19385-19388(1990).  
RN [7]  
RP SEQUENCE OF 27-37.  
RX MEDLINE=89174723; PubMed=2925659;  
RA Roche P.C., Ryan R.J.,  
RT "Purification, characterization, and amino-terminal sequence of rat  
ovarian receptor for luteinizing hormone/human chorogonadotropin.",  
RL J. Biol. Chem. 264:4636-4641(1989).  
RN [8]  
RP MUTAGENESIS.  
RX MEDLINE=91332007; PubMed=1714448;  
RA Ji T.H.,  
RT "Asp183 in the second transmembrane domain of the lutropin receptor  
is important for high affinity hormone binding and cAMP production.",  
RL J. Biol. Chem. 266:14953-14957(1991).  
CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.  
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
CC ACTIVATE ADENYLATE CYCLASE.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 11 ISOFORMS WHICH DIFFER IN  
CC SUBCELLULAR LOCATION ARE PRODUCED BY ALTERNATIVE SPLICING  
CC OF THE SAME GENE.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -1- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).  
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CC -----  
DR EXBL: M26199; AAA1528.1;  
DR EXBL: M61212; AAA1527.1;  
DR EXBL: M61211; AAA1527.1; JOINED.  
DR EXBL: S40803; AAB22680.1;  
DR EXBL: S40787; AAB22680.1; JOINED.  
DR EXBL: S40903; AAB22680.1; JOINED.  
DR EXBL: S40905; AAB22680.1; JOINED.  
DR EXBL: S40907; AAB22680.1; JOINED.  
DR EXBL: S40909; AAB22680.1; JOINED.  
DR EXBL: S40918; AAB22680.1; JOINED.  
DR EXBL: S40920; AAB22680.1; JOINED.  
DR EXBL: S40795; AAB22680.1; JOINED.  
DR EXBL: S40798; AAB22680.1; JOINED.

DR	ENBL;	S40795;	AAB22681.1;	-
DR	ENBL;	S40787;	AAB22681.1;	JOINED.
DR	ENBL;	S40903;	AAB22681.1;	JOINED.
DR	ENBL;	S40904;	AAB22681.1;	JOINED.
DR	ENBL;	S40905;	AAB22681.1;	JOINED.
DR	ENBL;	S40907;	AAB22681.1;	JOINED.
DR	ENBL;	S40909;	AAB22681.1;	JOINED.
DR	ENBL;	S40918;	AAB22681.1;	JOINED.
DR	ENBL;	S40920;	AAB22681.1;	JOINED.
DR	ENBL;	S40803;	AAB22682.2;	-
DR	ENBL;	S40787;	AAB22682.2;	JOINED.
DR	ENBL;	S40903;	AAB22682.2;	JOINED.
DR	ENBL;	S40907;	AAB22682.2;	JOINED.
DR	ENBL;	S40909;	AAB22682.2;	JOINED.
DR	ENBL;	S40918;	AAB22682.2;	JOINED.
DR	ENBL;	S40920;	AAB22682.2;	JOINED.
DR	ENBL;	S40795;	AAB22682.2;	JOINED.
DR	ENBL;	S40798;	AAB22682.2;	JOINED.
DR	ENBL;	S40803;	AAB22683.1;	-
DR	ENBL;	S40787;	AAB22683.1;	JOINED.
DR	ENBL;	S40903;	AAB22683.1;	JOINED.
DR	ENBL;	S40904;	AAB22683.1;	JOINED.
DR	ENBL;	S40905;	AAB22683.1;	JOINED.
DR	ENBL;	S40907;	AAB22683.1;	JOINED.
DR	ENBL;	S40909;	AAB22683.1;	JOINED.
DR	ENBL;	S40918;	AAB22683.1;	JOINED.
DR	ENBL;	S40920;	AAB22683.1;	JOINED.
DR	ENBL;	S40795;	AAB22683.1;	JOINED.
DR	ENBL;	S40798;	AAB22683.1;	JOINED.
DR	ENBL;	S40803;	AAB22684.2;	-
DR	ENBL;	S40787;	AAB22684.2;	JOINED.
DR	ENBL;	S40903;	AAB22684.2;	JOINED.
DR	ENBL;	S40904;	AAB22684.2;	JOINED.
DR	ENBL;	S40905;	AAB22684.2;	JOINED.
DR	ENBL;	S40909;	AAB22684.2;	JOINED.
DR	ENBL;	S40918;	AAB22684.2;	JOINED.
DR	ENBL;	S40920;	AAB22684.2;	JOINED.
DR	ENBL;	S40795;	AAB22684.2;	JOINED.
DR	ENBL;	S40798;	AAB22684.2;	JOINED.
DR	ENBL;	M68928;	AAA41529.1;	-
DR	ENBL;	M68917;	AAA41529.1;	JOINED.
DR	ENBL;	M68918;	AAA41529.1;	JOINED.
DR	ENBL;	M68919;	AAA41529.1;	JOINED.
DR	ENBL;	M68920;	AAA41529.1;	JOINED.
DR	ENBL;	M68921;	AAA41529.1;	JOINED.
DR	ENBL;	M68922;	AAA41529.1;	JOINED.
DR	ENBL;	M68923;	AAA41529.1;	JOINED.
DR	ENBL;	M68925;	AAA41529.1;	JOINED.
DR	ENBL;	M68926;	AAA41529.1;	JOINED.
DR	ENBL;	M68927;	AAA41529.1;	JOINED.
DR	PIR;	A32460;	A32460.	
DR	HSP;	P22888;	ILUT.	
DR	InterPro;	IPR000276;	GPCR_Rhodpsn.	
DR	InterPro;	IPR001611;	LRR.	
DR	InterPro;	IPR000372;	LRR_Nterm.	
DR	Pfam;	PF00001;	7tm_1; 1.	
DR	Pfam;	PF00560;	Lrrt; 1.	
DR	SMART;	SM00013;	LRRT; 1.	
DR	PROSITE;	PS00237;	G_PROTEIN_RECP_FL1_1; 1.	
DR	PROSITE;	PS00262;	G_PROTEIN_RECP_FL2_1; 1.	
KW	g-protein coupled receptor; Transmembrane; Glycoprotein; Signal;			
KW	phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing			
FT	SIGNAL	1	26	
FT	CHAIN	27	700	LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR.
FT	DOMAIN	27	362	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	363	390	1 (POTENTIAL).
FT	DOMAIN	391	399	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	400	422	2 (POTENTIAL).
FT	DOMAIN	423	443	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	444	466	3 (POTENTIAL).
FT	DOMAIN	467	486	CYTOPLASMIC (POTENTIAL).

RESULT 15  
LSHR HUMAN  
ID LSHR HUMAN STANDARD; PRT: 699 AA.  
AC P2388;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lutropin-chorionadotropin hormone receptor precursor (LH/CG-R)  
DE (LSH-R) (luteinizing hormone receptor).  
GN LHCR OR LHRR OR LCR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
PC TISSUE:Ovary;  
RC TISSUE:Ovary;  
RX MINEIGH T.; Nakamura K., Takakura Y., Miyamoto K., Hasegawa Y.,  
RX Ibuki Y., Igarashi M.;  
RT "Cloning and sequencing of human LH/hCG receptor cDNA.";  
RL Biochem. Biophys. Res. Commun. 172:1049-1054(1990).  
RN [2]  
RC TISSUE:Ovary;  
RX Frazier A.L., Robbins L.S., Scott P.J., Sprengel R., Segaloff D.L.,  
RX Cone R.D.;  
RT "Isolation of TSH and LH/CG receptor cDNAs from human thyroid:  
RT regulation by tissue specific splicing.";  
RL Mol. Endocrinol. 4:1264-1276(1990).  
RN [4]  
RN 3D-STRUCTURE MODELING OF 51-232.  
RX MEDLINE-96363672; PubMed-8747461;  
RX Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A.; Wu H.,  
RX Hendrickson W.A., el Teyar N.;  
RT "Structural predictions for the ligand-binding region of glycoprotein  
RT hormone receptors and the nature of hormone-receptor interactions.";  
RN Structure 3:1341-1353(1995).  
RN [5]  
RX VARIANT FMPP GLY-578.  
RX Shenker A., Laue L., Kosugi S., Merendino J.J. Jr., Minegishi T.,  
RX Cutler G.B. Jr.;  
RT "A constitutively activating mutation of the luteinizing hormone  
RT receptor in familial male precocious puberty.";  
RL Nature 365:652-654(1993).  
RN [6]  
RX VARIANTS FMPP ILE-571 AND GLY-578.  
RX MEDLINE-94108425; PubMed-8281137;  
RX Kremer H., Mariman E., Otten B.J., Moll G.W. Jr., Stoeltinga G.B.A.,  
RX Wit J.M., Jansen M., Drop S.L., Paas B., Ropers H.-H., Brunner H.G.;  
RT "Coregulation of missense mutations of the luteinizing hormone  
RT receptor gene in familial male limited precocious puberty.";  
RL Hum. Mol. Genet. 2:1779-1782(1993).  
RN [7]  
RX VARIANT FMPP ILE-577.  
RX MEDLINE-95276728; PubMed-7757065;  
RX Kosugi S., van Dop C., Geffner M.E., Rabl W., Carel J.-C.,  
RX Chaussain J.-L., Mori T., Merendino J.J. Jr., Shenker A.;  
RT "Characterization of heterogeneous mutations causing constitutive  
RT activation of the luteinizing hormone receptor in familial male  
RT precocious puberty.";

Hum. Mol. Genet. 4:183-188(1995).  
RN [8]  
RX VARIANT FMPP VAL-572.  
RX MEDLINE-95220804; PubMed-7714085;  
RX Yotsumoto S., Seiji M., Hatake A., Moriya N., Okuno A., Kohn L.D.,  
RX Cutler G.B. Jr.;  
RT "A new constitutively activating point mutation in the luteinizing  
RT hormone/chorionadotropin receptor gene in cases of male-limited  
RT precocious puberty.";  
RL J. Clin. Endocrinol. Metab. 80:1162-1168(1995).  
RN [9]  
RX VARIANT FMPP VAL-568.  
RX MEDLINE-95555560; PubMed-7629248;  
RX Latronico A.C., Anastasi J., Arnhold I.J., Mendonca B.B., Domenice S.,  
RX Albano M.C., Zachman K., Wajchenberg B.L., Taigos C.;  
RT "A novel mutation of the luteinizing hormone receptor gene causing  
RT male gonadotropin-independent precocious puberty.";  
RL J. Clin. Endocrinol. Metab. 80:2490-2494(1995).  
RN [10]  
RX VARIANT LCH PRO-593.  
RX MEDLINE-55235561; PubMed-7719343;  
RX Kremer H., Kralj R., Toledo S.P.A., Post M., Fridman J.B.,  
RX Hayashida C.Y., van Reen H.G.;  
RT "Male pseudohermaphroditism due to a homozygous missense mutation of  
RT the luteinizing hormone receptor gene.";  
RL Nat. Genet. 9:160-164(1995).  
RN [11]  
RX VARIANT FMPP ILE-577.  
RX MEDLINE-96233936; PubMed-8829636;  
RX Cocco S., Meloni A., Marini M.G., Cao A., Mol P.;  
RT "A missense (T577I) mutation in the luteinizing hormone receptor gene  
RT associated with familial male-limited precocious puberty.";  
RL Hum. Mutat. 7:164-166(1996).  
RN [12]  
RX VARIANT FMPP THR-398.  
RX MEDLINE-97083378; PubMed-8929952;  
RX Evans B.J., Bernal J., Smith P.J., Clayton P.E., Gregory J.M.;  
RT "A new point mutation in the luteinizing hormone receptor gene in  
RT familial and sporadic male limited precocious puberty: genotype does  
RT not always correlate with phenotype.";  
RL J. Med. Genet. 33:143-147(1996).  
RN [13]  
RX VARIANT LCH TYR-616.  
RX MEDLINE-96157015; PubMed-8559204;  
RX Latronico A.C., Anastasi J., Arnhold I.J.P., Rapaport R., Mendonca B.B.,  
RX Bloise W., Castro M., Tsigos C., Chrousos G.P.;  
RT "Brief report: testicular and ovarian resistance to luteinizing  
RT hormone caused by inactivating mutations of the luteinizing  
RT hormone-receptor gene.";  
RL N. Engl. J. Med. 334:507-512(1996).  
RN [14]  
RX VARIANT LCH ARG-131.  
RX MEDLINE-97358168; PubMed-9215288;  
RX Misrahi M., Meduri G., Plessard S., Bouvattier C., Beau I.,  
RX Loosfelt H., Jollivet A., Rapaport R., Milgrom E., Bougneres P.;  
RT "Comparison of immunocytochemical and molecular features with the  
RT phenotype in a case of incomplete male pseudohermaphroditism  
RT associated with a mutation of the luteinizing hormone receptor.";  
RL J. Clin. Endocrinol. Metab. 82:2159-2165(1997).  
RN [15]  
RX VARIANTS LEU-CLN-13 INS; SER-284 AND ASN-306.  
RX Wu S.-M., Jose M., Hallmeier K., Rennert O.M., Chan W.-Y.;  
RT "Polymorphisms in the coding exons of the human luteinizing hormone  
RT receptor gene.";  
RL Mutat. 11:333-334(1998).  
RN [16]  
RX VARIANT FMPP VAL-373.  
RX MEDLINE-98128689; PubMed-9467560;  
RX Gromell J., Partsch C.-J., Simoni M., Nordhoff V., Sippell W.G.,  
RX Mieschlag E., Saxena B.B.;  
RT "A mutation in the first transmembrane domain of the lutropin receptor  
RT causes male precocious puberty.";







KW Receptor. 688 AA; 77341 MW; 441F0D9E7D01DF18 CRC64;  
SQ SEQUENCE 688 AA; 77341 MW; 441F0D9E7D01DF18 CRC64;  
Query Match 99.1%; Score 3560; DB 11; Length 688;  
Best Local Similarity 99.3%; Pred. No. 1.4e-256;  
Matches 687; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 MALLVSLAFLGTGGCHHMLCHCSNRVFLQDSKVTEIPTDLPNATIELRVLTCLR 60  
DB 1 MALLVSLAFLGTGGCHHMLCHCSNRVFLQDSKVTEIPTDLPNATIELRVLTCLR 60  
QY 61 IPKGSFAGDLEKIEISQNDVLEADVFNPLKHEIRIEKANNLLYINPEAFONLP 120  
DB 61 IPKGSFAGDLEKIEISQNDVLEADVFNPLKHEIRIEKANNLLYINPEAFONLP 120  
QY 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIODNINIHIVARNSPMGLSFESVILWLSKN 180  
DB 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIODNINIHIVARNSPMGLSFESVILWLSKN 180  
QY 181 GIEEIHNCFAFNGTQDDELNLSDNNLELPNDVFOGASGPVILDISRTKVHSLPNHGLN 240  
DB 177 GIEEIHNCFAFNGTQDDELNLSDNNLELPNDVFOGASGPVILDISRTKVHSLPNHGLN 236  
QY 241 LKLLRARSYRLKLPNLDKFTVLMASLTYPHCCAFANLKRQISELHPICNKSILROD 300  
DB 237 LKLLRARSYRLKLPNLDKFTVLMASLTYPHCCAFANLKRQISELHPICNKSILROD 296  
QY 301 IDDMTOIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIM 360  
DB 297 IDDMTOIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIM 356  
QY 361 YNLRVLWIFISILAITGNTVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLIASV 420  
DB 357 YNLRVLWIFISILAITGNTVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLIASV 416  
QY 421 DIHTKSOYHNYAIDMOTGAGDAAGFTVFASLSVYTLTATLERWHITTHAMOLECKV 480  
DB 417 DIHTKSOYHNYAIDMOTGAGDAAGFTVFASLSVYTLTATLERWHITTHAMOLECKV 476  
QY 481 QLRHAASVMVLTGTFATAALPFIIGISSYKMKVSIKLPMDIDSPLSQLYMALLVNLVA 540  
DB 477 QLRHAASVMVLTGTFATAALPFIIGISSYKMKVSIKLPMDIDSPLSQLYMALLVNLVA 536  
QY 541 FVVICGCTHYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFAISASLKVP 600  
DB 537 FVVICGCTHYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFAISASLKVP 596  
QY 601 ITVSKAKILLVFPINSCANPLYAIFTKNFRDRFFILLSKFGCYEMQAQIYRTTSSA 660  
DB 597 ITVSKAKILLVFPINSCANPLYAIFTKNFRDRFFILLSKFGCYEMQAQIYRTTSSA 656  
QY 661 THNFHARKSHCSSAPRVTSYVLPVPLNHSSQN 692  
DB 657 THNFHARKSHCSSAPRVTSYVLPVPLNHSSQN 688

RESULT 2  
Q8R428 PRELIMINARY; PRT; 695 AA.  
AC Q8R428;  
DT 01-JUN-2002 (T-EMBLrel. 21, Created)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
DE Follicle stimulating hormone receptor.  
GN FSHR.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA SUZUKI O.;

RT \*Guinea pig follicle stimulating hormone receptor.\*;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY082514; AAL92577.1;  
KW Receptor.  
SQ SEQUENCE 695 AA; 77838 MW; 9A3ECF419C45227B CRC64;  
Query Match 87.5%; Score 3144.5; DB 11; Length 695;  
Best Local Similarity 87.1%; Pred. No. 1.2e-225;  
Matches 605; Conservative 38; Mismatches 49; Indels 3; Gaps 2;

QY 1 MALLVSLAFLGTGGCHHMLCHCSNRVFLQDSKVTEIPTDLPNATIELRVLTCLR 60  
DB 1 MALLVSLAFLGTGGCHHMLCHCSNRVFLQDSKVTEIPTDLPNATIELRVLTCLR 60  
QY 61 IPKGSFAGDLEKIEISQNDVLEADVFNPLKHEIRIEKANNLLYINPEAFONLP 120  
DB 61 IPKGSFAGDLEKIEISQNDVLEADVFNPLKHEIRIEKANNLLYINPEAFONLP 120  
QY 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIODNINIHIVARNSPMGLSFESVILWLSKN 180  
DB 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIODNINIHIVARNSPMGLSFESVILWLSKN 180  
QY 181 GIEEIHNCFAFNGTQDDELNLSDNNLELPNDVFOGASGPVILDISRTKVHSLPNHGLN 240  
DB 181 GIEEIHNCFAFNGTQDDELNLSDNNLELPNDVFOGASGPVILDISRTKVHSLPNHGLN 240  
QY 241 LKLLRARSYRLKLPNLDKFTVLMASLTYPHCCAFANLKRQISELHPICNKSILROD 300  
DB 241 LKLLRARSYRLKLPNLDKFTVLMASLTYPHCCAFANLKRQISELHPICNKSILROD 300  
QY 301 IDDMTOIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIM 359  
DB 301 VNDITQAGAQVSLAEDDEFYSRGFDYAEFDYDLCEVVDVTCSPKPDAPNCPEDIM 360  
QY 360 GYNILRVLWIFISILAITGNTVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLIAS 419  
DB 361 GYNILRVLWIFISILAITGNTVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLIAS 420  
QY 420 VDIHTKSOYHNYAIDMOTGAGDAAGFTVFASLSVYTLTATLERWHITTHAMOLECK 479  
DB 421 VDVHTRTLHNYAIDMOTGAGDAAGFTVFASLSVYTLTATLERWHITTHAMOLECK 480  
QY 480 VQLRHAASVMVLTGTFATAALPFIIGISSYKMKVSIKLPMDIDSPLSQLYMALLVNLVA 539  
DB 481 VQLRHAASVMVLTGTFATAALPFIIGISSYKMKVSIKLPMDIDSPLSQLYMALLVNLVA 540  
QY 540 AFVVICGCTHYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFAISASLKVP 599  
DB 541 AFVVICGCTHYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFAISASLKVP 600  
QY 600 LITVSKAKILLVFPINSCANPLYAIFTKNFRDRFFILLSKFGCYEMQAQIYRTTSS 659  
DB 601 LITVSKAKILLVFPINSCANPLYAIFTKNFRDRFFILLSKFGCYEMQAQIYRTTSS 660  
QY 660 ATHNFHARKSHCSSAPRVTSYVLPVPLNHSSQN 692  
DB 661 TANHSHPRNGSHSSSVSRVTNGSSYILAPLNHLAQN 695

RESULT 3  
Q9DGF5 PRELIMINARY; PRT; 696 AA.  
AC Q9DGF5;  
DT 01-MAR-2001 (T-EMBLrel. 16, Created)  
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
DE Follicle-stimulating hormone receptor precursor.  
OS Cynops pyrrhogaster (Japanese common newt).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae; Cynops.  
OX NCBI\_TaxID=8330;  
RN [1]  
RP SEQUENCE FROM N.A.

TISSUE-TESTIS; PubMed-10944452;  
RA Nakayama Y., Yamamoto T., Oba Y., Nagahama Y., Abe S.-I.:  
RT "Molecular cloning, functional characterization, and gene expression  
of a follicle-stimulating hormone receptor in the testis of newt  
Cynops pyrrhogaster";  
RL Biochem. Biophys. Res. Commun. 275:121-128(2000).  
DR HSP: P23945; 1XUN.  
DR EMBL: AB005587; BAB13501.1; .  
DR InterPro: IPR000276; GPCR\_Rhodopsin.  
DR InterPro: IPR001611; LRR.  
DR Pfam: PF00560; LRR; 2.  
DR Pfam: PF00560; LRR; 1.  
DR SMART: SM00017; GPCR\_Rhodopsin.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE: PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KN Receptor; Signal.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 696 POTENTIAL.  
SQ SEQUENCE 696 AA; 78633 MW; 179A6FC80B71E57 CRC64;  
Query Match 69.8%; Score 2507; DB 13; Length 696;  
Best Local Similarity 70.5%; Pred. No. 3.3e-178;  
Matches 490; Conservative 84; Mismatches 113; Indels 8; Gaps 5;  
OY 1 MALLVSLLAFLATGSGCHHLCNSRVFLCQDSKVTETPTDLPNRIATELRFVTLKRV 60  
DB 1 MSIAIICLLAVGSSPCCHP-VCRCLARVFTQCSHVQIPRIPRNSTELRFVTLKRV 59  
OY 61 IPKSGFAGGLEKIEISONDVLEYDAVFSNLPKLHEIRIEKANLLTYINPEAFON 120  
DB 60 IPRAKSGFEDVNEIISONDVLEIKTIANFSLHPLKYEIRIEKANLLTYINPEAFON 119  
OY 121 SLRYLLISNTGKIHLPVAVKIQSLQKVLVDODNINIHVARNSPAGLSFESVILMLS 180  
DB 120 SLKYLISNTGIVLPVAVKIRSFHSLVQVODNINIRHIGKSFAGLSFESVITRLAKN 179  
OY 181 GEEITHKAFNCTGLDELNSDNNHLEPNDFOGASGPVILDSRTKYVHSLPNGLN 240  
DB 180 GEEITHKAFNCTGLDELNSDNNHLEPNDFOGASGPVILDSRTKYVHSLPNGLN 239  
OY 241 LKLRARSTYRLKLPNLDKFTVILMEASLTPSHCCAFANLKROISELHPICNKSILROD 300  
DB 240 IKYFRANFTLKLPLLEAFLEATLNTLTPSHCCAFANRERKSEHHPICNKSFGKHD 299  
OY 301 IDDMTOIGD-QRYSLIDDESGKSGDMN--EPDYP--LCNEVDVYTCSPKPAFNPC 355  
DB 300 SAEKPEKHLRSNEDLSYSGPSYSLVENCDEFYDYLCEVHEDVYCFKPDAPNCP 359  
OY 356 EDIMGNILRWLWFLPISLITAGTNTVVLVLTTSQYKLTVPRLMCLNLAFAOLCIGIYLL 415  
DB 360 EDIMGNILRWLWFLPISLITAGTNTVVLVLTTSQYKLTVPRLMCLNLAFAOLCIGIYLL 419  
OY 416 LIASVDHTKSOYHNTAIDMOTGACGACGFFTFVASELSYVTLTALTLEWHHTTHAQ 475  
DB 420 LIASVDHTKSOYHNTAIDMOTGACGACGFFTFVASELSYVTLTALTLEWHHTTHAQ 479  
OY 476 LECVKVLRHAASVYVLTGTPAALAFPIFGISSTMYKVSICLPMIDSPLSQLYNALLY 535  
DB 480 LORVAFRHTAHVYVLTGTPAALAFPIFGISSTMYKVSICLPMIDSPLSQLYNALLY 539  
OY 536 LNVLPVWICCGTHYLTVRNPTVSSSDPKTAKRMATLITDPLCMAPISFALSAS 595  
DB 540 LNVCAFLICACTIGIYLTVRNPTVSSSDPKTAKRMATLITDPLCMAPISFALSAS 599  
OY 596 LKVLPTVSKARILLVYPTVNSCANPLVAFKTRNDFDFLLSKFGCYEKQAIYRT 655  
DB 600 LKVLPTVSKARILLVYPTVNSCANPLVAFKTRNDFDFLLSKFGCYEKQAIYRT 659  
OY 656 ETSSTANTENFARKSHCSAPR--VTNSYVLPVPLNR 688  
DB 655 ETSSTANTENFARKSHCSAPR--VTNSYVLPVPLNR 688

DB 660 EYSSLSHNSHNRHGRVTPAPKYSASHTLVPLNN 694  
RESULT 4  
O90MP8  
ID O90MP8 PRELIMINARY; PRT: 673 AA.  
AC O90MP8  
DT 01-DEC-2001 (TRENBLREL. 19, Created)  
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)  
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
DE FSH receptor.  
OS FSH RECEPTOR.  
OS Podarcis sicula.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Scincomorpha; Lacertoides;  
OC Lacertidae; Podarcis.  
OX NCBI\_TaxID=63484;  
RN [1]  
RC SEQUENCE FROM N.A.  
RS NCBI\_TaxID=63484;  
RX MEDLINE=21459565; PubMed=11574163;  
RA Borrelli L, De Stefano R, Parigi G., Filosa S.;  
RT "Molecular cloning, sequence and expression of follicle-stimulating  
hormone receptor in the lizard Podarcis sicula";  
RL EMBL: AJ292553; CAC82173.1; .  
DR InterPro: IPR000276; GPCR\_Rhodopsin.  
DR InterPro: IPR001611; LRR.  
DR Pfam: PF00560; LRR; 1.  
DR Pfam: PF00560; LRR; 2.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE: PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 673 AA; 76288 MW; 688994C8B5F67B5 CRC64;  
Query Match 55.1%; Score 1979; DB 13; Length 673;  
Best Local Similarity 59.5%; Pred. No. 6.3e-13;  
Matches 414; Conservative 81; Mismatches 151; Indels 50; Gaps 12;  
OY 8 LLALFLATGSGCHHLC--CSNRVFLCQDSKVTETP--TOLPRNATELRFVTLKRVIP--- 62  
DB 11 LLLALGSGSG--HPTCPLDNLMTCDQSKVTQPTQSERHG-----TGIPPHON 59  
OY 63 ----KGSFAGGLEKIEISONDVLEYDAVFSNLPKLHEIRIEKANLLTYINPEAFON 118  
DB 60 KHTERAFVGLDVEKIEISONDALGTIESVFLKPLKYEIRIEKANLLTYINPEAFON 119  
OY 119 LPSRYLLISNTGKIHLPVAVKIQSLQKVLVDODNINIHVARNSPAGLSFESVILMLS 178  
DB 120 LPSRYLLISNTGKIHLPVAVKIQSLQKVLVDODNINIHVARNSPAGLSFESVILMLS 179  
OY 179 KNGTEITHKAFNCTGLDELNSDNNHLEPNDFOGASGPVILDSRTKYVHSLPNGL 238  
DB 180 KNGTEITHKAFNCTGLDELNSDNNHLEPNDFOGASGPVILDSRTKYVHSLPNGL 239  
OY 239 ENLKRARSTYRLKLPNLDKFTVILMEASLTPSHCCAFANLKROISELHPICNKSILR 298  
DB 240 EKINKLARSAYNLKRVPLDKFASLLEANTLTPSHCCAFANMTKONSPFHPICNKSIL 299  
OY 299 ODIDDMTOIGDQRYSLIDDESGYKSGDM--MYNEFDY--DLCNEVDVYTCSPKPAFNPC 355  
DB 300 LQTD-----G-----GTFDLDDEHDYQSLCEEYEVICFPDAPNCP 338  
OY 356 EDIMGNILRWLWFLPISLITAGTNTVVLVLTTSQYKLTVPRLMCLNLAFAOLCIGIYLL 415  
DB 339 EDIMGNILRWLWFLPISLITAGTNTVVLVLTTSQYKLTVPRLMCLNLAFAOLCIGIYLL 398  
OY 416 LIASVDHTKSOYHNTAIDMOTGACGACGFFTFVASELSYVTLTALTLEWHHTTHAQ 475  
DB 399 LIATKIDQTSKSOYHNTAIDMOTGACGACGFFTFVASELSYVTLTALTLEWHHTTHAQ 457  
OY 476 LECVKVLRHAASVYVLTGTPAALAFPIFGISSTMYKVSICLPMIDSPLSQLYNALLY 535  
DB 475 LECVKVLRHAASVYVLTGTPAALAFPIFGISSTMYKVSICLPMIDSPLSQLYNALLY 535

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Db 458 LNKVRFQAVAPMLVGMFAFTVAIPFQVSSYMKVSLCLPMDIETPPCOAYINFLV 517
QY 536 LNVAFVWICGCTHYLYVRNPRTIVSSSDTKIAKRMATLFTDFLCMAPISFFAISAS 595
Db 518 LNLAFLLIISTYISYITVTRNTIISNDTKIAKRMATLFTDFLCMAPISFFAISAS 577
QY 596 LKPLITVSKAKILLVLPINSCAN-PFLYAIFTKNFRDRPFIILSKFCGYEMOQAIYR 654
Db 578 LKPLITVSKAKILLVLPINSCAN-PFLYAIFTKNFRDRPFIILSKFCGYEMOQAIYR 635
QY 655 TETSTATHNPHARKSHCSSAPRTN--SYVLVPLNH 688
Db 636 TETSTVPTSHMKNHGCTPASKASEGPAVALVPLNY 671

RESULT 5
Q16225 PRELIMINARY; PRT; 410 AA.
AC Q16225;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Follicle-stimulating hormone receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95000244; PubMed=7916967;
RA Gromoll J., Ried T., Holtgreve-Grez H., Nieschlag E., Gudermann T.;
RT "Localization of the human FSH receptor to chromosome 2 p21 using a
RT genonic probe comprising exon 10.";
RL J. Mol. Endocrinol. 12:265-271(1994).
DR EMBL; S73526; AAB32225.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT SIGNAL 1 22 POTENTIAL.
FT NON_TER 1
SQ SEQUENCE 410 AA; 46008 MW; F345E029C16BC792 CRC64;

Query Match 52.98; Score 1901.5; DB 4; Length 410;
Best Local Similarity 89.58; Pred. No. 2e-133;
Matches 367; Conservative 15; Mismatches 25; Indels 3; Gaps 2;

QY 286 SELHPICNKSILRQIDDMQIGDQVSLIDD-EPYSGKSDMMYNEFDYDLCNEVDVT 344
Db 1 SELHPICNKSILRQVDYDMQTRQORSLAEDNESSYRGFDYTYEFDYDLCNEVDVT 60
QY 345 CSPKPDAPNCPEDIMGVNIILRVLIWFTSILAIGNTTVLVLTQSYKLVPRFLMCLNLA 404
Db 61 CSPKPDAPNCPEDIMGVNIILRVLIWFTSILAIGNTTVLVLTQSYKLVPRFLMCLNLA 120
QY 405 FADLCIGYILLTASVDIHTKSOYHNYAIDMOTGACDGAAGFTVFASLSVYTLTATL 464
Db 121 FADLCIGYILLTASVDIHTKSOYHNYAIDMOTGACDGAAGFTVFASLSVYTLTATL 180
QY 465 ERWHTITHAMOLECKVQLRHAASVWVLGWTFAFAAALPFIIGISSYMKVSIICLPMDIDSP 524
Db 181 ERWHTITHAMOLECKVQLRHAASVWVWVWIFAFAAALPFIIGISSYMKVSIICLPMDIDSP 240
QY 525 LSQLYVMALLVNLVAFVWICGCTHYLYVRNPRTIVSSSDTKIAKRMATLFTDFLCM 584
Db 241 LSQLYVMALLVNLVAFVWICGCTHYLYVRNPRTIVSSSDTKIAKRMATLFTDFLCM 300
QY 585 APISFFAISASLKVPLITVSKAKILLVLPINSCANPFLYAIFTKNFRDRPFIILSKFG 644
Db 301 APISFFAISASLKVPLITVSKAKILLVLPINSCANPFLYAIFTKNFRDRPFIILSKFG 360
QY 645 CYENQAOIYRTETSSATHNFHARKSHCSSAPRTV--NSYVLVPLNHSSQN 692
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Db 361 CYENQAOIYRTETSSATHNFHARKSHCSSAPRTVSGTTLVPLSHLAQN 410

RESULT 6
Q98T84 PRELIMINARY; PRT; 662 AA.
AC Q98T84;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Follicle-stimulating hormone receptor precursor.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Kumar R.S., Ijiri S., Trant J.M.;
RT "Molecular Biology of Channel Catfish Gonadotropin Receptors: 2. cDNA
RT Cloning, Functional Expression, and Seasonal Gene Expression of the
RT Follicle-Stimulating Hormone Receptor.";
RL Biol. Reprod. 0:0-0(2001).
DR EMBL; AF285182; AAK16067.1; -
DR HSSP; P23945; 1XUN.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF00360; LRR; 4.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 662 AA; 74846 MW; DC179F07A2CADEED CRC64;

Query Match 51.38; Score 1844; DB 13; Length 662;
Best Local Similarity 54.28; Pred. No. 6.9e-129;
Matches 361; Conservative 110; Mismatches 163; Indels 32; Gaps 6;

QY 1 MALLVSLLAFLGTGS-GCHHNLCHCSNRVFLCODSKVTEIPTDLPNATLRFVLTCLR 59
Db 2 MCFILSNLWMMHAGNMCGLGSYACLANGTTSFCLGSKVHOMPHIPKNTYVIEIKLRIL 61
QY 60 VIPKGSFAGDLEKIEISQNDVLEADVFNLSNPKLHEIRIEKANNLLYINPEAFQNL 119
Db 62 MLPSSAMSSLDLKLIVSENGVLQRIEAYAFANLTKLEBITTTKSNLVCMRHTFWGL 121
QY 120 PSRLYLLISNTGKHLPAVHKIOSLO-KVLLDQDNIHINIVARNSPGLSFESVI-LWL 177
Db 122 PKLRYLTISNTGTLVPDFSKVSOAAFEFLFLEDNMHIEVIPSNAFAGTSGITELRL 181
QY 178 SKNGIEIHCNACGQLDELNLSDNNLELNDVFOGASGVPVLDISRTKVHSLPNHG 237
Db 182 TKNIGTEVDNENAGNGKIEKFLMGQQLKRIINYAFAGLGLVLDISTATSSLPENM 241
QY 238 LENKLLKRASTVRLKPLNLDKFTVLMESALYPSHCCAFANLKRIOISELHPICNKSIL 297
Db 242 LRRLKLLIATSVYSLRWLPNLEIFTELTQANLTYPSHCCAFKPKKSEKNRLCNDSTI 301
QY 298 RODIDDMQIGDQVSLIDDPSYSGKSDMMYNEFDYDLCNEVDVTCSKPDAPNCPED 357
Db 302 R-----NOEP-----YFEEHCKDVIEVCYPEPDAFNPCED 333
QY 358 IMGYNILRVLIWFTSILAIGNTTVLVLTQSYKLVPRFLMCLNLAFAADLCIGYILLI 417
Db 334 IMGFTLRVLIWFTSILAIGNTTVLVLTQSYKLVPRFLMCLNLAFAADLCIGYILLI 393
QY 418 ASVDIHTKSOYHNYAIDMOTGACDGAAGFTVFASLSVYTLTATLTERWHTITHAMOLE 477
Db 394 GSVDLQTRSHYNYNGIEWQTGVCGTAGFLTVFASLSVYTLTATLTERWHTITHAMOLE 453
```

466	RHPIITHAHOLECKVOURHASVWVLGMTFAFAALPFGISSYHKVSICLPMIDISPL	525
OY	:     :     :     :     :     :     :     :     :     :	
DB	:     :     :     :     :     :     :     :     :	
466	RHHIITAIQOLKRLAPMLPWGLSGSTLIJLVGVNTNKKYSICLPMIDESTL	525
OY	:     :     :     :     :     :     :     :     :	
DB	:     :     :     :     :     :     :     :     :	
526	SOLVMALLVNLAFVYICGGYTHYLTVNPFTVSSSDSKTKRMATLILFDFLCMA	585
OY	:     :     :     :     :     :     :     :     :	
DB	:     :     :     :     :     :     :     :     :	
526	SOVYLTLTLLNYAIFIACACYIKIFYAVONPELMATNKDKIAKKHVALIFDFTCNA	585
OY	:     :     :     :     :     :     :     :     :	
DB	:     :     :     :     :     :     :     :     :	
586	PISPFAISAASKYPTIVTSKANILLVLPFPINSCANPLVAIFTKNRDRDEFLLSKGC	645
OY	:     :     :     :     :     :     :     :     :	
DB	:     :     :     :     :     :     :     :     :	
586	PISPFAISAALKRYPTIVTSKANILLVLPFPINSCANPLVAIFTKAQRDFLLLSKGC	645
OY	:     :     :     :     :     :     :     :     :	
DB	:     :     :     :     :     :     :     :     :	
646	VEMCAOVIKFTPTSSATINHARKSHCS	673
OY	:   :     :     :     :     :     :     :     :     :	
DB	:   :     :     :     :     :     :     :     :     :	
646	CKYRAELVRKK-----DFSAYINSCKN	667
OY	:     :     :     :     :     :     :     :     :	
DB	:     :     :     :     :     :     :     :     :	

RESULT	8
QSPWID	
ID	QSPH16
AC	QSPH16
DT	PRELIMINARY;
DT	PRT; 662 AA.
DT	
DT	01-MAY-2000 (T=EWBLrel_13, Created)
DT	01-MAY-2000 (T=EWBLrel_13, Sequence update)
DT	01-MAR-2002 (T=EWBLrel_20, Last annotation update)
DE	Follicle-stimulating hormone receptor precursor.
DS	FSH-R
GS	Clarias gariepinus (Sharptooth catfish) (African catfish).
ON	Eukaryota; Metazoa; Craniata; Vertebrate; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Siluriformes;
OC	Characidae; Clariidae.
OX	NCBI_Taxid-13013;
OX	

DR HSSP; P23945; 1XUN.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR001611; LRR.  
DR Pfam; PF00001; 7tm\_1; 1.

DR		Pfam: PF00560; LRR; 4.
DR		PRINTS: PR00237; GPCRHOOPS.
DR		PROSITE: PS00217; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR		PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR		Receptor: Signal.
FT	SIGNAL	1 22
FT	POTENTIAL,	
FT	FOLICLE-STIMULATING HORMONE RECEPTOR.	
FT	CHAIN	23 662
FT	SEQUENCE	662 AA: 74891 MW: 5CBA9EDDDBD1DAF5 CRC64:

Query Match	50.1%	Score 1802;	DB 13;	Length 662;
Best Local Similarity	53.5%	Pred. No. 9.2e-126;		
Matches 356;	Conservative 111;	Mismatches 164;	Indels 34;	Gaps 6

QY	14	TGS---	GCHH	LCHC	SNRV	FLQD	SKVTE	IP	TD	LP	NA	EL	RV	TK	LR	VP	KG	SF	AG	FG	70
		:			:							:		:		:	:	:	:	:	:
Db	13	TGN	FLGS	AC	LAGT	TS	FL	CG	SK	VQ	MP	HH	IP	INT	TV	EI	KL	QT	II	IP	YR
		:			:						:		:		:		:	:	:	:	:

QY	71	DLEKIEISONDVLEIV	EADVFSNLPKL	HEIRIEKANLLY	INPEAFONLPSRYLLISNT	130
		: : : :		: :	: : :	
Db	73	DLKRIMVSNGALORIE	AYAFANLTILEE	ITTKSKNLYSHDRDT	FWGLPKLRYLTISNT	132
		: : : :		: :	: : :	

OY 131 GIKHLPVHKIQSLQ-KVLVLDIODNINTHIVARNSPCLSFESI-LWLSKNGIEETHNC 188  
 : : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :  
db 133 GLTVLPDFSKVQSAAFEFLFDLEDNMHIETHSNAFAGLTSTITELRLTANGITEVERN 192

QY	189	AFNCTQLDELNLSDNNNLEELPNDVFOGASGPVILDISRKYHSLPNHGLENLKLRARS	248
		:::      :	
Db	193	AFNGTKMEKLFMGNQQLKRIDNHAFCAEGPVLDIRTASLSPENMLRLKLLIATS	252



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DR EMBL: X84755; CA59234.1; JOINED.
DR EMBL: X84756; CA59234.1; JOINED.
DR EMBL: X84757; CA59234.1; JOINED.
DR EMBL: X84758; CA59234.1; JOINED.
DR EMBL: X84759; CA59234.1; JOINED.
DR EMBL: X84760; CA59234.1; JOINED.
DR EMBL: X84761; CA59234.1; JOINED.
DR EMBL: X84762; CA59234.1; JOINED.
DR EMBL: X84763; CA59234.1; JOINED.
DR EMBL: AP082076; AAC98291.1; -.
DR HSSP: P22888; 11UT.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR Pfam: PF00001; 7tm_1; 1.
DR Pfam: PF00560; LRR; 3.
DR SMART: SM0013; LRRNT; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR RECEPTOR.
SQ SEQUENCE 701 AA: 78757 MW: 659FF5BABC409DA CRC64;
Query Match 49.4%; Score 1776; DB 4; Length 701;
Best Local Similarity 55.4%; Pred. No. 8.5e-124;
Matches 349; Conservative 107; Mismatches 148; Indels 26; Gaps 6;
QY 55 LTKL-----RVIPKGFAGFDGKLEIEISONDVLEYEADVFNLPKLRIEKANN 107
DB 53 LTRLSLAYLPVKVPSQAFGLNEVIEISDIOSLERTEANAFNLNLNLSILLIOTKN 112
QY 108 LYTINPAFONLSGLYLLSNGLKHLPAVHI-OSLQVLLDIDNNIHIHVARNSP 166
DB 113 LITLPTLPLGKLTGKLTGKLTGKLTGKLTGKLTGKLTGKLTGKLTGKLTGKLT 172
QY 167 GUSTEVNIAFLKNGEIEHNCAGTCDLDELSDNNLEELPNDVFOGASCPVLDIS 226
DB 173 GNNESYTLKLYNGFEVOSHAPNTTSLKLNKLVLEKHGAFRCAGTKPTLDS 232
QY 227 RTKVSLPHRGLNKLARSTYRLKLNLDKLVTLMEASLTYPSCCAFANLKRQIS 286
DB 233 STKQALPSTGLSILQRLATSYSLKLPSTREFVYNLLEATLTPSHCCAFNLL- 287
QY 287 ELHPICNKSILRODIDDMTOIGDQSVSLIDDEPSYK---GSDMMYNEFDYDLCNEVDV 343
DB 288 ---PTKQNPFSHSISNFKQCESTYRVKSNKLYSSMLAESLSGMDYEGFCLKTP- 343
QY 344 TCSKPDAPNCPEDINGTINILRVLIWIFSLIATGNTVLYLTTSQTKLTVPRPLMNL 403
DB 344 RCPNPDAPNCPEDINGTINILRVLIWIFSLIATGNTVLYLTTSQTKLTVPRPLMNL 403
QY 404 AFADLCIGIYLLIASVDIHTKSOYHNYAIDMOTGACDMAEFTVFASELSVYTLTAT 463
DB 404 SPADPCNGLYLLIASVDSQTKQYINHAIDMOTGSGCSTAGFTVFASELSVYTLTAT 463
QY 464 LERHRTITHAMOLECKVOLRHAASVYVLTGTFAPFAALPFIPIGISTYMKVSYCLPMDIS 523
DB 464 LERHRTITHAMOLECKVOLRHAASVYVLTGTFAPFAALPFIPIGISTYMKVSYCLPMDIS 523
QY 524 PLISQLYVALVLYLWLVFVYCCGTHYLTVRNPTIVSSSOTKIARMAATLIFTDFLC 583
DB 524 TISQLYVALVLYLWLVFVYCCGTHYLTVRNPTIVSSSOTKIARMAATLIFTDFLC 583
QY 584 MAPISPPATSAKLVPLTYSKAKILLVLYPTDINSCANPFLKATPKRPPDFILLSKP 643
DB 584 MAPISPPATSAKLVPLTYSKAKILLVLYPTDINSCANPFLKATPKRPPDFILLSKP 643
QY 644 GYENOAQIYRTTSSANTHNPARKSHCSS 673
DB 644 GCKKRAELYRK-----DPSATYSCKN 667
RESULT 11
Q9DGC6
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Db 242 PKGLEHLKELIARNTWTLKPLSLFSLHLRADLSYPSHCCAFKXKIRGILESJAC 301
Oy 293 NKSILR-----ODIDDMTOIGDORVSLIDDEPS----- 320
Db 302 NESSIRLSQRKSVNAVNCPTQYQVEEDLGD--SSVGNKNSKFDQTHSHSHYVFFEEQ 360
Oy 331 ---YKGSOM-----MYNEFDYDLCNEVVDVTCSPKPAFNPCEIDINGYILRLVL 367
Db 361 DEIIGFOELKHPQZETLQAFDSHYDVTYCGGSEDVYCTPKSDEFNPCEIDINGYILRLVL 420
Oy 368 INFISILATIGTTLVLTTSOYKLVPRFLMKNLAFADLCIGIYILLIASVDIHTKSO 427
Db 421 VNFVSLALLGNFVVLVILTSYKLVPRFLMKNLAFADLCIGIYILLIASVDIHTKSO 480
Oy 428 YHNAIDMTGAGCDAGFFVFASELSYTLTATLERMTITHAMOLECKVQLRHAS 487
Db 481 YHNAIDMTGAGCDAGFFVFASELSYTLTATLERMTITHAMOLECKVQLRHAS 540
Oy 488 VMLGWTFAAALPFIQISYKMYKVSICLPMDSPLSOLYVALLVNLVAFVWICGC 547
Db 541 IMAGWCYCCFLALLPLVGISYKMYKVSICLPMDSPLSOLYVALLVNLVAFVWICGC 600
Oy 548 YTHIYLVNRPTIVSSSDTKIAKRMATLIFDFLCMAPISFAISASLVKPLVTSKAK 607
Db 601 ILLVLTPLNSCAMPFLAIFTANFRDRDFILLSKFCGYEQAOIYR-----TE 656
Oy 657 TSSATHFHARKSCSAPRVTSYVLYPLNH 688
Db 721 VQKVTQNR-----OSLPNQDDYELLENSH 746

RESULT 14
Q8SP9
ID Q8SP9 PRELIMINARY: PRT: 764 AA.
AC Q8SP9;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Thyroid stimulating hormone receptor.
OS TSUR.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1],TaxID=9823;
RP SEQUENCE FROM N.A.
RA Igornani M., Nagata A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF082015; AAL2560.1;
KW Receptor.
SQ SEQUENCE 764 AA: 86647 MW: 12828D1B617E7032 CRC64;

Query Match 46.5%; Score 1670.5; DB 6; Length 764;
Best Local Similarity 46.8%; Pred. No. 6.7e-116;
Matches 352; Conservative 115; Mismatches 208; Indels 77; Gaps 14;

Oy 3 LLLVSLAFLG---TSGCHRWKCHSN---RVPLQDSKRYEIPDLPNNAIERPVL 55
Db 6 LQQLALLALPSLKGCCFPCECHQEDDFRV-TCKD--IHSIP-PLPPTQTLATIE 61
Oy 56 TKLVRIKPSGAPGDLKIEISQNDVLEADVFNKPLKIEKANKELLYNDEA 115
Db 62 TLKLTIPSAPSLNPNISILVSLDATALQLESOSFYNSLKTHERTISLTLYNGA 121
Oy 116 FQMLPSLYALLISMTGKILPAVHKIOSLOK-VLLDIDNININIHVARNSPGLSPESVI 174
Db 122 LKDLPLALGIFMTGLRIFPDLTVYSTDVPVILEITDNPMTYSIPANAFGLCNETLT 181
Oy 175 LWLKNGIEIHNCAFNQGTQDELNLSDNNILNLELPNDVFOGA-SGFDLDSRTKVHSL 233
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Db 182 LALYNGFTSVOGNFNGTLDQYVLRNKKLYTVIDKQFGVSGFTLLDYSVTSL 241
Oy 234 PKHGLEHLKELIARNTWTLKPLSLFSLHLRADLSYPSHCCAFKXKIRGILESJAC 292
Db 242 PKGLEHLKELIARNTWTLKPLSLFSLHLRADLSYPSHCCAFKXKIRGILESJAC 301
Oy 293 NKSILR-----ODIDDMTOIGDORVSLIDDEPS----- 320
Db 302 NESSIRLSQRKSVNAVNCPTQYQVEEDLGD--SSVGNKNSKFDQTHSHSHYVFFEEQ 360
Oy 331 ---YKGSOM-----MYNEFDYDLCNEVVDVTCSPKPAFNPCEIDINGYILRLVL 367
Db 361 DEIIGFOELKHPQZETLQAFDSHYDVTYCGGSEDVYCTPKSDEFNPCEIDINGYILRLVL 420
Oy 368 INFISILATIGTTLVLTTSOYKLVPRFLMKNLAFADLCIGIYILLIASVDIHTKSO 427
Db 421 VNFVSLALLGNFVVLVILTSYKLVPRFLMKNLAFADLCIGIYILLIASVDIHTKSO 480
Oy 428 YHNAIDMTGAGCDAGFFVFASELSYTLTATLERMTITHAMOLECKVQLRHAS 487
Db 481 YHNAIDMTGAGCDAGFFVFASELSYTLTATLERMTITHAMOLECKVQLRHAS 540
Oy 488 VMLGWTFAAALPFIQISYKMYKVSICLPMDSPLSOLYVALLVNLVAFVWICGC 547
Db 541 IMAGWCYCCFLALLPLVGISYKMYKVSICLPMDSPLSOLYVALLVNLVAFVWICGC 600
Oy 548 YTHIYLVNRPTIVSSSDTKIAKRMATLIFDFLCMAPISFAISASLVKPLVTSKAK 607
Db 601 ILLVLTPLNSCAMPFLAIFTANFRDRDFILLSKFCGYEQAOIYR-----TE 656
Oy 657 TSSATHFHARKSCSAPRVTSYVLYPLNH 688
Db 721 VQKVTQNR-----OSLPNQDDYELLENSH 746

RESULT 15
Q42500
ID Q42500 PRELIMINARY: PRT: 601 AA.
AC Q42500;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Lateinizing hormone receptor (fragment).
OS Melagris gallopavo (Common turkey).
OC Akaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Neognathae; Galliformes; Meleagrididae; Meleagris.
RN [1],TaxID=9103;
RP SEQUENCE FROM N.A.
RA MEDLINE-20078926; PubMed-10611074;
RA You S., Kim H., Hsu C.C., El Halawani M.E., Foster D.N.;
RT Three different turkey lateinizing hormone receptor (tLH-R) isoforms
RT I: characterization of alternatively spliced tLH-R isoforms and their
RT regulated expression in diverse tissues.*;
RL Biol. Reprod. 62:108-116(2000).
DR EMBL: U92082; AAB64409.1;
DR HSPB; P22888; 1LUT.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR Pfam; PF00001; 7cm1.1.
DR PROSITE; PS00337; GPCR_Rhodopn.
DR PROSITE; PS00337; GPCR_Rhodopn.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
PT NON_TER.
SQ SEQUENCE 601 AA: 67380 MW: 71402FD6D5E28PDC CRC64;

Query Match 46.1%; Score 1658.5; DB 13; Length 601;
Best Local Similarity 55.6%; Pred. No. 3.9e-115;
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	Matches	330;	Conservative	99;	Mismatches	118;	Indels	47;	Gaps	8;
QY	102	IEKANNLLYINPEAFONLPSRLYLTISNTGKHLPAVHKIQSLQ-KVLLDIODNINIHIV	160							
Db	2	ILNTRNLLHIEDGAFNLPRLAYLSICNTGIIIEFDLTOIFSEAHFILELCONLHMTYI	61							
QY	161	ARNSPFGLSFESVILWLSKNGIEEIHNCAFNGTQDLENLSDNNNLEELPNDVFOGASGP	220							
Db	62	PONAFQGMNESITLKYNGFEDIHSHAFNGTKLNQILKDNKLNRRHNDALRGATGP	121							
QY	221	VILDISRTKVSHPNHLKLRARSTYRLKLPNDKFTVLMPEASTYPSHCCAFAN	280							
Db	122	DVLDISSTALESLPSYGLAEIQVLNAESSYSLKRLPDLKFSLSLEAVLTPSHCCAFRN	181							
QY	281	LK--RQISELHPICN-----KSLRODIDDM-----TOIGDQVSLID-DEPSYKGK	324							
Db	182	LATEKONMSLIFDNFSKCEISIVKRTSEIFYRDSFNTSLGQRKSTRTHEQPKI---	238							
QY	325	SDMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMGNILRVLIWFISILAITGNTVLV	384							
Db	239	-----LTCPEPDAPNCPEDILGYSFLRVLIWFINILAGNLIVLL	280							
QY	385	VLTTQYKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSOYHNYAIDMOTGAGCDA	444							
Db	281	VLITSHYKLMVPRFLMCLNLFADFCMGLYLVLIASVDAQTSQYYNHAIYMQTSGCSTA	340							
QY	445	GFETVFASELSVYTLTAITLERWHITTHAMOLECKVOLRHAASVMVLGWTFAFAALFPI	504							
Db	341	GFETVFASELSVYTLVITIERWHITTYAMQLDRLRLHRAVLIMLGGWVFSILITAVLPL	400							
QY	505	FGISSYMKVSIKLPMDIDSPLSQLYMALLVLNLVAFVVICGYTHIYLTVRNPTIVSS	564							
Db	401	LGVSVMKVSIKLPMDIETGLSQAYILLILVLNNAFVVICACYIKIYIYAVONPELYAAN	460							
QY	565	SDTKAKRMATLIFTDFLCMAPISEFAISASLKVPLITVSKAKILLVLFPYVNSCANPFL	624							
Db	461	KDTKIARMAIILIFTDFTCMAPISEFAISAFKVPPLITVTNSKILLVLFPYVNSCANPFL	520							
QY	625	YAIFTKFRDRDFILLSKFCGYEMOAOIYRTETSSATHNFARKSHC-----SSAP	675							
Db	521	YAIFTKAFORDFELLSKLGCCCKSRAEICR-----MNYFSAYTSNCKNGSSAP	568							

Search completed: June 16, 2003, 13:35:54  
 Job time : 47.5347 secs

GenCore version 5.1.6  
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OK protein - protein search, using sw model

Run on: June 16, 2003, 11:37:21 : Search time 46.4155 Seconds  
(without alignments)  
1937.804 Million cell updates/sec.

Title: US-09-877-804-7

Perfect score: 3516

Sequence: 1 CHRMCHCSNRFVLCDSKV.....SAPRVTNSYLVPLNHSN 675

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues 908470

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*

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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3511	99.9	692	11	Rat testicular lut
2	3511	99.9	692	11	Rat testicular lut
3	3444	98.2	695	14	N-terminal of LH r
4	3444	98.0	695	14	N-terminal of LH r
5	3441.5	97.9	696	14	N-terminal of LH r
6	3268.5	93.0	696	14	N-terminal of LH r
7	3194.5	90.9	696	14	N-terminal of LH r
8	3169.5	90.1	695	14	FSH receptor. Hom
9	3169.5	90.1	695	18	AAH4782
10	3164.5	90.0	695	13	AAH27558

11	3151.5	89.6	634	14	AAH30520	N-terminal of LH r
12	3109.5	88.4	696	14	AAH30513	N-terminal of LH r
13	3109.5	88.4	696	14	AAH30521	N-terminal of LH r
14	3036.5	86.4	620	14	AAH30522	N-terminal of LH r
15	2894	83.7	689	14	AAH30509	N-terminal of LH r
16	2894	83.7	705	14	AAH30505	N-terminal of LH r
17	2831	80.5	690	14	AAH30514	N-terminal of LH r
18	2632.5	74.9	690	14	AAH30514	N-terminal of LH r
19	2552.5	72.6	699	14	AAH30515	N-terminal of LH r
20	2474	70.4	692	14	AAH30508	N-terminal of LH r
21	2354	67.0	697	14	AAH30503	N-terminal of LH r
22	2276	64.7	706	14	AAH30504	N-terminal of LH r
23	2189.5	62.3	699	14	AAH30517	N-terminal of LH r
24	2075.5	59.0	693	14	AAH30510	N-terminal of LH r
25	2043.5	58.1	699	14	AAH30512	N-terminal of LH r
26	1941	55.2	700	14	AAH30516	N-terminal of LH r
27	1940	55.2	700	14	AAH30511	N-terminal of LH r
28	1901.5	54.1	410	22	AAH2468	Human follicle sti
29	1816	51.6	650	14	AAH30518	N-terminal of LH r
30	1797	51.1	700	11	AAH08037	Rat ovarian lutein
31	1787	51.1	702	14	AAH08038	N-terminal of LH r
32	1783	51.0	705	14	AAH30502	N-terminal of LH r
33	1783	51.0	705	14	AAH30502	N-terminal of LH r
34	1778	50.6	699	13	AAH2187	Sequence of luteal
35	1756.5	50.0	685	12	AAH11331	Human testis luteo
36	1690.5	48.1	679	19	AAH5041	Human testis luteo
37	1650.5	46.9	714	12	AAH12915	Human TSH Receptor
38	1648	46.9	764	12	AAH12504	Canine thyroid sti
39	1642.5	46.7	764	12	AAH13269	Human thyroid stim
40	1641.5	46.7	764	12	AAH12505	Human thyroid stim
41	1638.5	46.6	764	23	AAH56308	Non-endogenous hum
42	1638.5	46.6	764	23	AAH56308	Non-endogenous hum
43	1638	46.6	756	12	AAH12916	Human TSH Receptor
44	1637.5	46.6	764	12	AAH12914	Human thyroid stim
45	1637.5	46.6	764	22	AAH56310	Non-endogenous hum

ALIGNMENTS

RESULT 1  
AAH08038  
ID AAH08038 standard; protein; 692 AA.  
XX  
AC AAH08038;  
DT 26-FEB-1991 (first entry)  
XX  
DE Rat testicular luteinising hormone/choriogonadotropin receptor.  
XX  
KW LH/CG receptor; FSH receptor; TSH receptor; fertility; breast cancer;  
XX prostate cancer; thyroid cancer; osteoporosis; Graves disease;  
XX polycystic ovarian disease; vasomotor instability.  
XX  
OS Rattus rattus.  
XX  
PN WO9013643-A.  
XX  
PD 15-NOV-1990.  
XX  
PF 04-MAY-1990; 90WO-US02488.  
XX  
PR 05-MAY-1989; 89US-0347683.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Nikolic K, McFarland KC, Segaloff DL, Seeburg PH;  
XX WPT, 1990-361478/48.  
XX N-PSDB; AAQ06634.  
XX  
PT Pharmaceutical compsn. contrg. hormone receptor mol - used for  
PT treating fertility, breast-and prostate-cancer and osteoporosis,

PT etc.  
PS Disclosure; fig 6; 78pp; English.  
XX  
CC This rat testicular follicle-stimulating hormone (FSH) receptor.  
CC This receptor is useful in a pharmaceutical compan. for treating  
CC e.g. breast-, prostate- and thyroid cancer, fertility, osteopor-  
CC osis, vasomotor instability and polycystronic ovarian disease.  
CC LH/CG- or TSH-receptors can also be used, to treat e.g. Graves  
CC disease. Abs can be used to inhibit receptor binding and for imag-  
CC ing and therapy... See also AAR08015-23, AAR08035-36 and AAR06633.  
XX  
SQ Sequence 692 AA;  
Query Match 99.9%; Score 3513; DB 11; Length 692;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 674; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CHWLCHCSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 60  
DB 18 CHWLCHCSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 77  
QY 61 SONDVLEIADVFSLPKLHEIRIEKANNLLINPEAFONLPSRLYLLISNTGIKHLPA 120  
DB 78 SONDVLEIADVFSLPKLHEIRIEKANNLLINPEAFONLPSRLYLLISNTGIKHLPA 137  
QY 121 VHKIQSLQKLVLLDQDNIHIVARNSEFGLSFESVTLWLSKNGIEIHNCAFNGLTOLDE 180  
DB 138 VHKIQSLQKLVLLDQDNIHIVARNSEFGLSFESVTLWLSKNGIEIHNCAFNGLTOLDE 197  
QY 181 LNLSDNNLEELPNDVFGAGSGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKLLPN 240  
DB 198 LNLSDNNLEELPNDVFGAGSGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKLLPN 257  
QY 241 LDRFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLIDD 300  
DB 258 LDRFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLIDD 317  
QY 301 EPSYKGSDMYNEFDYDLGNEVDVTCSPKPAFNPCEIDIMGNILRVLIWIFISILAIT 360  
DB 318 EPSYKGSDMYNEFDYDLGNEVDVTCSPKPAFNPCEIDIMGNILRVLIWIFISILAIT 377  
QY 361 GNTTVLVLTTSQYKLTVPRLMCLNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQT 420  
DB 378 GNTTVLVLTTSQYKLTVPRLMCLNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQT 437  
QY 421 GAGCDAAGPFTVFASLSVYTLTAITLERWHTITHAMOLECKVOLRHAASVWVLGWTFAF 480  
DB 438 GAGCDAAGPFTVFASLSVYTLTAITLERWHTITHAMOLECKVOLRHAASVWVLGWTFAF 497  
QY 481 AAALFPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVNLVAFVVCGCYTHYLTVRN 540  
DB 498 AAALFPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVNLVAFVVCGCYTHYLTVRN 557  
QY 541 PTIVSSSDTKIAKRNATLIFTDFLCMAPIISFPAISASLKVPLITVSKAKILLVLPYIN 600  
DB 558 PTIVSSSDTKIAKRNATLIFTDFLCMAPIISFPAISASLKVPLITVSKAKILLVLPYIN 617  
QY 601 SCANPFLYALFTKNERDRFPILLKFCGYEQMAQIYRTETSSATHNPHARKSHCSSAPRV 660  
DB 618 SCANPFLYALFTKNERDRFPILLKFCGYEQMAQIYRTETSSATHNPHARKSHCSSAPRV 677  
QY 661 TNSYVLVPLNHSN 675  
DB 678 TNSYVLVPLNHSN 692

RESULT 2  
AAR30506  
ID AAR30506 standard; protein; 695 AA.  
XX  
AC AAR30506;  
XX

DT 10-MAY-1993 (first entry)  
XX  
DE N-terminal of LH receptor/FSH receptor chimaera #15.  
XX  
KW Follicle stimulating hormone receptor; luteinising hormone receptor;  
KW human chorionic gonadotrophin; glycoprotein hormone receptor;  
KW chimaera; chimera.  
XX  
OS Chimaeric; homo sapiens.  
XX  
PN WO9222667-A.  
XX  
PD 23-DEC-1992.  
XX  
PF 12-JUN-1992; 92WO-US04987.  
XX  
PR 14-JUN-1991; 91US-0715911.  
XX  
PA (UYNE-) UNIV NEW JERSEY.  
PI Bernard M, Moyle WR, Myers R;  
XX  
WPI; 1993-018150/02.  
XX  
Glyco:protein hormone receptor analogues - having binding  
affinity to human chorionic gonadotrophin, luteinising and  
follicle stimulating hormones, useful in bio:immunoassays  
Examples; Fig 12; 103pp; English.  
XX  
This sequence represents the N-terminal of a novel protein having a  
binding affinity for human chorionic gonadotrophin (hCG), luteinising  
hormone (LH), and follicle stimulating hormone (FSH). The protein  
itself is a chimaera having residues from both the FSH receptor,  
and LH receptor. The receptor analogues can be used in bio:immunoassays  
for the simultaneous detection of both LH (or hCG) and FSH as  
well as their ratio of biological activities. The analogues can also  
be used for raising, purifying and assaying antibodies to the  
analogues. Coding sequence for the chimaera was produced by two step  
PCR.  
SQ Sequence 695 AA;  
Query Match 99.9%; Score 3511; DB 14; Length 695;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 674; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CHWLCHCSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 60  
DB 18 CHWLCHCSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 77  
QY 61 SONDVLEIADVFSLPKLHEIRIEKANNLLINPEAFONLPSRLYLLISNTGIKHLPA 120  
DB 78 SONDVLEIADVFSLPKLHEIRIEKANNLLINPEAFONLPSRLYLLISNTGIKHLPA 137  
QY 121 VHKIQSLQKLVLLDQDNIHIVARNSEFGLSFESVTLWLSKNGIEIHNCAFNGLTOLDE 180  
DB 138 VHKIQSLQKLVLLDQDNIHIVARNSEFGLSFESVTLWLSKNGIEIHNCAFNGLTOLDE 197  
QY 181 LNLSDNNLEELPNDVFGAGSGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKLLPN 240  
DB 198 LNLSDNNLEELPNDVFGAGSGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKLLPN 257  
QY 241 LDRFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLIDD 300  
DB 258 LDRFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLIDD 317  
QY 301 EPSYKGSDMYNEFDYDLGNEVDVTCSPKPAFNPCEIDIMGNILRVLIWIFISILAIT 360  
DB 318 EPSYKGSDMYNEFDYDLGNEVDVTCSPKPAFNPCEIDIMGNILRVLIWIFISILAIT 377  
QY 361 GNTTVLVLTTSQYKLTVPRLMCLNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQT 420  
DB 378 GNTTVLVLTTSQYKLTVPRLMCLNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQT 437  
QY 421 GAGCDAAGPFTVFASLSVYTLTAITLERWHTITHAMOLECKVOLRHAASVWVLGWTFAF 480  
DB 438 GAGCDAAGPFTVFASLSVYTLTAITLERWHTITHAMOLECKVOLRHAASVWVLGWTFAF 497  
QY 481 AAALFPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVNLVAFVVCGCYTHYLTVRN 540  
DB 498 AAALFPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVNLVAFVVCGCYTHYLTVRN 557  
QY 541 PTIVSSSDTKIAKRNATLIFTDFLCMAPIISFPAISASLKVPLITVSKAKILLVLPYIN 600  
DB 558 PTIVSSSDTKIAKRNATLIFTDFLCMAPIISFPAISASLKVPLITVSKAKILLVLPYIN 617  
QY 601 SCANPFLYALFTKNERDRFPILLKFCGYEQMAQIYRTETSSATHNPHARKSHCSSAPRV 660  
DB 618 SCANPFLYALFTKNERDRFPILLKFCGYEQMAQIYRTETSSATHNPHARKSHCSSAPRV 677  
QY 661 TNSYVLVPLNHSN 675  
DB 678 TNSYVLVPLNHSN 692

Db 378 GNTVLVLTTSQKLTVPRLMCLAFADLCIGYLLLIASVDIHTKSOYHNTAIDMOT 437  
Qy 421 GAGCDAAGFFTVFASLSVYTLTATLERHHTITHAMQLECKVOLRHAASVWVLTGTFAP 480  
Db 438 GAGCDAAGFFTVFASLSVYTLTATLERHHTITHAMQLECKVOLRHAASVWVLTGTFAP 497  
Qy 481 AALPPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVLAFFVYICGCTHYILTVRN 540  
Db 498 AALPPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVLAFFVYICGCTHYILTVRN 557  
Qy 541 PTIVSSSDTKIARMATLIFTDFLCMAPISFPAISASLKVPILTYSKAKILLVLPYIN 600  
Db 558 PTIVSSSDTKIARMATLIFTDFLCMAPISFPAISASLKVPILTYSKAKILLVLPYIN 617  
Qy 601 SCANPLYAIPTFNPRDFPILLSKFCYEMAOIYRTTSSATHNPHARKSHCSSAPRV 660  
Db 618 SCANPLYAIPTFNPRDFPILLSKFCYEMAOIYRTTSSATHNPHARKSHCSSAPRV 677  
Qy 661 TNSYVLPVPLNHSOON 675  
Db 678 TNSYVLPVPLNHSOON 692

RESULT 3

AAR30524 standard; protein; 695 AA.  
XX ID AAR30524 standard; protein; 695 AA.  
XX AC AAR30524;  
XX DT 10-MAY-1993 (first entry)  
XX DE N-terminal of LH receptor/FSH receptor chimaera #33.  
XX KW Follicle stimulating hormone receptor; luteinising hormone receptor;  
XX KW human chorionic gonadotrophin; glycoprotein hormone receptor;  
XX KW chimaera; chimera.  
XX OS Chimaeric; homo sapiens.  
XX PN MO9222667-A.  
XX PD 23-DEC-1992.  
XX PR 12-JUN-1992; 92MO-US04987.  
XX PR 14-JUN-1993; 91US-0715911.  
XX PA (UTNE-) UNIV NEW JERSEY.  
XX P1 Bernard M. Moyle MR, Myers R;  
XX DR MPI; 1993-018150/02.  
XX PT Glyco:protein hormone receptor analogues - having binding  
XX PT affinity to human chorionic gonadotrophin, luteinising and  
XX PT follicle stimulating hormones, useful in bio:immunoassays  
XX XS Examples; Fig 12; 103pp; English.

CC This sequence represents the N-terminal of a novel protein having a  
CC binding affinity to human chorionic gonadotrophin (hCG), luteinising  
CC hormone (LH), and follicle stimulating hormone (FSH). The protein  
CC itself is a chimaera having residues from both the FSH receptor  
CC and LH receptor. The receptor analogues can be used in bio:immunoassays  
CC for the simultaneous detection of both LH (or hCG) and FSH as  
CC well as their ratio of biological activities. The analogues can also  
CC be used for raising, purifying and assaying antibodies to the  
CC analogues. Coding sequence for the chimaera was produced by two step  
CC PCR.  
XX SQ Sequence 695 AA;

Query Match 98.21; Score 3454; DB 14; Length 695;

Best Local Similarity 98.18; Pred. No. 0;  
Matches 662; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 CHHWLCHCSNRFVLCQDSKVTEIPTDLPRNAIELRFLVTLKRVIPKGSFAGGDELEKIEI 60  
Db 18 CHHWLCHCSNRFVLCQDSKVTEIPTDLPRNAIELRFLVTLKRVIPKGSFAGGDELEKIEI 77  
Qy 61 SONOVLEVTEADVFNLPKHEIRIEKANNLLYINPEAFQNLPSRLYLLISNTGKILPA 120  
Db 78 SONOVLEVTEADVFNLPKHEIRIEKANNLLYINPEAFQNLPSRLYLLISNTGKILPA 137  
Qy 121 VHKTSIQKLVLDIOONINIHIVANSFNGLSFESVILWLSKNGICEEIHNCAPNGTOLDE 180  
Db 138 VHKTSIQKLVLDIOONLHTTIPGNAFOGHNNESVILWLSKNGICEEIHNCAPNGTOLDE 197  
Qy 181 LNLSDNNLEELNDVDFOGASGPVLDISRTKYVSLPWGLLENLKLBARSTYRLKLPN 240  
Db 198 LNLSDNNLEELNDVDFOGASGPVLDISRTKYVSLPWGLLENLKLBARSTYRLKLPN 257  
Qy 241 LDKFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQDIDDMTQIGDQVSLIDD 300  
Db 258 LDKFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQDIDDMTQIGDQVSLIDD 317  
Qy 301 EPSYKGSOMYNEFDYDLCNEVDVTCSPKPAFNPCEDIMGYNILRVLINFTISILAIT 360  
Db 318 EPSYKGSOMYNEFDYDLCNEVDVTCSPKPAFNPCEDIMGYNILRVLINFTISILAIT 377  
Qy 361 GNTVLVLTTSQKLTVPRLMCLAFADLCIGYLLLIASVDIHTKSOYHNTAIDMOT 420  
Db 378 GNTVLVLTTSQKLTVPRLMCLAFADLCIGYLLLIASVDIHTKSOYHNTAIDMOT 437  
Qy 421 GAGCDAAGFFTVFASLSVYTLTATLERHHTITHAMQLECKVOLRHAASVWVLTGTFAP 480  
Db 438 GAGCDAAGFFTVFASLSVYTLTATLERHHTITHAMQLECKVOLRHAASVWVLTGTFAP 497  
Qy 481 AALPPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVLAFFVYICGCTHYILTVRN 540  
Db 498 AALPPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVLAFFVYICGCTHYILTVRN 557  
Qy 541 PTIVSSSDTKIARMATLIFTDFLCMAPISFPAISASLKVPILTYSKAKILLVLPYIN 600  
Db 558 PTIVSSSDTKIARMATLIFTDFLCMAPISFPAISASLKVPILTYSKAKILLVLPYIN 617  
Qy 601 SCANPLYAIPTFNPRDFPILLSKFCYEMAOIYRTTSSATHNPHARKSHCSSAPRV 660  
Db 618 SCANPLYAIPTFNPRDFPILLSKFCYEMAOIYRTTSSATHNPHARKSHCSSAPRV 677  
Qy 661 TNSYVLPVPLNHSOON 675  
Db 678 TNSYVLPVPLNHSOON 692

RESULT 4

AAR30525  
XX ID AAR30525 standard; protein; 695 AA.  
XX AC AAR30525;  
XX DT 10-MAY-1993 (first entry)  
XX DE N-terminal of LH receptor/FSH receptor chimaera #34.  
XX KW Follicle stimulating hormone receptor; luteinising hormone receptor;  
XX KW human chorionic gonadotrophin; glycoprotein hormone receptor;  
XX KW chimaera; chimera.  
XX OS Chimaeric; homo sapiens.  
XX PN MO9222667-A.  
XX PD 23-DEC-1992.  
XX PR 12-JUN-1992; 92MO-US04987.

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XX PR 14-JUN-1991; 91US-0715911.
XX PA (UYNE-) UNIV NEW JERSEY.
XX PI Bernard M, Moyle WR, Myers R;
XX XX WPI; 1993-018150/02.
XX
XX Glyco:protein hormone receptor analogues - having binding
PT affinity to human chorionic gonadotrophin, luteinising and
PT follicle stimulating hormones, useful in bio:immunoassays
XX
XX Examples; Fig 12; 103pp; English.
XX
XX This sequence represents the N-terminal of a novel protein having a
CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
CC hormone (LH), and follicle stimulating hormone (FSH). The protein
CC itself is a chimera having residues from both the FSH receptor,
CC and LH receptor. The receptor analogues can be used in bioimmunoassays
CC for the simultaneous detection of both LH (or hCG) and FSH as
CC well as their ratio of biological activities. The analogues can also
CC be used for raising, purifying and assaying antibodies to the
CC analogues. Coding sequence for the chimera was produced by two step
CC PCR.
XX
XX Sequence 695 AA;
SQ
Query Match 98.0%; Score 3445; DB 14; Length 695;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 664; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 CHHWLCHCSNRVFLCQDSKVTETPTDLPRAIELRVLTPLKRVIPKGSFAGDLEKIEI 60
DB 18 CHHWLCHCSNRVFLCQDSKVTETPTDLPRAIELRVLTPLKRVIPKGSFAGDLEKIEI 77
QY 61 SONDVLEIADVFSLNPKLHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 120
DB 78 SONDVLEIADVFSLNPKLHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 137
QY 121 VHKLQSLQKVLDDIQQDNIHIVARNFSGMGLSFESVILWLSKNGIEEIHNCFAFNGTQDLE 180
DB 138 VHKLQSLQKVLDDIQQDNIHIVARNFSGMGLSFESVILWLSKNGIEEIHNCFAFNGTQDLE 197
QY 181 LNLSDNNLEELPNDVFCASGPIVDISRTKVHSLPNHGLENLKRLARSTYRLKLPN 240
DB 198 LNLSDNNLEELPNDVFCASGPIVDISRTKVHSLPNHGLENLKRLARSTYRLKLPN 257
QY 241 LDKFVTLMEASLTYPSSHCCAFANLKRQISELHPICNKSILRODIDMTQIGDQVSLIDD 300
DB 258 LDKFVTLMEASLTYPSSHCCAFANLKRQISELHPICNKSILRODIDMTQIGDQVSLIDD 317
QY 301 EPSYKSGSDMYNEFDYDLNCEYVDVTCSPKPDAPNCPEDIMGYNLRVLIWFISTLAIT 360
DB 318 EPSYKSGSDMYNEFDYDLNCEYVDVTCSPKPDAPNCPEDIMGYNLRVLIWFISTLAIT 377
QY 361 GNTTVLWLTTSQYKLTVPFLMCNLAFLADLCIGIYLLLIASVDIHTKSOYHNYADWQT 420
DB 378 GNTTVLWLTTSQYKLTVPFLMCNLAFLADLCIGIYLLLIASVDIHTKSOYHNYADWQT 437
QY 421 GAGCDAAGFTTVPASLSVYTLTAITLERWHTTHAMOLECKVOLRAHASVMVLGWTFEF 480
DB 438 GAGCDAAGFTTVPASLSVYTLTAITLERWHTTHAMOLECKVOLRAHASVMVLGWTFEF 497
QY 481 AALFPFIFGSSYMKYSICLPMDDISPLSQYVALLVNLVLAFFVYICGCTHYILTVRN 540
DB 498 AALFPFIFGSSYMKYSICLPMDDISPLSQYVALLVNLVLAFFVYICGCTHYILTVRN 557
QY 541 PTIVSSSDTKIAKRNATLIFTDFLCMAPISFPAISASLKVPLITVSKAKILLVLFPYPIN 600
DB 558 PTIVSSSDTKIAKRNATLIFTDFLCMAPISFPAISASLKVPLITVSKAKILLVLFPYPIN 617
QY 601 SCANPELYAIFTKNFRDFILLSKFCGYEMOQAIYRTETSSATHNFARKHSCSAPRV 660

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DB 618 SCANPELYAIFTKNFRDFILLSKFCGYEMOQAIYRTETSSATHNFARKHSCSAPRV 677
QY 661 TNSYVLVPLNHSSQN 675
DB 678 TNSYVLVPLNHSSQN 692
RESULT 5
AAR30523
ID AAR30523 standard; protein: 696 AA.
XX
XX AAR30523;
XX
XX 10-MAY-1993 (first entry)
XX
XX N-terminal of LH receptor/FSH receptor chimera #32.
XX
XX Follicle stimulating hormone receptor; luteinising hormone receptor;
XX human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimera: chimera.
XX
XX Chimaeric: homo sapiens.
XX
XX WO9222667-A.
XX
XX 23-DEC-1992.
XX
XX 12-JUN-1992; 92WO-US04987.
XX
XX 14-JUN-1991; 91US-0715911.
XX
XX (UYNE-) UNIV NEW JERSEY.
XX
XX Bernard M, Moyle WR, Myers R;
XX
XX WPI; 1993-018150/02.
XX
XX Glyco:protein hormone receptor analogues - having binding
PT affinity to human chorionic gonadotrophin, luteinising and
PT follicle stimulating hormones, useful in bio:immunoassays
XX
XX Examples; Fig 12; 103pp; English.
XX
XX This sequence represents the N-terminal of a novel protein having a
CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
CC hormone (LH), and follicle stimulating hormone (FSH). The protein
CC itself is a chimera having residues from both the FSH receptor,
CC and LH receptor. The receptor analogues can be used in bioimmunoassays
CC for the simultaneous detection of both LH (or hCG) and FSH as
CC well as their ratio of biological activities. The analogues can also
CC be used for raising, purifying and assaying antibodies to the
CC analogues. Coding sequence for the chimera was produced by two step
CC PCR.
XX
XX Sequence 696 AA;
SQ
Query Match 97.9%; Score 3441.5; DB 14; Length 696;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 663; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 CHHWLCHCSNRVFLCQDSKVTETPTDLPRAIELRVLTPLKRVIPKGSFAGDLEKIEI 60
DB 18 CHHWLCHCSNRVFLCQDSKVTETPTDLPRAIELRVLTPLKRVIPKGSFAGDLEKIEI 77
QY 61 SONDVLEIADVFSLNPKLHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 120
DB 78 SONDVLEIADVFSLNPKLHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 137
QY 121 VHKLQSLQKVLDDIQQDNIHIVARNFSGMGLSFESVILWLSKNGIEEIHNCFAFNGTQDLE 179
DB 138 VTKISSEFNFLEIQDNIHIVARNFSGMGLSFESVILWLSKNGIEEIHNCFAFNGTQDLE 197

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XX N-terminal of LH receptor/FSH receptor chimera #35.  
 DE Follicle stimulating hormone receptor; luteinising hormone receptor;  
 XX human chorionic gonadotrophin; glycoprotein hormone receptor;  
 KW chimera; chimera.  
 KW Chimeric; homo sapiens.  
 OS  
 XX W09222667-A.  
 PN  
 XX 23-DEC-1992.  
 PD  
 XX 12-JUN-1992; 92MO-US04987.  
 XX  
 XX 14-JUN-1991; 91US-0715911.  
 PR  
 XX (UYNE-) UNIV NEW JERSEY.  
 XX  
 XX Bernard M, Moyle WR, Myers R;  
 PI  
 XX WPI; 1993-018150/02.  
 DR  
 XX Glyco:protein hormone receptor analogues - having binding  
 XX affinity to human chorionic gonadotrophin, luteinising and  
 PT follicle stimulating hormones, useful in bio:immunoassays  
 PT  
 XX Examples; Fig 12; 103pp; English.  
 PS  
 XX This sequence represents the N-terminal of a novel protein having a  
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinising  
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein  
 CC itself is a chimera having residues from both the FSH receptor,  
 CC and LH receptor. The receptor analogues can be used in bioimmunoassays  
 CC for the simultaneous detection of both LH (or hCG) and FSH as  
 CC well as their ratio of biological activities. The analogues can also  
 CC be used for raising, purifying and assaying antibodies to the  
 CC analogues. Coding sequence for the chimera was produced by two step  
 CC PCR.  
 XX  
 XX Sequence 696 AA;  
 SQ

Query Match 90.9%; Score 3194.5; DB 14; Length 696;  
 Best Local Similarity 91.6%; Pred. No. 1.5e-298;  
 Matches 619; Conservative 17; Mismatches 39; Indels 1; Gaps 1;

QY 1 CHHWLCHCSNRVFLQDSKVTETPTDLPNRIELRVLTUKLRVTPKGSFAGDLEKIEI 60  
 DB 18 CHHWLCHCSNRVFLQDSKVTETPTDLPNRIELRVLTUKLRVTPKGSFAGDLEKIEI 77  
 QY 61 SONDVLEIADVFENLPLKLEIRIEKANNLLYINPEAFONLPSRLYLLISNTGIKHLP 120  
 DB 78 SOSDSLRIEAFANFONLNLSELLQNTKNNLYIEPGAFTNLPRLKYLISICWTGRTLPD 137  
 QY 121 VHKIQSLQ-KVLLDQDNINIHIVARNFGLSFESVILMSKNGIEIHCNCAFGTOLD 179  
 DB 138 VTKISSSENFLEICDNLHITIPGNAFQGNNSVTLKLYNGFEEVQSHAFNGTOLD 197  
 QY 180 ELNLSNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLP 239  
 DB 198 ELNLSNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLP 257  
 QY 240 NLDKFTVLEASITYPESHCCAFANLKRQISELHPICNKSILRQDDIMTQIGDQRVSLID 299  
 DB 258 NLDKFTVLEASITYPESHCCAFANLKRQISELHPICNKSILRQDDIMTQIGDQRVSLID 317  
 QY 300 DEPSYKSGSDMYNEFDYDLCEWVDVTCSPKPDAPNCPEDINGYNILRVLIWFISILAI 359  
 DB 318 DEPSYKSGSDMYNEFDYDLCEWVDVTCSPKPDAPNCPEDINGYNILRVLIWFISILAI 377  
 QY 360 TGNVTVLVLTTSQYKLTVPRLFMCLNAPADICIGIYLLIASVDHTKSOYHNAIDNQ 419  
 DB 378 TGNVTVLVLTTSQYKLTVPRLFMCLNAPADICIGIYLLIASVDHTKSOYHNAIDNQ 437

QY 420 TGAGCDAAGFTTVFASSELVYTLTAITLERWHTITHAMQLECKVQLRHAASVMVLGWTFA 479  
 DB 438 TGAGCDAAGFTTVFASSELVYTLTAITLERWHTITHAMQLECKVQLRHAASVMVLGWTFA 497  
 QY 480 FFAALPPIGICISSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCTHYIYLTVR 539  
 DB 498 FFAALPPIGICISSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCTHYIYLTVR 557  
 QY 540 NPTIVSSSDTKIAKRMTATLIFTDFLCMAPIISFFAISASLKVPPLITYSKAKILLVLFYPI 599  
 DB 558 NPTIVSSSDTKIAKRMTATLIFTDFLCMAPIISFFAISASLKVPPLITYSKAKILLVLFYPI 617  
 QY 600 NSCANPELYAIFTKNFRDRDFILLSKFCGYEMOQIYRTETSSATHNFHARKSHCSSAPR 659  
 DB 618 NSCANPELYAIFTKNFRDRDFILLSKFCGYEMOQIYRTETSSATHNFHARKSHCSSAPR 677  
 QY 660 VTNSYVLVPLNHSSON 675  
 DB 678 VTNSYVLVPLNHSSON 693

## RESULT 8

AAR42082  
 ID AAR42082 standard; Protein: 695 AA.

XX AAR42082;

XX 05-MAY-1994 (first entry)

XX FSH receptor.

XX FSH; receptor; follicle stimulating hormone; GST;  
 KW glutathione-S-transferase; primer; PCR; amplification;  
 KW polymerase chain reaction; probe; antibody; overstimulation.

XX Homo sapiens.

XX WO9320199-A.

XX 14-OCT-1993.

XX 29-MAR-1993; 93WO-EP00780.

XX 30-MAR-1992; 92EP-0200886.

XX (ALKU) AKZO NV.

XX De Leeuw R, Dijkema R;

XX WPI; 1993-336907/42.

XX N-PSDB; AAQ50013.

XX New follicle stimulating hormone receptor - and derived  
 PT antibodies, anti-idiotypic antibodies, and transfected cells,  
 PT useful e.g. in diagnosis and as antidote for FSH overstimulation

XX Claim 7; Page 20-23; 42pp; English.

XX The primers given in AAQ50029-34 were used in the cloning of GST-FSH-  
 CC R1, GST-FSH-R2 and GST-FSH-R3 fusion protein constructs.  
 CC Screening of the human testis cDNA library with a hFSH-R specific  
 CC probe resulted in five recombinant phages positive in hybridisation.  
 CC Sequence analysis was performed of the 2222 bp fragment of pGEM32c1  
 CC (AAQ50013).

XX Sequence 695 AA;

XX Query Match 90.1%; Score 3169.5; DB 14; Length 695;  
 XX Best Local Similarity 89.5%; Pred. No. 3.9e-296;  
 XX Matches 607; Conservative 31; Mismatches 37; Indels 3; Gaps 2;

QY 1 CHHWLCHCSNRVFLQDSKVTETPTDLPNRIELRVLTUKLRVTPKGSFAGDLEKIEI 60

DB 18 CHIRICHCHNRVFLCQSKVTEIPSDLPNRIELRVLTAKVIOKAFSGFGDLEKIEI 77  
OY 61 SONDVLEVIADVFSNLPKLEIRIEKANNLLYINPEAFONLPSPRYLLISNTGKHLPA 120  
DB 78 SONDVLEVIADVFSNLPKLEIRIEKANNLLYINPEAFONLPSPRYLLISNTGKHLPA 137  
OY 121 VHKIQSLQKVLDDIQDNIHIVARNSPGLSFESVILWLSKNGIEIHNKAFNGTOLDE 180  
DB 138 VHKIQSLQKVLDDIQDNIHIVARNSPGLSFESVILWLSKNGIEIHNKAFNGTOLDE 197  
OY 181 LNSDNNLLELPNDVPHGASGVILDSRTKVPKLEIRIEKANNLLYINPEAFONLPSPRYLLISNTGKHLPA 240  
DB 241 LNSDNNLLELPNDVPHGASGVILDSRTKVPKLEIRIEKANNLLYINPEAFONLPSPRYLLISNTGKHLPA 257  
OY 301 -EPSTYKSGDMYNEFDYDLCNEVVDVTCSPKDPAPNCPEDIMGYNLRVLFISILAI 359  
DB 318 NESYSRGFDMYTFEFDYDLCNEVVDVTCSPKDPAPNCPEDIMGYNLRVLFISILAI 377  
OY 360 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 419  
DB 420 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 437  
OY 438 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 497  
DB 480 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 539  
OY 498 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 557  
DB 540 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 599  
OY 558 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 617  
DB 600 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 659  
OY 618 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 677  
DB 678 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 695

RESULT 9  
AAM14782  
ID AAM14782 standard; Protein; 695 AA.  
AC AAM14782;  
DT 20-JUN-1997 (first entry)  
DE FSH receptor.  
XX Follicle stimulating hormone receptor; FSH receptor;  
KW ovarian dysgenesis; hypergonadotropic hypogonadism; diagnosis.  
XX Homo sapiens.  
PN WO9711194-A1.  
XX 27-MAR-1997.  
PD 20-SEP-1996; 96WO-F100501.  
PP 20-SEP-1995; 95US-0531070.  
PR (UYHE-) UNIV HELSINKI LICENSING LTD OY.  
PA  
XX

PI Alttomaeki K, De La Chapelle A, Huhtaniemi I;  
XX WPI: 1997-202900/18.  
DR N-PSDB: AAT63181.  
XX  
XX Diagnosis of ovarian dysgenesis and carriers from DNA abnormalities  
XX - by amplifying DNA including follicle stimulating hormone receptor  
XX allele(s), i.e. codon 189, cleaving fragments, and examination  
XX  
XX Disclosure: Page 18-21: 43pp; English.  
XX  
XX The human follicle stimulating hormone (FSH) receptor (AAM14782)  
XX is a G-protein coupled transmembrane receptor. A mutation in the  
XX fsh gene (see also AAT63181) is associated with ovarian dysgenesis,  
XX and methods for provided for the diagnosis of this disorder.  
XX  
XX Sequence 695 AA:  
Query Match 90.18; Score 3169.5; DB 18; Length 695;  
Best Local Similarity 89.34; Pred. No. 3; 9e-296;  
Matches 607; Conservative 31; Mismatches 37; Indels 3; Gaps 2;  
OY 1 CHIRICHCHNRVFLCQSKVTEIPSDLPNRIELRVLTAKVIOKAFSGFGDLEKIEI 60  
DB 18 CHIRICHCHNRVFLCQSKVTEIPSDLPNRIELRVLTAKVIOKAFSGFGDLEKIEI 77  
OY 61 SONDVLEVIADVFSNLPKLEIRIEKANNLLYINPEAFONLPSPRYLLISNTGKHLPA 120  
DB 78 SONDVLEVIADVFSNLPKLEIRIEKANNLLYINPEAFONLPSPRYLLISNTGKHLPA 137  
OY 121 VHKIQSLQKVLDDIQDNIHIVARNSPGLSFESVILWLSKNGIEIHNKAFNGTOLDE 180  
DB 138 VHKIQSLQKVLDDIQDNIHIVARNSPGLSFESVILWLSKNGIEIHNKAFNGTOLDE 197  
OY 181 LNSDNNLLELPNDVPHGASGVILDSRTKVPKLEIRIEKANNLLYINPEAFONLPSPRYLLISNTGKHLPA 240  
DB 241 LNSDNNLLELPNDVPHGASGVILDSRTKVPKLEIRIEKANNLLYINPEAFONLPSPRYLLISNTGKHLPA 257  
OY 241 LNSDNNLLELPNDVPHGASGVILDSRTKVPKLEIRIEKANNLLYINPEAFONLPSPRYLLISNTGKHLPA 300  
DB 258 LNSDNNLLELPNDVPHGASGVILDSRTKVPKLEIRIEKANNLLYINPEAFONLPSPRYLLISNTGKHLPA 317  
OY 301 -EPSTYKSGDMYNEFDYDLCNEVVDVTCSPKDPAPNCPEDIMGYNLRVLFISILAI 359  
DB 318 NESYSRGFDMYTFEFDYDLCNEVVDVTCSPKDPAPNCPEDIMGYNLRVLFISILAI 377  
OY 360 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 419  
DB 420 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 437  
OY 438 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 497  
DB 480 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 539  
OY 498 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 557  
DB 540 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 599  
OY 558 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 617  
DB 600 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 659  
OY 618 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 677  
DB 678 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 695

RESULT 10  
AAR27558





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XX 12-JUN-1992: 92MO-US04987.
XX 14-JUN-1991: 91US-0715911.
XX (UYNE-) UNIV NEW JERSEY.
XX Bernard M. Moyle WR, Myers R;
XX WPI; 1993-018150/02.
XX
XX Glyco:protein hormone receptor analogues - having binding
XX affinity to human chorionic gonadotrophin, luteinising and
XX follicle stimulating hormones, useful in bio:immunoassays
XX
XX Examples: Fig 12: 103pp: English.
XX
XX This sequence represents the N-terminal of a novel protein having a
XX binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX hormone (LH), and follicle stimulating hormone (FSH). The protein
XX itself is a chimera having residues from both the FSH receptor,
XX and LH receptor. The receptor analogues can be used in bio:assays
XX for the simultaneous detection of both LH (or hCG) and FSH as
XX well as their ratio of biological activities. The analogues can also
XX be used for raising, purifying and assaying antibodies to the
XX analogues. Coding sequence for the chimera was produced by two step
XX PCR.
XX
XX Sequence 634 AA:
XX
Query Match 89.6%; Score 3151.5; DB 14; Length 634;
Best Local Similarity 90.8%; Pred. No. 1.8e-294;
Matches 613; Conservative 0; Mismatches 1; Indels 61; Gaps 1;
XX 1 CHHILCHSRRVFLCQDSKVTETPTDLPNNALRFLVTKLRVYPKGSFAGFQGLEKIEI 60
XX 18 CHHILCHSRRVFLCQDSKVTETPTDLPNNALRFLVTKLRVYPKGSFAGFQGLEKIEI 77
XX
XX 61 SONDVLEYEADVSNLPKHEIRIEKANLLYINPEAFONLPSLRLLISNTGKHLPA 120
XX
XX 78 SONDVLEYEADVSNLPKHEIRIEKANLLYINPEAFONLPSLRLLISNTGKHLPA 137
XX
XX 131 VHKIOSLQKYLQDODNINIHIVARNSPGLSFESVILMSKNGIEIHNCAFNQTOLDE 180
XX
XX 138 VHKIOSLQKYLQDODNINIHIVARNSPGLSFESVILMSKNGIEIHNCAFNQTOLDE 197
XX
XX 181 LNLSDNNLLEELPNDVFCASGPVILDISRTKYHSLPNHGLENLKLRARSTYRLKLPN 240
XX
XX 198 LNLSDNNLLEELPNDVFCASGPVILDISRTKYHSLPNHGLENLKLRARSTYRLKLPN 223
XX
XX 241 LDKFVTLMEASLTPSNCNPAFLKQISELHPICNKSILRODIDMTQICQORVSLDD 300
XX
XX 224 -----ISELHPICNKSILRODIDMTQICQORVSLDD 256
XX
XX 301 EPSYKGSQDMNTEPDYDLCEVNVYVTCSPKPAFNCEDIMGTNLRVLWFLSTLALT 360
XX
XX 257 EPSYKGSQDMNTEPDYDLCEVNVYVTCSPKPAFNCEDIMGTNLRVLWFLSTLALT 316
XX
XX 361 GNTTVLVYLTTSQYKLTVPFLMCLNLAFLADLCIGYLLLTASVDIHTKSQYHAYDMQT 420
XX
XX 317 GNTTVLVYLTTSQYKLTVPFLMCLNLAFLADLCIGYLLLTASVDIHTKSQYHAYDMQT 376
XX
XX 421 GACDDAGFTTFVASELSVYTLTAITLERWHITTHAMOLECKVOLRRMAAAYVGLMTFAP 480
XX
XX 377 GACDDAGFTTFVASELSVYTLTAITLERWHITTHAMOLECKVOLRRMAAAYVGLMTFAP 436
XX
XX 481 AALAPPIFGISSTKVSICGLPMDISPLQYVYLLALVNLATVPYCCGTHYILTVRN 540
XX
XX 437 AALAPPIFGISSTKVSICGLPMDISPLQYVYLLALVNLATVPYCCGTHYILTVRN 496
XX
XX 541 PTVVSSSDTKIARMATLITPDLFCHAPISFPATSAKVPPLITYSKAKLVLPYPTIN 600
XX
XX 497 PTVVSSSDTKIARMATLITPDLFCHAPISFPATSAKVPPLITYSKAKLVLPYPTIN 556

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OY 601 SCANFLYAIFTRNFRDFFILLSKFCYEMQAIYRTETSSATHNPHARKSCSSAPRV 660
DB 557 SCANFLYAIFTRNFRDFFILLSKFCYEMQAIYRTETSSATHNPHARKSCSSAPRV 616
OY 661 TNSYVLVPLNHSQN 675
DB 617 TNSYVLVPLNHSQN 631
XX
XX RESULT 12
XX AAR30513
XX ID AAR30513 standard; protein; 696 AA.
XX AC AAR30513;
XX DT 10-MAY-1993 (first entry)
XX DE N-terminal of LH receptor/FSH receptor chimera #22.
XX KW Follicle stimulating hormone receptor; luteinising hormone receptor;
XX human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimera; chimera.
XX OS Chimeraic; homo sapiens.
XX PN MO9222667-A.
XX PD 23-DEC-1992.
XX PF 12-JUN-1992: 92MO-US04987.
XX PR 14-JUN-1991: 91US-0715911.
XX (UYNE-) UNIV NEW JERSEY.
XX Bernard M. Moyle WR, Myers R;
XX WPI; 1993-018150/02.
XX Glyco:protein hormone receptor analogues - having binding
XX affinity to human chorionic gonadotrophin, luteinising and
XX follicle stimulating hormones, useful in bio:immunoassays
XX
XX Examples: Fig 12: 103pp: English.
XX
XX This sequence represents the N-terminal of a novel protein having a
XX binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX hormone (LH), and follicle stimulating hormone (FSH). The protein
XX itself is a chimera having residues from both the FSH receptor,
XX and LH receptor. The receptor analogues can be used in bio:immunoassays
XX for the simultaneous detection of both LH (or hCG) and FSH as
XX well as their ratio of biological activities. The analogues can also
XX be used for raising, purifying and assaying antibodies to the
XX analogues. Coding sequence for the chimera was produced by two step
XX PCR.
XX
XX Sequence 696 AA:
XX
Query Match 88.4%; Score 3109.5; DB 14; Length 696;
Best Local Similarity 89.3%; Pred. No. 2.3e-290;
Matches 604; Conservative 22; Mismatches 49; Indels 1; Gaps 1;
OY 1 CHHILCHSRRVFLCQDSKVTETPTDLPNNALRFLVTKLRVYPKGSFAGFQGLEKIEI 60
DB 18 CHHILCHSRRVFLCQDSKVTETPTDLPNNALRFLVTKLRVYPKGSFAGFQGLEKIEI 77
OY 61 SONDVLEYEADVSNLPKHEIRIEKANLLYINPEAFONLPSLRLLISNTGKHLPA 120
DB 78 SONDVLEYEADVSNLPKHEIRIEKANLLYINPEAFONLPSLRLLISNTGKHLPA 137
OY 121 VHKIOSLQ-KVLLDIOONINIHIVARNSPGLSFESVILMSKNGIEIHNCAFNQTOLD 179
DB 121 VHKIOSLQ-KVLLDIOONINIHIVARNSPGLSFESVILMSKNGIEIHNCAFNQTOLD 179

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Db 138 VTKISSSEFNFILEICNDLHITTPGNFQGMNNESTLKLXNGFEEVQSHAFNGTTLI 197  
QY 180 ELNLSNNLEELPNDFOGASGPVILDSRTKVSHPNHLNKLKLRARSTYRLKKLP 239  
Db 198 SLEKENIYLEKMHSAFOGATGPVILDSRTKVSHPNHLNKLKLRARSTYRLKKLP 257  
QY 240 NLDKFVTLMEASLTYPSSHCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLID 299  
Db 258 NLDKFVTLMEASLTYPSSHCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLID 317  
QY 300 DEPSYKSGSDMYNEFDYDLCLNEVDVTCSPKPDAPNCPEDINGYNILRVLIWFIILAI 359  
Db 318 DEPSYKSGSDMYNEFDYDLCLNEVDVTCSPKPDAPNCPEDINGYNILRVLIWFIILAI 377  
QY 360 TGNNTVLVLTTSOYKLTVPFLMCLNLAFLADLCIGIYLLIASVDIHTKSOYHNYAIDMQ 419  
Db 378 TGNNTVLVLTTSOYKLTVPFLMCLNLAFLADLCIGIYLLIASVDIHTKSOYHNYAIDMQ 437  
QY 420 TGAGCDAAGFTVFASLSVYTLTALTLEWHHTITHAMQLECKVQLRHAASVMVLGWTFA 479  
Db 438 TGAGCDAAGFTVFASLSVYTLTALTLEWHHTITHAMQLECKVQLRHAASVMVLGWTFA 497  
QY 480 FFAALFPFIIGISSYMKVSCICLPMDIDSPLSQLYMALLVNLVLAFFVVICGCTHYIYLTVR 539  
Db 498 FFAALFPFIIGISSYMKVSCICLPMDIDSPLSQLYMALLVNLVLAFFVVICGCTHYIYLTVR 557  
QY 540 NPTIVSSSDTKIAKRMATLIPTDFLCMAPISFPAISASLKVPLITVSKAKILLVLPYPI 599  
Db 558 NPTIVSSSDTKIAKRMATLIPTDFLCMAPISFPAISASLKVPLITVSKAKILLVLPYPI 617  
QY 600 NSCANPFLYAIFTKNFRDFFILLSKFGCYEMQAQIYRTTSSATHNFARKSHCSAPR 659  
Db 618 NSCANPFLYAIFTKNFRDFFILLSKFGCYEMQAQIYRTTSSATHNFARKSHCSAPR 677  
QY 660 VTNSYVLVPLNHSQN 675  
Db 678 VTNSYVLVPLNHSQN 693

## RESULT 13

AAR30521  
ID AAR30521 standard; protein: 696 AA.

XX AC AAR30521;

XX DT 10-MAY-1993. (first entry)

XX DE N-terminal of LH receptor/FSH receptor chimaera #30.

XX KW Follicle stimulating hormone receptor; luteinising hormone receptor;  
KW human chorionic gonadotrophin; glycoprotein hormone receptor;  
XX chimaera; chimera.

XX OS Chimeric; homo sapiens.

XX PN W09222667-A.

XX PD 23-DEC-1992.

XX PF 12-JUN-1992; 92WO-US04987.

XX PR 14-JUN-1991; 91US-0715911.

XX PA (UYNE-) UNIV NEW JERSEY.

XX PI Bernard M, Moyle WR, Myers R;

XX DR WPI; 1993-018150/02.

XX Glyco:protein hormone receptor analogues - having binding  
PT affinity to human chorionic gonadotrophin, luteinising and  
PT follicle stimulating hormones, useful in bio:immunoassays  
XX

Examples: Fig 12: 103pp; English.

PS This sequence represents the N-terminal of a novel protein having a  
XX binding affinity for human chorionic gonadotrophin (hCG), luteinising  
CC hormone (LH), and follicle stimulating hormone (FSH). The protein  
CC itself is a chimaera having residues from both the FSH receptor,  
CC and LH receptor. The receptor analogues can be used in immunoassays  
CC for the simultaneous detection of both LH (or hCG) and FSH as  
CC well as their ratio of biological activities. The analogues can also  
CC be used for raising, purifying and assaying antibodies to the  
CC analogues. Coding sequence for the chimaera was produced by two step  
CC PCR.  
XX SQ Sequence 696 AA;

Query Match 88.4%; Score 3109.5; DB 14; Length 696;  
Best Local Similarity 89.3%; Pred. No. 2.3e-290;  
Matches 604; Conservative 22; Mismatches 49; Indels 1; Gaps 1;

QY 1 CHHLCHCSNRVFLCODSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 60  
Db 18 CHHLCHCSNRVFLCODSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 77  
QY 61 SQNDVLEIVADVFSNLPKLHEIRIEKANNLLYINPEAFQNLPSRLYLLISNTGKHLPA 120  
Db 78 SQSDSLERIEANAFDNLNLSSELLIQNTKNLLYIEGAPTNLPRLKVLSTCNTGIRLPD 137  
QY 121 VHKIQSLQ-KVLDDIQDNIHIVARNSPMGLSFESVILMSKNGIEEIHNCAPNGTOLD 179  
Db 138 VTKISSSEFNFILEICNDLHITTPGNFQGMNNESTLKLXNGFEEVQSHAFNGTTLI 197  
QY 180 ELNLSNNLEELPNDFOGASGPVILDSRTKVSHPNHLNKLKLRARSTYRLKKLP 239  
Db 198 SLEKENIYLEKMHSAFOGATGPVILDSRTKVSHPNHLNKLKLRARSTYRLKKLP 257  
QY 240 NLDKFVTLMEASLTYPSSHCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLID 299  
Db 258 NLDKFVTLMEASLTYPSSHCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLID 317  
QY 300 DEPSYKSGSDMYNEFDYDLCLNEVDVTCSPKPDAPNCPEDINGYNILRVLIWFIILAI 359  
Db 318 DEPSYKSGSDMYNEFDYDLCLNEVDVTCSPKPDAPNCPEDINGYNILRVLIWFIILAI 377  
QY 360 TGNNTVLVLTTSOYKLTVPFLMCLNLAFLADLCIGIYLLIASVDIHTKSOYHNYAIDMQ 419  
Db 378 TGNNTVLVLTTSOYKLTVPFLMCLNLAFLADLCIGIYLLIASVDIHTKSOYHNYAIDMQ 437  
QY 420 TGAGCDAAGFTVFASLSVYTLTALTLEWHHTITHAMQLECKVQLRHAASVMVLGWTFA 479  
Db 438 TGAGCDAAGFTVFASLSVYTLTALTLEWHHTITHAMQLECKVQLRHAASVMVLGWTFA 497  
QY 480 FFAALFPFIIGISSYMKVSCICLPMDIDSPLSQLYMALLVNLVLAFFVVICGCTHYIYLTVR 539  
Db 498 FFAALFPFIIGISSYMKVSCICLPMDIDSPLSQLYMALLVNLVLAFFVVICGCTHYIYLTVR 557  
QY 540 NPTIVSSSDTKIAKRMATLIPTDFLCMAPISFPAISASLKVPLITVSKAKILLVLPYPI 599  
Db 558 NPTIVSSSDTKIAKRMATLIPTDFLCMAPISFPAISASLKVPLITVSKAKILLVLPYPI 617  
QY 600 NSCANPFLYAIFTKNFRDFFILLSKFGCYEMQAQIYRTTSSATHNFARKSHCSAPR 659  
Db 618 NSCANPFLYAIFTKNFRDFFILLSKFGCYEMQAQIYRTTSSATHNFARKSHCSAPR 677  
QY 660 VTNSYVLVPLNHSQN 675  
Db 678 VTNSYVLVPLNHSQN 693

## RESULT 14

AAR30522  
ID AAR30522 standard; protein: 620 AA.  
XX AC AAR30522;

XX 10-MAY-1993 (first entry)  
 XX N-terminal of LH receptor/FSH receptor chimera #31.  
 XX Follicle stimulating hormone receptor; luteinising hormone receptor;  
 XX human chorionic gonadotrophin; glycoprotein hormone receptor;  
 XX chimera; chimera.  
 XX Chimeraic; homo sapiens.  
 XX OS  
 XX W09222667-A.  
 XX 23-DEC-1992.  
 XX 12-JUN-1992; 92MO-US04987.  
 XX 14-JUN-1991; 91US-0715911.  
 XX (UYNE-) UNIV NEW JERSEY.  
 XX Bernard M, Moyle WR, Myers R;  
 XX MPI; 1993-018150/02.  
 XX Glyco:protein hormone receptor analogues - having binding  
 PT affinity to human chorionic gonadotrophin, luteinising and  
 PT follicle stimulating hormones, useful in bio:immunoassays  
 XX Examples; Fig 12: 103pp: English.  
 XX This sequence represents the N-terminal of a novel protein having a  
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinising  
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein  
 CC itself is a chimera having residues from both the FSH receptor,  
 CC and LH receptor. The receptor analogues can be used in bio:immunoassays  
 CC for the simultaneous detection of both LH<sup>h</sup> (or hCG) and FSH as  
 CC well as their ratio of biological activities. The analogues can also  
 CC be used for raising, purifying and assaying antibodies to the  
 CC analogues. Coding sequence for the chimera was produced by two step  
 CC PCR.  
 XX Sequence 620 AA;  
 XX 50

Query Match 86.4%; Score 3036.5; DB 14; Length 620;  
 Best Local Similarity 87.74; Pred. No. 2.le-293;  
 Matches 592; Conservative 1; Mismatches 7; Indels 75; Gaps 1;  
 OY 1 CHHNLCHSNRVFLCOBCKVTEIPTDLPNNALIEFLVTLKLVIPKGSFAGGLEKIEI 60  
 DB 18 CHHNLCHSNRVFLCOBCKVTEIPTDLPNNALIEFLVTLKLVIPKGSFAGGLEKIEI 77  
 OY 61 SONDVLEIVADVFNPLKHEIRIEKANNLLYINPEAFONLPSLYLLIWTGKHLPA 120  
 DB 78 SONDVLEIVADVFNPLKHEIRIEKANNLLYIEGAPNLPRLKYLSTGKHLPA 137  
 OY 121 VHKIQSLQKVLDDIQDMMINIHIVARNSEFGLSPESVYLWLSKNGIEIHCNFAFNGTOLDE 180  
 DB 138 VHKIQSLQKVLDD----- 150  
 OY 181 LKLSNNHLELPNDVPOGASGVILDISRTKVHSLPNHGLEKALKLRARSTYRLKKLPN 240  
 DB 151 -----SRTKVHSLPNHGLEKALKLRARSTYRLKKLPN 182  
 OY 241 LKFPVTLAEASLTYPSCCAPANLKRQISELHPICNTSLRQDIDDTQIGDORVSLDD 300  
 DB 183 LKFPVTLAEASLTYPSCCAPANLKRQISELHPICNTSLRQDIDDTQIGDORVSLDD 242  
 OY 301 EPSYVGSGDMMYNEFDVDCNVDVTCSPKPAQNPCCEDIMCVNLRVLNFTSLAIT 360  
 DB 243 EFSYVGSGDMMYNEFDVDCNVDVTCSPKPAQNPCCEDIMCVNLRVLNFTSLAIT 302  
 OY 361 GNTTVLVLTTSQTKLVTPFLMCLNLAFLADLCIGYLLLIASVDIHTKSYQHNTAIDMQT 420

DB 303 GNTTVLVLTTSQTKLVTPFLMCLNLAFLADLCIGYLLLIASVDIHTKSYQHNTAIDMQT 362  
 OY 421 GAGCDNAGEFTVFASLSVYTLTAITLERHHTITHAMOLECKVQLRHAASVWVLTGTFAP 480  
 DB 363 GAGCDNAGEFTVFASLSVYTLTAITLERHHTITHAMOLECKVQLRHAASVWVLTGTFAP 422  
 OY 481 AALPFPFGIGISSYKVSICLPMIDISPLSOLYVALLVNLVAFVYVGGCYTHIYLVN 540  
 DB 423 AALPFPFGIGISSYKVSICLPMIDISPLSOLYVALLVNLVAFVYVGGCYTHIYLVN 482  
 OY 541 PTIVSSSDTKIAKRMATLIPTDFLCHAPISFSAISLAKVPLITVSKAKILLVLFYPI 600  
 DB 483 PTIVSSSDTKIAKRMATLIPTDFLCHAPISFSAISLAKVPLITVSKAKILLVLFYPI 542  
 OY 601 SCANPFLYAIPTKFRDRDFILLSPFCGYEQAOIYRTTSSATHNPHARKSHCSSAPRV 660  
 DB 543 SCANPFLYAIPTKFRDRDFILLSPFCGYEQAOIYRTTSSATHNPHARKSHCSSAPRV 602  
 OY 661 TNSYVLVPLNHSSQN 675  
 DB 603 TNSYVLVPLNHSSQN 617  
 XX RESULT 15  
 XX AAR30509  
 XX ID AAR30509 standard; protein: 689 AA.  
 XX AC AAR30509;  
 XX DT 10-MAY-1993 (first entry)  
 XX DE N-terminal of LH receptor/FSH receptor chimera #18.  
 XX Follicle stimulating hormone receptor; luteinising hormone receptor;  
 XX human chorionic gonadotrophin; glycoprotein hormone receptor;  
 XX chimera; chimera.  
 XX OS Chimeraic; homo sapiens.  
 XX PN W09222667-A.  
 XX PD 23-DEC-1992.  
 XX PF 12-JUN-1992; 92MO-US04987.  
 XX PR 14-JUN-1991; 91US-0715911.  
 XX (UYNE-) UNIV NEW JERSEY.  
 XX Bernard M, Moyle WR, Myers R;  
 XX MPI; 1993-018150/02.  
 XX Glyco:protein hormone receptor analogues - having binding  
 PT affinity to human chorionic gonadotrophin, luteinising and  
 PT follicle stimulating hormones, useful in bio:immunoassays  
 XX Examples; Fig 12: 103pp: English.  
 XX This sequence represents the N-terminal of a novel protein having a  
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinising  
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein  
 CC itself is a chimera having residues from both the FSH receptor,  
 CC and LH receptor. The receptor analogues can be used in bio:immunoassays  
 CC for the simultaneous detection of both LH<sup>h</sup> (or hCG) and FSH as  
 CC well as their ratio of biological activities. The analogues can also  
 CC be used for raising, purifying and assaying antibodies to the  
 CC analogues. Coding sequence for the chimera was produced by two step  
 CC PCR.  
 XX Sequence 689 AA;  
 XX 50

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Query Match      86.3%; Score 3034; DB 14; Length 689;
Best Local Similarity 87.0%; Pred. No. 4.4e-283;
Matches 590; Conservative 32; Mismatches 44; Indels 12; Gaps 3;

QY 1 CHHWLCHCSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 60
DB 18 CHHWLCHCSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 77
QY 61 SONDVLEIADVFNLPKLHEIRIEKANNLLYINPEAFONLPRLYLLISNTGKHLPA 120
DB 78 SONDVLEIADVFNLPKLHEIRIEKANNLLYINPEAFONLPRLYLLISNTGKHLPA 137
QY 121 VHKIOSLQKVLDDIODNINIHIVARNFPMGLSFESVILWLSKNGIEEIHNCFAFNGTQDLE 180
DB 138 VHKIOSLQKVLDDIODNINIHIVARNFPMGLSFESVILWLSKNGIEEIHNCFAFNGTQDLE 197
QY 181 LNLSDNNLEELPNDVFOGASGPVILDISRKVHSLPNHGLENLKLRARSTYRKLKLPN 240
DB 198 LNLSDNNLEELPNDVFOGASGPVILDISRKVHSLPNHGLENLKLRARSTYRKLKLPN 257
QY 241 LDKFVTLMEASLTYPHCHCAFANLKRQISELHPICNKSILRODIDDMTOIGDORYSLIDD 300
DB 258 KEKFTSLVATITYSHCCAFNLPK-----EQNESFISFENFSKQCESTVRKADN 309
QY 301 EPSYG---KGDMMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIMGYNILRVLIWFISIL 357
DB 310 ETLYSATFEENELSGWDYDYGCSPT-LQCAPEPDAPNCPEDIMGYAFRLVLIWFISITL 368
QY 358 AITGNTTVLVLTTSQYKLTVPFLMCNLAFLADLCIGIYLLIASVDIHTKSQYHNYAID 417
DB 369 AITGNTTVLVLTTSQYKLTVPFLMCNLAFLADLCIGIYLLIASVDIHTKSQYHNYAID 428
QY 418 WOTGAGCDAAGFTVPFASLSVYTLTATLERWHTITHAMQLECKVQLRHAASVMVLGWT 477
DB 429 WOTGAGCDAAGFTVPFASLSVYTLTATLERWHTITHAMQLECKVQLRHAASVMVLGWT 488
QY 478 FAFAAALPFIIGISSYMKVSIPLMDIDSPLSQLYVMALLVNLVLAFFVVCGYTHIYIT 537
DB 489 FAFAAALPFIIGISSYMKVSIPLMDIDSPLSQLYVMALLVNLVLAFFVVCGYTHIYIT 548
QY 538 VRNPTIVSSSDTKAKRMATLIPTDFLCMAPISFFAISASLKVPILTVSKAKILLVLFY 597
DB 549 VRNPTIVSSSDTKAKRMATLIPTDFLCMAPISFFAISASLKVPILTVSKAKILLVLFY 608
QY 598 PINSKANPLYAIFTKNFRDFFILLSKFGCYEMOQIYRTETSSATHNFHARKSHCSSA 657
DB 609 PINSKANPLYAIFTKNFRDFFILLSKFGCYEMOQIYRTETSSATHNFHARKSHCSSA 668
QY 658 PRVTNSYVLVPLNHSSQN 675
DB 669 PRVTNSYVLVPLNHSSQN 686
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Search completed: June 16, 2003, 13:33:21  
Job time : 48.4155 secs

Result	Query No.	Score	Match	Length	DB	ID	Description
1	3516	100.0	632	4	US-07-757-342D-6	Sequence 6, Appl	
2	3169.5	90.1	695	1	US-08-487-885-2	Sequence 2, Appl	
3	3169.5	90.1	695	3	US-08-482-855-2	Sequence 2, Appl	
4	3169.5	90.1	695	4	US-08-474-986-2	GENERAL INFORMAT	
5	1807	51.4	696	4	US-07-757-342D-4	Sequence 4, Appl	
6	1789	51.2	764	4	US-07-741-453A-60	Sequence 60, Appl	
7	1789	51.2	764	4	US-07-757-342D-3	Sequence 3, Appl	
8	1772	51.1	700	4	US-07-757-342D-1	Sequence 10, Appl	
9	1776	50.5	692	4	US-07-757-342D-5	Sequence 56, Appl	
10	1670	47.5	793	4	US-07-741-453A-56	Sequence 56, Appl	
11	1656.5	47.1	764	4	US-07-741-453A-61	Sequence 61, Appl	
12	1655	47.1	764	4	US-07-741-453A-54	Sequence 54, Appl	
13	1652.5	47.0	795	4	US-07-741-453A-55	Sequence 55, Appl	
14	1641.5	46.7	764	4	US-07-741-453A-59	Sequence 59, Appl	
15	1640.5	45.7	764	4	US-07-757-342D-5	Sequence 5, Appl	
16	1605.5	45.7	390	3	US-08-460-576-2	Sequence 2, Appl	
17	1598	45.4	420	4	US-08-795-876-33	Sequence 33, Appl	
18	1598	45.4	423	4	US-08-795-876-38	Sequence 38, Appl	
19	1578	43.6	436	4	US-08-795-876-2	Sequence 2, Appl	
20	1567.5	44.6	636	4	US-07-757-342D-9	Sequence 9, Appl	
21	1567.5	44.6	636	4	US-07-757-342D-9	Sequence 29, Appl	
22	1532.5	43.3	393	4	US-07-741-453A-29	Sequence 29, Appl	
23	1474.5	41.9	337	3	US-08-118-270-55	Sequence 55, Appl	
24	1474.5	41.9	337	3	PCT-US93-08528-55	Sequence 55, Appl	
25	1037.5	29.2	336	1	US-08-118-270-54	Sequence 54, Appl	
26	1037.5	29.2	336	1	PCT-US93-08528-54	Sequence 54, Appl	
27	993.5	28.0	332	1	US-08-118-270-53	Sequence 53, Appl	

\_\_\_\_\_

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Query Match      100.0%  Score 3516;  DB 4;  Length 692;
Best Local Similarity 100.0%  Pred. No. 3,36-77;
Matches 675;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

1 CHWILCHSNRFLVCDSDKVTETPTDPRNATLRFVLTKLVIRPGSGAGCDLKEIT 50

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Db 18 CHHWLCHCSNRVFLCDSKVTEIPTDLPRAIELRVLTKLRIKPGSFAGFGDLEKIEI 77  
QY 61 SONDLVLEADVFNLPKLEIRLEKANNLLYINPEAFONLPRLYLLISNTGKHLPA 120  
Db 78 SONDLVLEADVFNLPKLEIRLEKANNLLYINPEAFONLPRLYLLISNTGKHLPA 137  
QY 121 VHKIOSLQKVLDDIODNIHIVARNSPFGLSFESVILWLSKNGIEEIHNCFAFGTQDLE 180  
Db 138 VHKIOSLQKVLDDIODNIHIVARNSPFGLSFESVILWLSKNGIEEIHNCFAFGTQDLE 197  
QY 181 LNLSDNNLEELPNDVFOGASGVILDISRTKVHSLPNHGLNKKLRARSTYRLKKLPN 240  
Db 198 LNLSDNNLEELPNDVFOGASGVILDISRTKVHSLPNHGLNKKLRARSTYRLKKLPN 257  
QY 241 LKFTVLMASITYPSSHCAFLNKLROISELHPICKNSILRODIDMTQIGDQVSLIDD 300  
Db 258 LKFTVLMASITYPSSHCAFLNKLROISELHPICKNSILRODIDMTQIGDQVSLIDD 317  
QY 301 EPSYKSGSDMYNEFDYDLCLNEVDVTCSPKPDAPNCPEDIMGYNLRLVLIWFISILAIT 360  
Db 318 EPSYKSGSDMYNEFDYDLCLNEVDVTCSPKPDAPNCPEDIMGYNLRLVLIWFISILAIT 377  
QY 361 GNTTVLVLTTSOYKLTVPREFLMCNLAFADLCIGIYVLLLIASVDIHTKSQYHNYAIDMOT 420  
Db 378 GNTTVLVLTTSOYKLTVPREFLMCNLAFADLCIGIYVLLLIASVDIHTKSQYHNYAIDMOT 437  
QY 421 GAGCDAAAGFTTFASELSVYITATLERWHITTHAMQLECKVQLRHAASVMVLGWTAF 480  
Db 438 GAGCDAAAGFTTFASELSVYITATLERWHITTHAMQLECKVQLRHAASVMVLGWTAF 497  
QY 481 AALPFIFIGISYMKVSIKLPMDIDSPLSOLVPMALLVNLVAFVVICGCTHYIYLVN 540  
Db 498 AALPFIFIGISYMKVSIKLPMDIDSPLSOLVPMALLVNLVAFVVICGCTHYIYLVN 557  
QY 541 PTIVSSSDTKIAKRMATLIFTDFLCMAPIISFAISASLKVPPLITVSRAKILLVLFYFIPN 600  
Db 558 PTIVSSSDTKIAKRMATLIFTDFLCMAPIISFAISASLKVPPLITVSRAKILLVLFYFIPN 617  
QY 601 SCANPLXYAFTKFNRRDFILLKFGCYEQMAQIYRTTSSATINFHARKSHCSAPRV 660  
Db 618 SCANPLXYAFTKFNRRDFILLKFGCYEQMAQIYRTTSSATINFHARKSHCSAPRV 677  
QY 661 TNSYVLVPLNHSQN 675  
Db 678 TNSYVLVPLNHSQN 692

RESULT 2  
US-08-487-886-2  
; Sequence 2, Application US/08487886  
; Patent No. 574448  
; GENERAL INFORMATION:  
; APPLICANT: Kelton, Christie Ann  
; APPLICANT: Schweickhardt, Rene Lynn  
; APPLICANT: Cheng, Shirley Vui Yen  
; APPLICANT: Nugent, No. 574448een Patrice  
; TITLE OF INVENTION: Human Follicle Stimulating  
; TITLE OF INVENTION: Hormone Receptor  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Stephan P. Williams,  
; ADDRESSEE: Ares-Serono, Inc.  
; STREET: Exchange Place, 37th floor  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density  
; COMPUTER: IBM PS/2, model 55 SX  
; OPERATING SYSTEM: MS-DOS version 4.0  
; SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,886  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/670,085  
FILING DATE: 15-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Stephan P.  
REGISTRATION NUMBER: 28546  
REFERENCE/DOCKET NUMBER: US/252  
TELEPHONE: (617) 723-1300  
TELEFAX: (617) 723-8923  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 695  
TYPE: Amino acid  
TOPOLOGY: Linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: signal sequence  
LOCATION: -17 to -1  
IDENTIFICATION METHOD: hydrophobic  
FEATURE:  
NAME/KEY: putative amino-terminal extracellular domain  
LOCATION: 1 to 349  
IDENTIFICATION METHOD: similarity with other  
IDENTIFICATION METHOD: dimeric glycoprotein receptor extracellular  
IDENTIFICATION METHOD: domains, hydrophilic  
FEATURE:  
NAME/KEY: transmembrane domain  
LOCATION: 350 to 613  
IDENTIFICATION METHOD: similarity to other G  
IDENTIFICATION METHOD: protein-coupled receptor transmembrane domains  
FEATURE:  
NAME/KEY: putative transmembrane region I  
LOCATION: 350 to 370  
IDENTIFICATION METHOD: similarity to other G  
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
FEATURE:  
NAME/KEY: putative transmembrane region II  
LOCATION: 382 to 404  
IDENTIFICATION METHOD: similarity to other G  
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
FEATURE:  
NAME/KEY: putative transmembrane region III  
LOCATION: 427 to 448  
IDENTIFICATION METHOD: similarity to other G  
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
FEATURE:  
NAME/KEY: putative transmembrane region IV  
LOCATION: 469 to 491  
IDENTIFICATION METHOD: similarity to other G  
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
FEATURE:  
NAME/KEY: putative transmembrane region V  
LOCATION: 512 to 533  
IDENTIFICATION METHOD: similarity to other G  
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
FEATURE:  
NAME/KEY: putative transmembrane region VI  
LOCATION: 557 to 580  
IDENTIFICATION METHOD: similarity to other G  
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
FEATURE:  
NAME/KEY: putative transmembrane region VII  
LOCATION: 592 to 613





FEATURE:  
: NAME/KEY: putative transmembrane region V  
: LOCATION: 512 to 533  
: IDENTIFICATION METHOD: similarity to other G  
: IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
: IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
: FEATURE:  
: NAME/KEY: putative transmembrane region VI  
: LOCATION: 557 to 580  
: IDENTIFICATION METHOD: similarity to other G  
: IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
: IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
: FEATURE:  
: NAME/KEY: putative transmembrane region VII  
: LOCATION: 592 to 613  
: IDENTIFICATION METHOD: similarity to other G  
: IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
: IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
: FEATURE:  
: NAME/KEY: putative carboxy-terminal intracellular  
: NAME/KEY: domain  
: LOCATION: 614 to 678  
US-08-482-855-2

Query Match 90.1%; Score 3169.5; DB 3; Length 695;  
Best Local Similarity 89.5%; Pred. No. 4.4e-249;  
Matches 607; Conservative 31; Mismatches 37; Indels 3; Gaps 2;

Qy 1 CHHWLCHS NRVLFCQDSKVTEIPTDLPRNAIELRVLTTLKRLVPIPKGSPAGFGDLEKIEI 60  
Db 18 CHHRICHCS NRVLFCQESKVTEIPSDLPNAIELRVLTTLKRLVIQKGFSGDLEKIEI 77  
Qy 61 SONDVLEIADVFNSLPKLEHRIEIKANNLLINPEAFONLPSRLYLLISNTGIRKHPA 120  
Db 78 SONDVLEIADVFNSLPKLEHRIEIKANNLLINPEAFONLPSRLYLLISNTGIRKHPD 137  
Qy 121 VHKIQSLQKVLDDIQDNNIINHIVARNFMSFVSLKSGIEIHNCAFNGLTOLDE 180  
Db 138 VHKIHSLOKVLDDIQDNNIINHIVARNFMSFVSLKSGIEIHNCAFNGLTOLDE 197  
Qy 181 LNSDNNLEELNDVFOGASGVILDISTKTVHSLPNHGLENNKLLRARSYTLRKLPN 240  
Db 198 LNSDNNLEELNDVFOGASGVILDISTKTVHSLPNHGLENNKLLRARSYTLRKLPN 257  
Qy 420 TGACDAAAGFTVFASLSVYTLTALERWHITAMOLECKVOLRHAASVVLGTFPA 479  
Db 438 TGACDAAAGFTVFASLSVYTLTALERWHITAMOLECKVOLRHAASVVLGTFPA 497  
Qy 480 FAALPFIPIGSIYMKVSIKPLMDIDSPLSQVMSLLVNLVAFVVICGYTHIYLTVR 539  
Db 498 FAALPFIPIGSIYMKVSIKPLMDIDSPLSQVMSLLVNLVAFVVICGYTHIYLTVR 557  
Qy 540 NPPIVSSSDTKAKRWATLITFDLCMAPISEFASLSKLVPLITVSKAKILLVLYPI 599  
Db 558 NPPIVSSSDTKAKRWATLITFDLCMAPISEFASLSKLVPLITVSKAKILLVLYPI 617  
Qy 600 NSCANPLYAIFTKNRRDFILLSKFGCYEMAQIYRTETSSATNFHARKSHCSAPR 659  
Db 618 NSCANPLYAIFTKNRRDFILLSKFGCYEMAQIYRTETSSATNFHARKSHCSAPR 677  
Qy 660 VTN--SYVLPLNHSQN 675.

Db 678 VTNGSYILVPLSHLAQN 695  
III :I:IIII:I:I:II  
RESULT 4  
US-08-474-986-2  
: GENERAL INFORMATION:  
: APPLICANT: Kelton, Christie Ann  
: Schwickhardt, Rene Lynn  
: Cheng, Shirley Vui Yen  
: Nugent, No. 637271leen Patrice  
: TITLE OF INVENTION: Human Follicle Stimulating  
: Hormone Receptor  
: NUMBER OF SEQUENCES: 2  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Stephan P. Williams,  
: Ares-Serono, Inc.  
: STREET: Exchange Place, 37th floor  
: CITY: Boston  
: STATE: MA  
: COUNTRY: USA  
: ZIP: 02109  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density  
: COMPUTER: IBM PS/2, model 55 SX  
: OPERATING SYSTEM: MS-DOS version 4.0  
: SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/474,986  
: FILING DATE: 07-Jun-1995  
: CLASSIFICATION: <Unknown>  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 07/670,085  
: FILING DATE: <Unknown>  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Williams, Stephan P.  
: REGISTRATION NUMBER: 28546  
: REFERENCE/DOCKET NUMBER: US/252  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (617) 723-1300  
: TELEFAX: (617) 723-8923  
: LOCATION: 614 to 678  
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-08-474-986-2

Query Match 90.1%; Score 3169.5; DB 4; Length 695;  
Best Local Similarity 89.5%; Pred. No. 4.4e-249;  
Matches 607; Conservative 31; Mismatches 37; Indels 3; Gaps 2;

Qy 1 CHHWLCHS NRVLFCQDSKVTEIPTDLPRNAIELRVLTTLKRLVPIPKGSPAGFGDLEKIEI 60  
Db 18 CHHRICHCS NRVLFCQESKVTEIPSDLPNAIELRVLTTLKRLVIQKGFSGDLEKIEI 77  
Qy 61 SONDVLEIADVFNSLPKLEHRIEIKANNLLINPEAFONLPSRLYLLISNTGIRKHPA 120  
Db 78 SONDVLEIADVFNSLPKLEHRIEIKANNLLINPEAFONLPSRLYLLISNTGIRKHPD 137  
Qy 121 VHKIQSLQKVLDDIQDNNIINHIVARNFMSFVSLKSGIEIHNCAFNGLTOLDE 180  
Db 138 VHKIHSLOKVLDDIQDNNIINHIVARNFMSFVSLKSGIEIHNCAFNGLTOLDE 197  
Qy 181 LNSDNNLEELNDVFOGASGVILDISTKTVHSLPNHGLENNKLLRARSYTLRKLPN 240  
Db 198 LNSDNNLEELNDVFOGASGVILDISTKTVHSLPNHGLENNKLLRARSYTLRKLPN 257  
Qy 241 LDFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRODIDDMTOIGDORVSLDD 300  
Db 258 LKLVALMEASLYPSHCCAFANLKRQISELHPICNKSILRODIDDMTOIGDORVSLDD 317  
Qy 301 -EPSYKSGSDMYNEFDYDLCNEVDVTCSPKDPANPCEDIMGYNLRVLWIFISLAI 359  
Db 318 NESSYSGRFGDMTTEFDYDLCNEVDVTCSPKDPANPCEDIMGYNLRVLWIFISLAI 377

QY 360 TGNVTLLVLTSTQYKLTVPFLMKNLAPADLCIGIYLLIASVDHTKSOYHNTAIDQ 419  
DB 378 TGNVILVLTSTQYKLTVPFLMKNLAPADLCIGIYLLIASVDHTKSOYHNTAIDQ 437  
QY 420 TGACDAAGFFTFVASELSVTTTATILRHHHTITHAMOLECKVOLRHAASVNVGTF 479  
DB 438 TGACDAAGFFTFVASELSVTTTATILRHHHTITHAMOLECKVOLRHAASVNVGTF 497  
QY 480 FAAALFPITGISTSKVSYICUPMDIDSPLSQLYNALLVYLVAFVYICGCTHYIYTVR 539  
DB 498 FAAALFPITGISTSKVSYICUPMDIDSPLSQLYNALLVYLVAFVYICGCTHYIYTVR 557  
QY 540 NPTVSSSDPTKIKAMATLPTDPLCHAPISFAISASIKVPLTVSKAKILLVYPI 599  
DB 558 NPTVSSSDPTKIKAMATLPTDPLCHAPISFAISASIKVPLTVSKAKILLVYPI 617  
QY 600 NSCANPETAITPFRDPTILLSCCTCYEMOQIYRTSTSSATHARKSHCSSAPR 659  
DB 618 NSCANPETAITPFRDPTILLSCCTCYEMOQIYRTSTSSATHARKSHCSSAPR 677  
QY 660 VTN--STVLVPLHNSON 675  
DB 678 VTNGSTVLVPLHNSON 695

## RESULT 5

US-07-757-3420-4  
Sequence 4, Application US/07/7573420

Patent No. 429507  
GENERAL INFORMATION:

APPLICANT: IGARASHI, Masao  
NAGAMURA, Kazuo

TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
CUSHMAN

STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts

COUNTRY: US  
ZIP: 02109

COMPUTER READABLE FORM:  
SOURCE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25

APPLICATION NUMBER: US/07/757,3420  
FILING DATE: 10-Sep-1991

CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: BUCKLEY, Linda M.  
REGISTRATION NUMBER: 31003

REFERENCE/DOCKET NUMBER: 41226  
TELEPHONE: (617)523-3400

TELEFAX: (617)523-6440  
INFORMATION FOR SEQUENCE:

SEQUENCE CHARACTERISTICS:  
LENGTH: 696 amino acids

TOPOLOGY: linear  
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-07-757-3420-4

Query Match 51.4%; Score 1807; DB 4; Length 696;  
Best Local Similarity 57.6%; Pred.No.1.7e-138;  
Matches 361; Conservative 98; Mismatches 142; Indels 26; Gaps 8;

QY 28 PRNAILRPTVLTKL--RVIPKSPAGFGDLKIEISQNDVLEIVDAVFSNLPKLHRI 85  
DB 47 PRAGLS-RUSITVLTIKVFSQNFGLNEVYKILSOSLEKIANFNDLNLSEIL 105  
QY 86 EXANKLYINPAPOLFSLRYLLSNTGFKHLPVHKIOSLO-KVLDDIQDNINHI 144  
DB 106 ONTKNLVYTERGAPTHLPRLKLSICNTGIRKLPDVTKIPSEFNPILLECONLHITVP 165  
QY 145 RNSPGLSPESVILMLSNKNGIBEHNCAPNGTQDELINLNNLELPHNDVFCASGPV 204  
DB 166 ANAFOGNNESITLKLYGNGFEEIOSHAFNGTTLISLEKENAHLKKMHHDAFARGPS 225  
QY 205 ILDISRTKVLPHGLNKLKLRARSTYRLAKKLPNDKFTVLMKASLTYPSSHCAPNL 264  
DB 226 ILDISRTKVLPHGLNKLKLRARSTYRLAKKLPNDKFTVLMKASLTYPSSHCAPNL 285  
QY 265 --KRO-----ISELHPICNKSILRDOIDMFOIGORVSLIDDEPSYKGSMDMYNEFD 316  
DB 286 PTKDNFSPSIFPKNFSCSTARRPNNETL-----YSAFAG-----SELSMDYD 332  
QY 317 YDLNCEVVDVTCSPKDFAPNGEDIMGYNLRLVLIHFIISILATIGNTTVLVLTSTQYKL 376  
DB 333 YGFCSPKT-LOCAPEPDAFNPCEIDIMGYDLFVLIHFIISILATIGNTTVLVLTSTQYKL 391  
QY 377 TVPRLMCLNLAFLADLCIGIYLLIASVDHTKSOYHNTAIDQTAGCDAAGFFTFVASE 436  
DB 392 TVPRLMCLNLAFLADLCIGIYLLIASVDHTKSOYHNTAIDQTAGCDAAGFFTFVASE 451  
QY 437 LSVYTLTATILRHHHTITHAMOLECKVOLRHAASVNVGTFVASE 496  
DB 452 LSVYTLTATILRHHHTITHAMOLECKVOLRHAASVNVGTFVASE 511  
QY 497 SICLPMOVTLSQYKLTVPFLMKNLAPADLCIGIYLLIASVDHTKSOYHNTAIDQ 556  
DB 512 SICLPMOVTLSQYKLTVPFLMKNLAPADLCIGIYLLIASVDHTKSOYHNTAIDQ 571  
QY 557 ATLIPTDCHAPISFAISASIKVPLTVSKAKILLVYLVAFVYICGCTHYIYTVR 616  
DB 572 AVLIPTDCHAPISFAISASIKVPLTVSKAKILLVYLVAFVYICGCTHYIYTVR 631  
QY 617 RDPFTLLSKFCGYEMOQIYRTSTSSA 643  
DB 632 RDPFTLLSKFCGYEMOQIYRTSTSSA 658

## RESULT 6

US-07-741-453A-60  
Sequence 60, Application US/07/741453A

Patent No. 629897  
GENERAL INFORMATION:

APPLICANT: PARMENTIER, MARC  
APPLICANT: LIBERT, FREDERIC

APPLICANT: DUMONT, JACQUES  
APPLICANT: VASSART, GILBERT

TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS

NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1615 L STREET, N.W.

CITY: WASHINGTON, D.C.  
COUNTRY: U.S.A.

COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/741,453A

FILING DATE: 19911015  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, PAUL N.  
 REGISTRATION NUMBER: 16773  
 REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 861-3000  
 TELEFAX: (202) 822-0944  
 TELEX: 6714627 CUSH  
 INFORMATION FOR SEQ ID NO: 60:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 764 amino acids  
 TYPE: AMINO ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-741-453A-60

Query Match 51.2%; Score 1799; DB 4; Length 764;  
 Best Local Similarity 51.9%; Pred. No. 8.7e-138;  
 Matches 377; Conservative 92; Mismatches 197; Indels 60; Gaps 10;

QY 6 CHCSN----RVFLQDSKVTEPTDLPNRAIELRVTLKLRVPGSGFAGDGLKIEIS 61  
 DB 29 CECHOEDEFV--TKRD--IHRIPT-LPPSTQTLKFIETQLKTPISRAFSNLPNISRIYLS 84  
 QY 62 QNDVLEIADVFSLPKLHEIRIEKANNLLVINPEAFQNLPSRLYLLISNTGKIHLPV 121  
 DB 85 IDATLORLSESHFYSLKSMTHIEINTSLTSIDPAUKELPLKPLGIFNGLGVFPDV 144  
 QY 122 HKIOSLQK-VLLDIONINIHIVARNFPMGLSFESVILWLSKNGIEEIHNCFAFGNGTQDLE 180  
 DB 145 TKVYSTDFVFIETDNPYMASIPANAFQGLCNETTLTKLYNNGFTSIOGHAFNGTKLDA 204  
 QY 181 LNLSDNNLEELPNDVFOGA-SGPVILDSRTKRVHSLPNHGLEKLLKLRSTYRLKLP 239  
 DB 205 VTLNKKYLSAIDKDAFGVYSGTLLDVSYSVTALPSKGLKELIARNTWTWKLP 264  
 QY 240 NLDKFTVLEASLTYPSSHCCAFANLKRQISELHPI--CNKSILRQ-----DI 284  
 DB 265 LSLFHLTRADLSYPSHCCAFKQKIRGILESIMCNESIRSRQKSVNTLNGPDDQ 324  
 QY 285 DMTQIGDQVSLIDDEFSYSGSDMY-----NE 314  
 DB 325 EYEEYLGDSHAGYKNSQFQDTSNHYVFFEEQDETLGFGQELKPNQEEITLQAFDSH 384  
 QY 315 FPDYDLNVEVDVTCSPKDPAPNCPEDINGYNILRVLINFISILAITGNTTVLVLTTSOY 374  
 DB 385 IDYTVCGGNEDMVCTPKSDEFNCPEDIMGYKELRVVWFVSLALLGNVFLVILVLTSHY 444  
 QY 375 KLTVPFRFLMCLAFADLCIGIYLLIASVDIHTKSOYHNYAIDMTQAGCDAAGFTVFA 434  
 DB 445 KLTVPFRFLMCLAFADFCIGIYLLIASVDIHTKSOYHNYAIDMTQAGCDAAGFTVFA 504  
 QY 435 SELSVYTLTAITLERWHTITHAMQLECKVQLRHAASVMVGLWTFFAAALFFIFGSSYM 494  
 DB 505 SELSVYTLTAITLERWHTITHAMQLDCKVQLRHAASVMVGMVIFAFAAALFFIFGSSYM 564  
 QY 495 KYVICLPMDIDPSLSQLYMALLVNLVAFVVCCTHYIYTVRNPTIVSSSDTKIAK 554  
 DB 565 KYVICLPMDIDPSLSQLYMALLVNLVAFVVCCTHYIYTVRNPTIVSSSDTKIAK 624  
 QY 555 RNATLIFTDLCMAPISFAISLKVPLITYSKAKILLVLPVNSCANPELYAIFTKN 614  
 DB 625 RNATLIFTDLCMAPISFAISLKVPLITYSKAKILLVLPVNSCANPELYAIFTKN 684  
 QY 615 FRDFPILLSKGCYEMOQAIYRTETSSATHNF-----HARKSHGSSAPRVNTSVLPL 669  
 DB 685 FORDVILLSKGCYEMOQAIYRTETSSATHNF-----HARKSHGSSAPRVNTSVLPL 744  
 QY 670 NHSSQN 675  
 DB 745 SHLTNP 750

RESULT 7

US-07-757-342D-3  
 : Sequence 3, Application US/07757342D  
 : Patent No. 6218509  
 : GENERAL INFORMATION:  
 : APPLICANT: IGARASHI, Masao  
 : MINEGISHI, Takashi  
 : NAKAMURA, Kazuto  
 : TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
 : NUMBER OF SEQUENCES: 10  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
 : CUSHMAN  
 : STREET: 130 Water Street  
 : CITY: Boston  
 : STATE: Massachusetts  
 : COUNTRY: US  
 : ZIP: 02109  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent In Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA: US/07/757,342D  
 : APPLICATION NUMBER: US/07/757,342D  
 : FILING DATE: 10-Sep-1991  
 : CLASSIFICATION: <Unknown>  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: BUCKLEY, Linda M.  
 : REGISTRATION NUMBER: 31003  
 : REFERENCE/DOCKET NUMBER: 41226  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (617)523-3400  
 : TELEFAX: (617)523-6440  
 : TELEX: 200291 STRE UR  
 : INFORMATION FOR SEQ ID NO: 3:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 700 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-07-757-342D-3

Query Match 51.1%; Score 1797; DB 4; Length 700;  
 Best Local Similarity 56.5%; Pred. No. 1.1e-137;  
 Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

QY 28 PRNATELRFVLTKL--RVIPKGSFAGDGLKIEISQNDVLEIADVFSLPKLHEIRI 85  
 DB 51 PRAGI--ARLSLTLYLVKVPISQAFRLNEVVKIEISQSDSLERIEANAFDNLNLSELLI 109  
 QY 86 EKANNLLINPEAFONLPSRLYLLISNTGKIHLPVHKTQSLO--KVLLDIONINITHVA 144  
 DB 110 QNTKLLIYECAFNLPRLKLTSLTCTGIRTPDVTKISSSEFNFILEICIONLHITTP 169  
 QY 145 RNSFMGLSFESVILWLSKNGIEEIHNCFAFGNGTQDDELNLSDNNLEELPNDVFOGASGV 204  
 DB 170 GNAFGMNNESVTLKLYNGPPEVQSHAFNGTTLISLEKENIYLEKHNSHGAFOGATGFS 229  
 QY 205 ILDISRTKRVHSLPNHGLEKLLKLRSTYRLKLLPNLQKFTVLMASLTYPSSHCCAFANL 264  
 DB 230 ILDISRTKRVHSLPNHGLEKLLKLRSTYRLKLLPNLQKFTVLMASLTYPSSHCCAFANL 289  
 QY 265 KROISELHPICKNSLILRODIDDMTOIGQORVSLIDDEPSYG---KGDMMYNEFDVLCN 321  
 DB 290 PKK-----EQNFSFISFENFSKQCESTVRKADNETLYSAIFEENELSGWDYDYGFS 341  
 QY 322 EYVDVTCSPKDPAPNCPEDIMGYNILRVLINFISILAITGNTTVLVLTTSOYKLTVPFR 381  
 DB 342 PKT-LQCAPEPDAPNCPEDIMGYALRVLNLINILAFGNLTVLFLVLTTSYKLTVPFR 400

OY 392 LACNAPADLCIGYLLIASVDIHTKSOYHVAIDMOTGAGCDAGFFVASELSVYT 441  
DB 401 LACNLSFADFCMGLYLLIASVDSOTGQYHNAIDMOTGCGGAGFFVASELSVYT 450  
OY 442 LTAITLERHHTITHAMOLECKVOLRHAASVVLGHTFAAALFFPICISSYKVSICLP 501  
DB 461 LTVITLERHHTITAVOLQOKLRLRHAIPIMLGCMFSTLIATPMLVGISNTRKVSICLP 520  
OY 502 MDIDSPLSOLYVALLVAFVYVCGCYTHIYLVTRNPTIVSSSSDTKIAKRMATLIF 561  
DB 521 MDVSTLSOYVILSLILUNVAFVYVCGCYTHIYLVTRNPTIVSSSSDTKIAKRMATLIF 580  
OY 562 TOPICAPISFAISAKSVPLITVSKAKILLVLPYNSCANPFLYAIPTKFRFRDFFI 621  
DB 581 TOPICAPISFAISAKSVPLITVSKAKILLVLPYNSCANPFLYAIPTKFRFRDFFI 640  
OY 622 LLSRECFEYMOAOIVTETSATHNFAKSHCSS 656  
DB 641 LLSRFGCKRBAELTRK-----DFSATTSCKN 669

RESULT 8  
US-07-757-342D-10  
: Sequence 10, Application US/07757342D  
: Patent No. 6218509  
: GENERAL INFORMATION:  
: APPLICANT: IGARASHI, Masao  
: MINEGISHI, Takashi  
: NAKAMURA, Kazuto  
: TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
: NUMBER OF SEQUENCES: 10  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
: STREET: 130 Water Street  
: CITY: Boston  
: STATE: Massachusetts  
: COUNTRY: US  
: ZIP: 02109  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07/757,342D  
: FILING DATE: 10-Sep-1991  
: CLASSIFICATION: <Unknown>  
: ATTORNEY/AGENT INFORMATION:  
: NAME: BUCKLEY, Linda M.  
: REGISTRATION NUMBER: 31003  
: REFERENCE/DOCKET NUMBER: 41226  
: TELEPHONE: (617)523-3400  
: TELEFAX: (617)523-6440  
: TELEX: 200291 STRE UR  
: INFORMATION FOR SEQ ID NO: 10:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 674 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULAR WEIGHT: 74.2 kDa  
: SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-07-757-342D-10

Query Match 50.5%; Score 1776; DB 4; Length 674;  
Best Local Similarity 55.4%; Pred. No. 5.4e-136;  
Matches 349; Conservative 107; Mismatches 148; Indels 26; Gaps 6;  
OY 38 LTKL-----RVIPKGFAGFQDLREIISQNDVLEADVFNPLRIETREKANN 90  
DB 26 LTRLSLAYLPVKVIPSQAFGLNVEIKIISQIDSLRIETANAFNLLNSLILQNTKN 85

OY 91 LLYINPFAONFSLRYLLISHTGKIHLPAVHKI-OSLOKVLDDIQDNINIHIVARNSPM 149  
DB 86 LAYTECAFNLGKLYLSICTGIRFPDVTAFVSESFNLDEICNLNLTITTPGNAPQ 145  
OY 150 GLSPESVILMSKNGEIEHNCANFCTQDDELNLSNNLELPNDVFOGASGPVTLDS 209  
DB 146 GNNESVTLKLYGNGFEVGSHPFNGTTLTSLKLNKLVHLEKMHGAFRGATGPKTLDIS 205  
OY 210 RTKVHSLPNHGLENLKRLARSTYRKLKLPNLDKFTVLTMEASLTPYSHCCAFANLAROIS 269  
DB 206 STKQALPSTGLSESQRLATSTSYSLKLPSTRETFVNLLEATLTPYSHCCAFNRL----- 260  
OY 270 ELHPICNKSILROIDMTOIGDQVSLIDDEFSYCK---GSDMHYNEFDYDLNNEVDV 326  
DB 261 ---PTEKNGSHSISENFSKQCESTVRKVSNTKLYSSMLAESLSGMDVEYGFCLKTP- 316  
OY 327 TCSKPDAPNCPEDINGNILKLVLPISLAIATGTTLVLTSTSOYKLVTPRFLMCLN 386  
DB 317 RCAFEPDAPNCPEDINGDPLAVLILHILAHGMYLVLLTSRLKLVTPRFLMCLN 376  
OY 387 APADLCIGYLLIASVDIHTKSOYHVAIDMOTGAGCDAGFFVASELSVYTITAIT 446  
DB 377 SFADFCMGLYLLIASVDSOTGQYHNAIDMOTGCGGAGFFVASELSVYTITVIT 436  
OY 447 LERMHTITHAMOLECKVOLRHAASVVLGHTFAAALFFPICISSYKVSICLPMDIDS 506  
DB 437 LERMHTITVATHLDOKLRLRHAIPIMLGCMFSSLIAMLPVGVSNTRKVSICPMDVET 496  
OY 507 PLSOLYVALLVAFVYVCGCYTHIYLVTRNPTIVSSSSDTKIAKRMATLIFTDFLC 566  
DB 497 TLSOVVILSLILUNVAFVYVCGCYTHIYLVTRNPTIVSSSSDTKIAKRMATLIFTDFTC 556  
OY 567 MAPISFAISAKSVPLITVSKAKILLVLPYNSCANPFLYAIPTKFRFRDFFILLSP 626  
DB 557 MAPISFAISAKSVPLITVSKAKILLVLPYNSCANPFLYAIPTKFRFRDFFILLSP 616  
OY 627 GCYEMOAOIVTETSATHNFAKSHCSS 656  
DB 617 GCKRBAELTRK-----DFSATTSCKN 640

RESULT 9  
US-07-757-342D-2  
: Sequence 2, Application US/07757342D  
: Patent No. 6218509  
: GENERAL INFORMATION:  
: APPLICANT: IGARASHI, Masao  
: MINEGISHI, Takashi  
: NAKAMURA, Kazuto  
: TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
: NUMBER OF SEQUENCES: 10  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
: STREET: 130 Water Street  
: CITY: Boston  
: STATE: Massachusetts  
: COUNTRY: US  
: ZIP: 02109  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07/757,342D  
: FILING DATE: 10-Sep-1991  
: CLASSIFICATION: <Unknown>  
: ATTORNEY/AGENT INFORMATION:  
: NAME: BUCKLEY, Linda M.  
: REGISTRATION NUMBER: 31003  
: REFERENCE/DOCKET NUMBER: 41226  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (617)523-3400  
: TELEFAX: (617)523-6440  
: TELEX: 200291 STRE UR  
: INFORMATION FOR SEQ ID NO: 10:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 674 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULAR WEIGHT: 74.2 kDa  
: SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-07-757-342D-10

TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 699 amino acids  
TYPE: amino acid  
MOLECULE TYPE: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-07-757-342D-2

Query Match 50.5%; Score 1776; DB 4; Length 699;  
Best Local Similarity 55.4%; Pred. No. 5.7e-136;  
Matches 349; Conservative 107; Mismatches 148; Indels 26; Gaps 6;

QY 38 LTKL-----RVIPKSPAGFGDLEKIEISONDVLEIVIEADVFSLPKLHEIRIEKANN 90  
DB 51 LTRLAYLPVKVIPSQAFGLNEVIEKIEISODSLERIEANAFDNLNLSILIQTKN 110  
QY 91 LLYINPEAFONLPSRLYLISNTGKHLPAVHKI-OSLQKVLDDIODNINHIVARNSEM 149  
DB 111 LRYEPGAFNLPGKLSLTCNTGIRKFPDVTYVSSSENFLEICDNLHITTPGNAFQ 170  
QY 150 GLSPESVILWLSKNGIEEIHNCANFGTQDLDELNLDNNLEELPNDVFGASGPVILDIS 209  
DB 171 GNNESVTLKLYNGPEEVQSHAFNGTTLTSLKENVHLEKMHNGAFRCATGPKTLDIS 230  
QY 210 RTKVHSLPNEGLENKLRARSYRLAKLNLNOKFVTLMEASLTYPHSCCAFLNKRQIS 269  
DB 231 STKLQALPSYGLSEIQRLIATSSYSLKLPSTRETFVNLLEATLTPSHCCAFRLN---- 285  
QY 270 ELHPICKNLSLRQDIDDMTOIGDORVSLIDDEPSYK--GSDMMYNEFDYDLCNEVVVD 326  
DB 286 ---PTKQNFSHSISENFKQCESTVRKVNKNTLYSSMLAESELSUGWDYETGCLPTP- 341  
QY 327 TCSKPKDAPNCPEDIMGYNLRLVIFISILAITGNTTVLVLTTSQYKLTVPFLMCNL 386  
DB 342 RCAPEAPNCPEDIMGYDFLRWLILINILAINGNMTLVFLVLTSLYKLTVPFLMCNL 401  
QY 387 AFADLCIGYLLLTASVDIHTKSOYHNAIDMTQAGCDAAGFTVPFASLSVYTLTAIT 446  
DB 402 SFADFCHGLVLLLTASVDSOTKGOYHNAIDMTQAGCDAAGFTVPFASLSVYTLTAIT 461  
QY 447 LERHHTTHAMOLECKVOLRHAASVMVLGWTFAFAALFPFTGSSYKMYKVICLPMDIDS 506  
DB 462 LERHHTTYAHLQKRLRHAAILIMLGGWLFSSLIAMLPVGVNSYKMYKVICPMDVET 521  
QY 507 PLSQLYMALVNLVAFVYICGCTHYILTVRNPTIVSSSDTKIAKRMATLIFTDFLC 566  
DB 522 TLSQVYILTILNVAVAFIICACYIKIYFAVRNPELMAKNKDTKIAKMAILLIFTDFTC 581  
QY 567 MAPISFAISASLKVLITVSKAKILLVLYPINSKANPELYAIFTKFNRRDPFILLSKF 626  
DB 582 MAPISFAISAAFLVITVNSVLLVLYPINSKANPELYAIFTKFNRRDPFILLSKF 641  
QY 627 GYEMOQIYRTTSSATHNFARKSHCSS 656  
DB 642 GCCRRALRYRK-----DPSATYSNCKN 665

RESULT 10  
US-07-741-453A-56  
Sequence 56, Application US/07741453A  
Patent No. 6228597  
GENERAL INFORMATION:  
APPLICANT: PARMENTIER, MARC  
APPLICANT: LIBERT, FREDERIC  
APPLICANT: DUMONT, JACQUES  
APPLICANT: VASSART, GILBERT  
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES

NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBAY & CUSHMAN  
STREET: 1615 L STREET, N.W.  
CITY: WASHINGTON, D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07741,453A  
FILING DATE: 19911015  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16773  
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 792 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-741-453A-56

Query Match 47.5%; Score 1670; DB 4; Length 792;  
Best Local Similarity 50.3%; Pred. No. 2.7e-127;  
Matches 368; Conservative 100; Mismatches 166; Indels 98; Gaps 21;

QY 28 PRNAIEFLVLTKL--RVIPKSPAGFGDLEKIEISONDVLE-----VIEADVFSLPK 79  
DB 59 PRAGLS--RLSTYLPKIPVISOAFRGVNVVVKIEISODSLEPIGHGCKIEANAFDNLN 117  
QY 80 LHEIRIEKANLLINPEAFONLPSRLYLISNTGIRK-----LPAVHKIQSLQ-KVLL 132  
DB 118 LSEILQNTKLVYIEPGAFTNLPRAYLSICNTGIRKPIGCHGCLPDTYKIFSSEFNIL 177  
QY 133 DIQDNIHIVARNFMSGLSFESVILWLSKNGIEEIHNC-----AFNGTQDELNLSDN 186  
DB 178 EICDNLHITVPAANAFQGMNNEITLKLNGNFEPIGHGCEIQSHAFNGTLLISLELKN 237  
QY 187 NNLDELNDVFOGASGVILDISRTKVHS-----LPHGLENLKLRLARSTYRLKLPN 240  
DB 238 AHLKMHNDAPFRGARGPSILDISSTKLOAPIGHGCLPSYGLSQTLLATSSYSLKLKPS 297  
QY 241 LDKFETLMEASLTYPHSCCAFLN-----KRQ-----ISELHPICKNLSLRQDIDD 286  
DB 298 REKFTNLLDATLTPSHCCAFRLNPPIGHGCTKQNFSESTFKNFKQCESTARRPNNET 357  
QY 287 MTQIGDORVSLIDDEPSYKGSDDMMYNEFDY-DLCNEVVVDVTCSPKDPAPNCPEDIMGYN 345  
DB 358 LYSIFAFAESELSDWDPIGHGCEYD--YGPIGHGCFSPKT-LQCAPEADAPNCPEDIMGYD 414  
QY 346 ILRVLIWFISTLATGTNTVLV-----LTTQYKLTVPFLMCNLAFADLCIGYLL 399  
DB 415 FLRVLIWILINILAINGNVTLFADIGHGCLTSHYKLTVPFLMCNLSFADFCMLGLLL 474  
QY 400 IASVDIHTKSOYHNAIDW-----QTGAGCDAAGFTVPFASLSVYTLTAITLERHWTI 453  
DB 475 IASVDAQTKGOYHNAIDWPIGHGCGTNGCSVAGFTVPFASLSVYTLTAITLERHWTI 534  
QY 454 THAMOLECKVOLRHA-----ASVMVLGWTFAFAALFPFTGSSYKMYKVICLPMDIDSP 507  
DB 535 TYAQLDQKLRHARPIGHGCGIPIMLGGWLFSTLIAMLPVGVSSYKMYKVICLPMDVETT 594

QY 508 LSQVYVALLY-----LVAFVYVCCGYHYIYVYVNTPIVSSSDTKIAKPMATLIF 561  
DB 595 LQVYVALLY-----LVAFVYVCCGYHYIYVYVNTPIVSSSDTKIAKPMATLIF 564  
QY 562 TQVYVALLY-----LVAFVYVCCGYHYIYVYVNTPIVSSSDTKIAKPMATLIF 564  
DB 655 TQVYVALLY-----LVAFVYVCCGYHYIYVYVNTPIVSSSDTKIAKPMATLIF 714  
QY 616 RRD-----PFLSKGCGYVQAOYRTTSSATHNPHARKSHC-----SSAP-RVTN 662  
DB 715 RRDPIGCHGCGPFLLSKCGCKNOAELYRRKDFSA-----YCKNGFTGSKNPSRSTL 765  
QY 663 SYLVPLNHSQ 674  
DB 766 KUTLPIGHCQ 777

RESULT 11  
US-07-741-453A-61  
Sequence 61, Application US/07741453A  
Patent No. 6228597  
GENERAL INFORMATION:  
APPLICANT: PARMENTIER, MARC  
APPLICANT: LIBERT, FREDERIC  
APPLICANT: DUMONT, JACQUES  
APPLICANT: VASSART, GILBERT  
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1615 L STREET, N.W.  
CITY: WASHINGTON, D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07741453A  
FILING DATE: 19911015  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16773  
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
TELEPHONE: (202) 821-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 764 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-741-453A-61

Query Match  
Best Local Similarity: 49.61  
Matches 339; Conservative 110; Mismatches 179; Indels 55; Gaps 11;

QY 6 CHSN-----RVFLCQSDSYTEPTDLPNATLEFVTLKRVTPKSGFAGOLEKIEIS 61  
DB 29 CEHOEDPRV-TCND--IQRIPS-LPPSTOTLALIEHTLTPSHAFSLNPSRIYVS 84  
QY 62 ONDVLVEADVSNLPKLEHRIEKANLVINPEAFONLPSRLYLLISMTGKHLPAV 121  
DB 85 IDLTQLOLESHTNLSKVTHIEINRNLTIIDPALKELPFLAFLGIFNTGLKMPDL 144

QY 122 HKISQ--KVLLDIODMINIHVARNSPNGLSFESVILMSKNGTEIEHNCFAFNQFOLDE 180  
DB 145 TVTSTDTDFILEITDMPHTSIPVPAQGLCNETLTKLYNNGFTSVOCYAFNGTKDA 204  
QY 181 LNLSDNNLEELNDVQGA-SGPVILDISHTKVSUPLNGLKLEKLBASSTYRLKLP 239  
DB 205 VYLNKKKYLTVIDKDAFGVYSGSLDVSOTSYALPSKLEHLEKLIARMTWLKLP 264  
QY 240 MLDFVTLMEASITTPSHCCAFANLAROISELHIPI-CNKSIL-----RODIDONT 288  
DB 265 LSLSPHLTRADLSYPSHCCAFKQKKIRGLTESLMCNESMSQSLRORKSYNALNSPLHQ 324  
QY 289 ----OIGDORVSLID-----DEPSYKGSMD-----MYNE 314  
DB 325 EYENLGDSIVGYKEKSKFOOTHANNAHYVFEDEDEIIGFQGLKNPOEITLQAFDSH 384  
QY 315 FQDLCNEVDVTCSPKPAOFNCPEDIMCYNILRVLWIFISLAIATGNTVTVVLTQY 374  
DB 385 TDYTCOSDWCYCTPSPDFNCPEDIMCYNILRVLWIFISLAIATGNTVTVVLTQY 444  
QY 375 LNVPPFLKNAFADICIGYLLIASVDIHTKSOYHNYATDMOTGACGACGPTVPA 434  
DB 445 KLVNPFKNAFADICIGYLLIASVDIHTKSOYHNYATDMOTGACGACGPTVPA 504  
QY 435 KLVNPFKNAFADICIGYLLIASVDIHTKSOYHNYATDMOTGACGACGPTVPA 494  
DB 505 SELSVTLTVTLERHMTATFAMLRDKIRLRHAAAINVGGWCCPCLALLPLVGLISYA 564  
QY 495 KVSICUPMDIDSPLSQVYVYVCCGYHYIYVYVNTPIVSSSDTKIAK 554  
DB 565 KVSICUPMDIDSPLSQVYVYVCCGYHYIYVYVNTPIVSSSDTKIAK 624  
QY 555 RMYLFTDFLCNATISFAISASLKVPLTVSKAKILLVLPYVINSANPELYATFKN 614  
DB 625 RMYLFTDFLCNATISFAISASLKVPLTVSKAKILLVLPYVINSANPELYATFKN 684  
QY 615 FROFTLLSKGCGYVQAOYR 637  
DB 685 FROFTLLSKGCGYVQAOYR 707

RESULT 12  
US-07-741-453A-54  
Sequence 54, Application US/07741453A  
Patent No. 6228597  
GENERAL INFORMATION:  
APPLICANT: PARMENTIER, MARC  
APPLICANT: LIBERT, FREDERIC  
APPLICANT: DUMONT, JACQUES  
APPLICANT: VASSART, GILBERT  
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1615 L STREET, N.W.  
CITY: WASHINGTON, D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07741453A  
FILING DATE: 19911015  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16773

REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 764 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-741-453A-54

Query Match 47.18; Score 1655; DB 4; Length 764;  
Best Local Similarity 47.28; Pred. No. 4.3e-126;  
Matches 343; Conservative 114; Mismatches 209; Indels 60; Gaps 10;  
Qy 6 CHGSDN----RVFLCQDSKVTEIPTDLPRAIELRFLVTLKRVIPKGSFAGFGDLEKIEIS 61  
Db 29 CECHOEDFRV-CKD--IHRIPT-LPPSTQTLKFTETQLKTPSRFSLNPLNISRIYLS 84  
Qy 62 QNDVLEIADVPSNPKLHEIRKANNLLYINPEAFQNLPSRLYLLISNTGKHLPAV 121  
Db 85 IDATLQRLSHSFVNLKSMTHIEIRNTRSLTSDPDALKELPLKFLGIPNTGLGVFPDV 144  
Qy 122 HKIQSLQK-VLLDIODNINHIVARNFMSGLSFESVILWLSKNGIEBIHNCAFNQTOLDE 180  
Db 145 TKYSTDVFLEITDNPYMASIPANAFGLCNETLTKLYNNGFTSIQGHAFNGTKLDA 204  
Qy 181 LNLSDNNLBELPNDVFOGA-SGVLIDISRTKVSHPNGLNKLKLRARSTYRKKLKLP 239  
Db 205 VYLNKMYLSAIDKADFGVYSGPTLDVSYTSVTPALPSGLEHKLIELIARNITWTKLKP 264  
Qy 240 NLDKFTVLEASITPSHCCAFANLKRQISELHPI-CNKSILRQ-----DI 284  
Db 265 LSLSLFLHTRADLSYPSHCCAFNOKKIRGILESLMCNESSIRSLRQKSVNTLNGFPDQ 324  
Qy 285 DDMTQIGDQVSLIDDPSPKGSDDMY-----NE 314  
Db 325 EYELGLDHAGYKDNQSQFQDTSNHSYVYFFEEQDEILGFOELKNPQOETLQAFDSDH 384  
Qy 315 FDYDLCEWVDVTSKRPDAFNPCEIDMGYNILRVLIWFISILAITGNTVVLVLTTSQY 374  
Db 385 YDITVCGNEDWCTPKSDENPCEDMGYKFLRIVVFWVSLALLGNVFLVLLTSHY 444  
Qy 375 KLVVPRFLMCLNAPADLCIGYLLIASVDIHTKSYHNYAIDMQTGAGCAAAGFTVFA 434  
Db 445 KLVVPRFLMCLNAPADFCMGYLLIASVDLYTHSEYNNHAIIDMQTGPGCNTAGFTVFA 504  
Qy 435 SELSVYTLTATLTERWITTHAMOLECKVOLRHAASVMVLGWTFAFAALFPFGISSYM 494  
Db 505 SELSVYTLVTLERWITATFAMLRDRIRLIRHAYAIMVGWCCFLLALLPLVGISSYA 564  
Qy 495 KVSICLPMIDSPISOLYVALLVNLVAFVIGCYTHIYTVRNPTVSSSDTKIAK 554  
Db 565 KVSICLPMIDTETPLAYIILVLLNIVAFIIVSCYKVIYTVRNPOYNPGDKTKIAK 624  
Qy 555 RMATLIFTDFLCMAPIFFAISLKVPLITVSKAKILLVFLYVINSKANPFLYAIPTKN 614  
Db 625 RMAYLIFTDFCMAPISFYALSALMNKPLITVTNSKILLVFLYPLNSCANPFLYAIPTKA 684  
Qy 615 PRDFFILLSKFGCYEMOAOIYRTETSATNHF-----HARKSHCSAPRVNTSYVLVPL 669  
Db 685 FORDVFIILSKFGICKRQAOAAYRGORVSPKNSAGIQIKQVTRDMRQSLPNMQDEYELLEN 744  
Qy 670 NHSSQN 675  
Db 745 SHLTPN 750

RESULT 13

US-07-741-453A-55

Sequence 55, Application US/07741453A  
Patent No. 6228597  
GENERAL INFORMATION:  
APPLICANT: PARMENTIER, MARC  
APPLICANT: LIBERT, FREDERIC  
APPLICANT: DUMONT, JACQUES  
APPLICANT: VASSART, GILBERT  
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1615 L STREET, N.W.  
CITY: WASHINGTON, D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/741.453A  
FILING DATE: 19911015  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16773  
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 795 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-741-453A-55

Query Match 47.08; Score 1652.5; DB 4; Length 795;  
Best Local Similarity 50.78; Pred. No. 7.2e-126;  
Matches 360; Conservative 96; Mismatches 159; Indels 95; Gaps 17;  
Qy 28 PRNAIELRFLVTLK--RVIPKGSFAGFGDLEKIEISQNDVLE-----VIEADVFSLNPK 79  
Db 63 PRAGL-ARLSITLVPKVIQAPRGLNEVVKIEISQDSLERATHCGRIENAFDNLN 121  
Qy 80 LHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGK-----HLPVHKIQSLQ-KVLL 132  
Db 122 LSELLIQNTKLLYIEPCAFTNLPRKLYLSICNTGIRATHCPGLPDVTKISSSEFNFL 181  
Qy 133 DIODNINHIVARNFMSGLSFESVILWLSKNGIEIHC-----AFNGTDELNLSDN 186  
Db 182 EICNLHITIPGNAFQGMNNESTVLKLYNGFRATHCGVQSHAFNGTLLISLEKEN 241  
Qy 187 NNLEELPNDFQSGASGVILDISRTKVS-----LPNHGLENLKLKRRSTYRLKLPN 240  
Db 242 IYLEKMHSGAFQAGTGSILDISSTKLQARATHCGLSHGLESIQTLIALSSYSLKTLPS 301  
Qy 241 LDKFVTLMESLTPSHCCAFANLKRQ-----ISELHPTCNKSIILRODIDD 286  
Db 302 KEKFTSLVATLTPSHCCAFANLPRATHCGKKBQNFSEFISFENFSKQCESTVRKADNET 361  
Qy 287 MTQIGDQVSLIDDPSPKGSDDMYNEFDYDLCEV-----VDVTCSPKPDAPNCPEDIM 342  
Db 362 L-----YSAIFEENELSGWDRATHCGYDGRATHCGFSPKTLOCAPEPAFNPCEDIM 414  
Qy 343 GYNILRVLIWFISILAITGNTTVLW-----LTTSOYKLTVPFRFLMCLNAPADLCIGIY 396  
|| ||||| :||| ||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 415 GYAFLEVLWLNINLAIGNLVLTVPVATHCOLLTSRKLTVPRFLMCLNLSFADPCNGLY 474  
QY 397 LLLIASVDIHTKSOYNVAIDW-----OTGAGCDAAGFTTVFASLSVYTLTATLERN 450  
Db 475 LLLIASVDSOTKGYNYNADWATHHCGGTGGCGAGFTTVFASLSVYTLTATLERN 534  
QY 451 HTITHAMOLECKVQLRAHAS-----VWVLGWTFAAALPPIFGISSTKMSVCLPMDI 504  
Db 535 HTIITVAOLDOKLRLHARATHCGIPMLGGMLESTLATMPVLGVSINMKVSVCLPMDV 594  
QY 505 DSPLSQVLYMALLV-----LNVLAFFVYICGCTHYIYLVTRNPTVSSSDTKIAKMAT 558  
Db 595 ESTLSQVYTLISLIRATHCGLVNVAFVYICACIRYFAVONPELTAPNKDKTIAKMAI 654  
QY 559 LIPTDFLCHA-----PISFAISASLVPLTVSKAKILLVLPFPINSCANPFLYAITF 612  
Db 655 LIPTDFCMAHATCCPISFPAISASLVPLTVSKAKILLVLPFPINSCANPFLYAITF 714  
QY 613 KNPRED-----PILLSKRCGYEMQAIYRTSSNTHNFKSHGSS 656  
Db 715 KAFORDRATHCGFLLLSRFGCCCKRAELYRK-----EFSAYTSNCKN 758

RESULT 14  
US-07-741-453A-59  
: Sequence 59, Application US/07741453A  
: Patent No. 6228597  
: GENERAL INFORMATION:  
: APPLICANT: PARMENTIER, MARC  
: APPLICANT: LIBERT, FREDERIC  
: APPLICANT: DOMONT, JACQUES  
: APPLICANT: VASSART, GILBERT  
: TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
: ACTIVITY; NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
: TITLE OF INVENTION: POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES  
: NUMBER OF SEQUENCES: 62  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: CUSHMAN DABBY & CUSHMAN  
: STREET: 1615 L STREET, N.W.  
: CITY: WASHINGTON, D.C.  
: COUNTRY: U.S.A.  
: ZIP: 20036  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07741453A  
: FILING DATE: 19911015  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: KOKULIS, PAUL N.  
: REGISTRATION NUMBER: 16773  
: REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (202) 861-3000  
: TELEFAX: (202) 822-0944  
: TELEX: 6714627 CUSH  
: INFORMATION FOR SEQ ID NO: 59:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 764 amino acids  
: TYPE: AMINO ACID  
: TOPOLOGY: single  
: MOLECULE TYPE: protein  
US-07-741-453A-59

Query Match 46.7% Score 1641.5; DB 4; Length 764;  
Best Local Similarity 49.3%; Pred. No. 5.3e-125;  
Matches 336; Conservative 110; Mismatches 182; Indels 55; Gaps 11;  
QY 6 CHCSN-----RVFLQDSKVTEIPTDLPNNAELRVLTKLVRPKGSFAGDGLEKIEIS 61

Db 29 CCEHQBDFRV-TCKD--IQRPIS-LPPSTOTLALETHLRTIPSHAFSNLPNTRIYSVS 84  
QY 62 QNDVLEVDADVSNLPKLHEIRIEKANMLYIMPFAQNLPISLYLLISNTGKIKHLPAY 121  
Db 85 IDLTLOOLESUSFVNSKYTHIEINTRNLTITDPAKLELPDLAFLOFTGLKAMPDL 144  
QY 132 HKIOSLO-KVLLIDQINENIHVARNSPGLSPESVILWLSKNGIEETHHCAFCNGTOLDE 180  
Db 145 TVKSTDTDFIETIDNPMYTSIPVNAFOGLCNETLTLKLYNGFTSVQCYAFNCTKLOA 204  
QY 181 LNLSDNNIEELPNDVFOGA--SGPVILDIISRTKVHSLPHGLNKLKLRRSTYRLKLP 239  
Db 205 VYLNKNKYLTVIKDAFGGVYSGPSLDVSVTSALPSKGLKELKELIARNTMTLKLKLP 264  
QY 240 NLDKFVTLMEASLTYPSCCAFNKLRKROISELHPI-CNKSIL-----RQDIDDMT----- 288  
Db 265 LSLGFLHLTRADLSYPSHCCAFKNOKKIRGILESIMCNESSHOSLRKSVNALNSPLHQ 324  
QY 289, ----QIGDQVSLID-----NOK-----DEPSYCKGSDM-----NYNE 314  
Db 325 EYENLQDSIVGYKSKSFQDTHNANYVFFEDQEDILQGLKLNQOETLOAFDSH 384  
QY 315 FQYDLCEVVDVYVTCSPKPDAPNCCEDIMGYNLRVLINPILSILATNGTNTLVYLTSSY 374  
Db 385 XYDTICGDSDEMVCPTKSDENPCEDIMGYKFLRIYVWEVSLALLGNVFLVLLILTSY 444  
QY 375 KLTVPRLMCLAFADLIGIYLLLIASVDIHTKSOYHNYAIDMOTGAGCDAAGFTTFA 434  
Db 445 KLVNPRELMLCLAFADPCMGVYLLLIASVDLTHSEYVYHNAIDMOTGPGCMTAGFTTFA 504  
QY 435 SELSVYTLTATLERHHTITHAKOLECKVQLRHAASVWYVLTGMTFAFAAALPFIIGISYM 494  
Db 505 SELSVYTLTATLERHHTITHAKOLECKVQLRHAASVWYVLTGMTFAFAAALPFIIGISYM 564  
QY 495 KVSICLPMDSPLSOLYVALLVUNLVAPVYICGCTHYIYLVTRNPTVSSSDTKIAK 554  
Db 565 KVSICLPMDSPLSOLYVALLVUNLVAPVYICGCTHYIYLVTRNPTVSSSDTKIAK 624  
QY 555 RNATLFTDPLCHAPISFAISAKVPLTVSKAKILLVLPFPINSCANPFLYAITKN 614  
Db 625 RNATLFTDPLCHAPISFAISAKVPLTVSKAKILLVLPFPINSCANPFLYAITKN 684  
QY 615 FRDPEFLLSKFCGYEMQAIYR 637  
Db 685 FORDVFTLLSKFCGYEMQAIYR 707

RESULT 15  
US-07-757-342D-5  
: Sequence 5, Application US/07757342D  
: Patent No. 6228597  
: GENERAL INFORMATION:  
: APPLICANT: ICARASHI, MASAO  
: APPLICANT: MINEGISHI, TAKASHI  
: APPLICANT: NAKAMURA, KAZUO  
: TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
: NUMBER OF SEQUENCES: 10  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
: CUSHMAN  
: STREET: 130 Water Street  
: CITY: Boston  
: STATE: Massachusetts  
: COUNTRY: US  
: ZIP: 02109  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07757342D



Job time : 23.2326 secs

```

;
; FILING DATE: 10-Sep-1991
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BUCKLEY, Linda M.
; REGISTRATION NUMBER: 31003
; REFERENCE/DOCKET NUMBER: 41226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
;
; INFORMATION FOR SEQ ID NO: 5:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 764 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-07-757-342D-5

Query Match      46.7%  Score 1640.5;  DB 4;  Length 764;
Best Local Similarity 49.2%  Pred. No. 6.4e-125;
Matches 336;  Conservative 110;  Mismatches 182;  Indels 55;  Gaps 11;

QY 6 CHCSN-----RVFLCDSKVTEIPTDLP RNAIELRVLT KLRV PKGSFAGFDLEKIEIS 61
Db  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
29 CECHOEDFRV--TKND--IQRI PS--LPPSTOTLKLIETHRLTIPSHAFSNLPNISRIYVS 84
QY 62 QNDVLEIVLEADVSNLPKLHEIRIEKANNLLYINPEAFQNLPSLRYLLISNTGIKHLPAY 121
Db  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
85 IDVTLQQLSHSFYNSLVKTHIEIRNTRNLTYIDPDALKELPLFLKLGIFNTGLKMFDDL 144
QY 122 HKIQSLQ--KVLIDIQDNIINIHVARNSPMGLSFSEVILWLSKNGTEETHNCAFNCTOLDE 180
Db  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
145 TKVYSTDIFILEITDNPYMTSIPVNAFGCLNEFTLKLNNNGFTSVQGYAFNGTKLDA 204
QY 181 LNLSDNNLEELPNDVFOGA--SGPVLDISRTKVHSLPNHGLENLKLRARSTYRLKKLP 239
Db  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
205 VYLNKNKYLTVIYDAFGVSGPSLDDVSOTSVTALPSKGLHKLKELIARNTWTLLKLP 264
QY 240 NLDKFTVLEASLTYPSCCAFANLKROISELHPI--CNKSL-----RQDIDDMT----- 288
Db  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
265 LSLSELHLTRADLSYPSHCCAFKNOKKIRGILESLMCNESSMQSLRQRKSVNALNSPLHQ 324
QY 289 ----QIGDQVSLID-----DEPSYKGKSDM-----MYNE 314
Db  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
325 EYEENLGDYSIVGYKEKSKFQDTHNNAHYVVFEEQDEIIGGQELKNPQETLQAFDSH 384
QY 315 FDYDLCLNEVDVTCSPKPDAPNCPEDIMGYNILRVLIWFISILATGNTTVLVLTTTQY 374
Db  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
385 YDYTCGDSSEDMVCTPKSDEFPNCPEDIMGYKFLRVVWVFSLLALLGNVFLVLLILLTSY 444
QY 375 KLTVPRELMCNLAFADLCIGIYVLLIASVDIHTKSOYHNYAIDMOTGAGCDAAGFTTVA 434
Db  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
445 KLVPRFLMCNLAFADFCMGMYLLIASVDLYTHSEYINHAIDMOTGPGCNTAGFTTVA 504
QY 435 SELSVYTLTATLERWHTITHAMQLECKVQLRHAASVMVLTWTFATAALPPIFGISSYM 494
Db  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
505 SELSVYTLTVITLERWYAITFAMRLDRKMRLEHACAIWVGWCCFLALLPLVGISSYA 564
QY 495 KVSICLPMDISPLSOLYVMALLVNLVAFVVICGYTHIYLTVRNPTIVSSSDTKIAK 554
Db  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
565 KVSICLPMDTETPLALIVFVLTNLNIVAFVIVCCYVKIYITVRNPQYNPGDKDKIAK 624
QY 555 RMATLIFTDFLCMAISFAISASLKVPLITVSKAKILLVLYFPINSCANPFLYAIPTKN 614
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625 RMALVIFTDFICMAISFALSAILNKPLITVSNKILLVLYFPLNSCANPFLYAIPTKE 684
QY 615 FRDFFILLSKFCGYEMOQAIYR 637
Db  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
685 FORDVFIILLKFCICKRQQAQR 707
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Search completed: June 16, 2003, 13:37:58

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2003, 13:36:01 : Search time 165.911 Seconds  
(without alignments)  
434.981 Million cell updates/sec

Title: US-09-877-804-7

Perfect score: 3516

Sequence: 1 CHHCHCSNRVFLCQSKV.....SAPRTNIVLPLNHSN 675

Scoring table: BLOSUM62

Gapop 10.0, Capet 0.5

Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:  
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2: /cgn2\_6/ptodata/2/pubpa/US08\_NEW\_PUB pep.\*  
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13: /cgn2\_6/ptodata/2/pubpa/US60\_NEW\_PUB pep.\*  
14: /cgn2\_6/ptodata/2/pubpa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3516	100.0	675	10	US-09-877-804-7 Sequence 7, Appl 1
2	3516	100.0	692	9	US-09-965-536A-11 Sequence 11, Appl 1
3	3516	100.0	692	10	US-09-877-804-6 Sequence 6, Appl 1
4	3482	99.0	688	9	US-09-965-536A-12 Sequence 12, Appl 1
5	3149.5	89.6	695	10	US-09-804-626-8 Sequence 8, Appl 1
6	3010.5	85.6	687	9	US-09-965-536A-13 Sequence 13, Appl 1
7	2577.5	73.3	693	9	US-09-965-536A-14 Sequence 14, Appl 1
8	2103.5	59.9	358	10	US-09-862-767A-9 Sequence 9, Appl 1
9	1997	52.1	676	10	US-09-877-804-8 Sequence 8, Appl 1
10	1797	51.1	700	10	US-09-877-804-2 Sequence 2, Appl 1
11	1797	50.7	676	9	US-09-804-626-15 Sequence 15, Appl 1
12	1783.5	50.7	699	10	US-09-965-536A-2 Sequence 6, Appl 1
13	1638.5	46.6	764	9	US-10-045-624B-2 Sequence 2, Appl 1
14	1505.5	42.8	516	10	US-09-804-626-4 Sequence 4, Appl 1
15	1353	38.5	458	10	US-09-862-767A-5 Sequence 5, Appl 1
16	1191	33.9	359	10	US-09-862-767A-7 Sequence 7, Appl 1
17	910.5	23.1	861	10	US-09-804-551B-20 Sequence 20, Appl 1
18	810.5	23.1	861	10	US-09-804-551B-20 Sequence 4, Appl 1
19	675	19.2	341	10	US-09-877-804-4 Sequence 4, Appl 1

ALIGNMENTS

RESULT 1  
US-09-877-804-7  
; Sequence 7, Application US/09877804  
; GENERAL INFORMATION:  
; APPLICANT: Nikolova, Karoly  
; APPLICANT: McFarland, Keith C.  
; APPLICANT: Seghal, Deborah L.  
; APPLICANT: Sebburg, Peter H.  
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules  
; FILE REFERENCE: P0576P1C2  
; CURRENT APPLICATION NUMBER: US/09/877.804  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: US 08/207.814  
; PRIOR FILING DATE: 1994-03-07  
; PRIOR APPLICATION NUMBER: US 07/701.153  
; PRIOR FILING DATE: 1991-10-31  
; PRIOR APPLICATION NUMBER: US 07/347.683  
; PRIOR FILING DATE: 1989-05-05  
; NUMBER OF SEQ ID NOS: 22  
; SEQ ID NO 7  
; LENGTH: 675  
; TYPE: PPT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: deduced sequence  
US-09-877-804-7  
Query Match 100.0%; Score 3516; DB 10; Length 675;  
Best Local Similarity 100.0%; Pred. No. 1.4e-284;  
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHHCHCSNRVFLCQSKVTEPTDLPNATLRLPVLTNLRVTPKGSFAGFGLKIEI 60  
Db 1 CHHCHCSNRVFLCQSKVTEPTDLPNATLRLPVLTNLRVTPKGSFAGFGLKIEI 60  
Qy 61 SONDYLEVLEADVFNSLKLHETRIEYKANNLLYNPFAONLPSLYLLISMTGKILPA 120  
Db 61 SONDYLEVLEADVFNSLKLHETRIEYKANNLLYNPFAONLPSLYLLISMTGKILPA 120  
Qy 121 VHKIQSLQKVLDTQNTINIRIVARNSPGLSFESVILWLSKNGIEEIHNCAPNCTQLOB 180  
Db 121 VHKIQSLQKVLDTQNTINIRIVARNSPGLSFESVILWLSKNGIEEIHNCAPNCTQLOB 180

Sequence 2, Appl 1  
Sequence 16, Appl 1  
Sequence 26, Appl 1  
Sequence 278, Appl 1  
Sequence 2, Appl 1  
Sequence 10, Appl 1  
Sequence 3, Appl 1  
Sequence 5, Appl 1  
Sequence 90, Appl 1  
Sequence 7, Appl 1  
Sequence 6, Appl 1  
Sequence 2, Appl 1  
Sequence 24, Appl 1  
Sequence 21, Appl 1  
Sequence 20, Appl 1  
Sequence 3, Appl 1  
Sequence 6, Appl 1  
Sequence 1, Appl 1  
Sequence 1, Appl 1  
Sequence 2, Appl 1  
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Sequence 8, Appl 1  
Sequence 7, Appl 1  
Sequence 8, Appl 1  
Sequence 4, Appl 1

Db 121 VHKIOSLQKVLDDIODNINIHIVARNFPMGLSFESVILWLSKNGIEEIHNCFAFNGTQOLDE 180  
QY 181 LNLSDNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKKLPN 240  
Db 181 LNLSDNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKKLPN 240  
QY 241 LKFTVLMASLTYSHCACAFANLKRQISELHPICNKSILRQIDIDMTQIGDQVSLIDD 300  
Db 241 LKFTVLMASLTYSHCACAFANLKRQISELHPICNKSILRQIDIDMTQIGDQVSLIDD 300  
QY 301 EPSYKGSMDMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMGYNLRVLIWIFISILAIT 360  
Db 301 EPSYKGSMDMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMGYNLRVLIWIFISILAIT 360  
QY 361 GNTTVLVLTTSQYKLTVPFLMCNLAFAADLCIGIYLLLIASVDIHTKSOYHNYAIDWQT 420  
Db 361 GNTTVLVLTTSQYKLTVPFLMCNLAFAADLCIGIYLLLIASVDIHTKSOYHNYAIDWQT 420  
QY 421 GAGCDAAGFTFVASELSVYTLTAITLERWHTITHAMQLECKVOLRHAASVMVLGWTFAF 480  
Db 421 GAGCDAAGFTFVASELSVYTLTAITLERWHTITHAMQLECKVOLRHAASVMVLGWTFAF 480  
QY 481 AAALPFIPIGSISSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCTHYIYLTVRN 540  
Db 481 AAALPFIPIGSISSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCTHYIYLTVRN 540  
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Db 541 PTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVPLITVSKAKILLVLFYPI 600  
QY 601 SCANPELYAIFTKFNRRDFFILLSKFCYEMQAOIYRTETSSATHNFHARKSHCSSAPRV 660  
Db 601 SCANPELYAIFTKFNRRDFFILLSKFCYEMQAOIYRTETSSATHNFHARKSHCSSAPRV 660  
QY 661 TNSYVLVPLNHSSQN 675  
Db 661 TNSYVLVPLNHSSQN 675

RESULT 2  
US-09-965-536A-11  
; Sequence 11, Application US/09965536A  
; Publication No. US20030027323A1  
; GENERAL INFORMATION:  
; APPLICANT: FEDER, J. N.  
; APPLICANT: MINTIER, G.  
; APPLICANT: RAMANATHAN, C. S.  
; APPLICANT: HAWKEN, D. R.  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV5,  
; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES  
; FILE REFERENCE: D0041NP  
; CURRENT APPLICATION NUMBER: US/09/965,536A  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/235,713  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/261,781  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/306,605  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/310,436  
; PRIOR FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 692  
; TYPE: PRT  
; ORGANISM: RAT  
US-09-965-536A-11

Query Match 100.0%; Score 3516; DB 9; Length 692;  
Best Local Similarity 100.0%; Pred. No. 1.4e-284;  
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHMLCHCSNRVFLCODSKVTEIPTDLPRNATELRFVLTKLRIYIPKGSFAGDLEKIEI 60  
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QY 61 SONDVLEVEADVFNLPKLHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGIKHLPA 120  
Db 78 SONDVLEVEADVFNLPKLHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGIKHLPA 137  
QY 121 VHKIOSLQKVLDDIODNINIHIVARNFPMGLSFESVILWLSKNGIEEIHNCFAFNGTQOLDE 180  
Db 138 VHKIOSLQKVLDDIODNINIHIVARNFPMGLSFESVILWLSKNGIEEIHNCFAFNGTQOLDE 197  
QY 181 LNLSDNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKKLPN 240  
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Db 258 LKFTVLMASLTYSHCACAFANLKRQISELHPICNKSILRQIDIDMTQIGDQVSLIDD 317  
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Db 318 EPSYKGSMDMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMGYNLRVLIWIFISILAIT 377  
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Db 378 GNTTVLVLTTSQYKLTVPFLMCNLAFAADLCIGIYLLLIASVDIHTKSOYHNYAIDWQT 437  
QY 421 GAGCDAAGFTFVASELSVYTLTAITLERWHTITHAMQLECKVOLRHAASVMVLGWTFAF 480  
Db 438 GAGCDAAGFTFVASELSVYTLTAITLERWHTITHAMQLECKVOLRHAASVMVLGWTFAF 497  
QY 481 AAALPFIPIGSISSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCTHYIYLTVRN 540  
Db 498 AAALPFIPIGSISSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCTHYIYLTVRN 557  
QY 541 PTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVPLITVSKAKILLVLFYPI 600  
Db 558 PTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVPLITVSKAKILLVLFYPI 617  
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Db 618 SCANPELYAIFTKFNRRDFFILLSKFCYEMQAOIYRTETSSATHNFHARKSHCSSAPRV 677  
QY 661 TNSYVLVPLNHSSQN 675  
Db 678 TNSYVLVPLNHSSQN 692

RESULT 3  
US-09-877-804-6  
; Sequence 6, Application US/09877804  
; Patent No. US20020061557A1  
; GENERAL INFORMATION:  
; APPLICANT: Nikolics, Karoly  
; APPLICANT: McFarland, Keith C.  
; APPLICANT: Segalo, Deborah L.  
; APPLICANT: Seeburg, Peter H.  
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules  
; FILE REFERENCE: P0576PIC2  
; CURRENT APPLICATION NUMBER: US/09/877,804  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: US 08/207,814  
; PRIOR FILING DATE: 1994-03-07  
; PRIOR APPLICATION NUMBER: US 07/781,153  
; PRIOR FILING DATE: 1991-10-31  
; PRIOR APPLICATION NUMBER: US 07/347,683  
; PRIOR FILING DATE: 1989-05-05  
; NUMBER OF SEQ ID NOS: 22  
; SEQ ID NO 6  
; LENGTH: 692  
; TYPE: PRT  
; ORGANISM: Artificial sequence

FEATURE:  
OTHER INFORMATION: deduced sequence  
US-09-877-804-6

Query Match 100.0%; Score 3516; DB 10; Length 692;  
Best Local Similarity 100.0%; Pred. No. 1.4e-284;  
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CHHMLCHSNNVFLQDSKVTEIPTDLPNNAIELRVLTAKRVIPKGSFAGFQDLEKIEI 60  
DB 18 CHHMLCHSNNVFLQDSKVTEIPTDLPNNAIELRVLTAKRVIPKGSFAGFQDLEKIEI 77  
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DB 78 SONDLVLEADVSNLPLKHEIRIEKANNLLYINPEAFONPLSLRYLLISNTGKHLPA 137  
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DB 198 LNLSDNNLLELPNDVFOGASGPVILDSRTKVVHSLPNHGLENLKLRARSTYRLKLLPN 257  
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DB 258 LOKFVTLMEASLTPSHCCAFANKRKQISELHPICNKSILROQIDDMTQIGDORVSLIDD 317  
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DB 318 EPSYSGSDMMYNEFDYDLCEVNDVTCSPKPDAPNCPEDIMGYNILRVLIWFISILAIT 377  
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DB 378 GNTTVLVLTTSQYKLTVPRLMKNLAFADLCIGIYLLLIASVDIHTKSOYHNTADMT 437  
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DB 498 AAALFFPICISSTMYKVSICLPMIDSPLSQLYNALLVNLVAFVYICGCTHYIYLVYRN 557  
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DB 618 SCANPFLTAIFTNFRDFFILLSKFCQYEMQAIYRTETSSATHNFARKSHCSSAPRV 677  
OY 661 TNSYVLVPLNHSN 675  
DB 678 TNSYVLVPLNHSN 692

RESULT 4  
US-09-965-536A-12  
Sequence 12; Application US/09965536A  
Patent No. US2003002733A1  
GENERAL INFORMATION  
APPLICANT: FREDERICK J. N.  
APPLICANT: KIMTIER, G.  
APPLICANT: RAMANATHAN, C. S.  
APPLICANT: HAWKEN, D. R.  
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBWY5,  
FILE REFERENCE: DOQ41NP  
CURRENT APPLICATION NUMBER: US/09/965.536A  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/235.713  
PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/261.781  
PRIOR FILING DATE: 2001-01-16  
PUBLICATION NUMBER: 09/306.605  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/310.436  
PRIOR FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 688  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-965-536A-12

Query Match 99.0%; Score 3482; DB 9; Length 688;  
Best Local Similarity 99.3%; Pred. No. 9.7e-282;  
Matches 670; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

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DB 18 CHHMLCHSNNVFLQDSKVTEIPTDLPNNAIELRVLTAKRVIPKGSFAGFQDLEKIEI 77  
OY 61 SONDLVLEADVSNLPLKHEIRIEKANNLLYINPEAFONPLSLRYLLISNTGKHLPA 120  
DB 78 SONDLVLEADVSNLPLKHEIRIEKANNLLYINPEAFONPLSLRYLLISNTGKHLPA 137  
OY 121 VHKIOSLOKVLDDIODNINIHIVARNSPFGLSFEVILMLSKNGIEEIHNCAPFNGTOLDE 180  
DB 138 VHKIOSLOKVLDDIODNINIHIVARNSPFGLSFEVILMLSKNGIEEIHNCAPFNGTOLDE 193  
OY 181 LNLSDNNLLELPNDVFOGASGPVILDSRTKVVHSLPNHGLENLKLRARSTYRLKLLPN 240  
DB 194 LNLSDNNLLELPNDVFOGASGPVILDSRTKVVHSLPNHGLENLKLRARSTYRLKLLPN 253  
OY 241 LOKFVTLMEASLTPSHCCAFANKRKQISELHPICNKSILROQIDDMTQIGDORVSLIDD 300  
DB 254 LOKFVTLMEASLTPSHCCAFANKRKQISELHPICNKSILROQIDDMTQIGDORVSLIDD 313  
OY 301 EPSYSGSDMMYNEFDYDLCEVNDVTCSPKPDAPNCPEDIMGYNILRVLIWFISILAIT 360  
DB 314 EPSYSGSDMMYNEFDYDLCEVNDVTCSPKPDAPNCPEDIMGYNILRVLIWFISILAIT 373  
OY 361 GNTTVLVLTTSQYKLTVPRLMKNLAFADLCIGIYLLLIASVDIHTKSOYHNTADMT 420  
DB 374 GNTTVLVLTTSQYKLTVPRLMKNLAFADLCIGIYLLLIASVDIHTKSOYHNTADMT 433  
OY 421 GAGCDAAGFFTFVASELSVYTLTATILERMHTITHAMOLECKVQLRHAASVNLGWTAF 480  
DB 434 GAGCDAAGFFTFVASELSVYTLTATILERMHTITHAMOLECKVQLRHAASVNLGWTAF 493  
OY 481 AAALFFPICISSTMYKVSICLPMIDSPLSQLYNALLVNLVAFVYICGCTHYIYLVYRN 540  
DB 494 AAALFFPICISSTMYKVSICLPMIDSPLSQLYNALLVNLVAFVYICGCTHYIYLVYRN 553  
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DB 554 PTIVSSSDTKIAKRMATLIFTDFLCMAPISFAISASLKVPLITVSKAKILLVLYFPIN 613  
OY 601 SCANPFLTAIFTNFRDFFILLSKFCQYEMQAIYRTETSSATHNFARKSHCSSAPRV 660  
DB 614 SCANPFLTAIFTNFRDFFILLSKFCQYEMQAIYRTETSSATHNFARKSHCSSAPRV 673  
OY 661 TNSYVLVPLNHSN 675  
DB 674 TNSYVLVPLNHSN 688

RESULT 5  
US-09-804-626-8  
Sequence 8; Application US/09804626  
Patent No. US20020128190A1  
GENERAL INFORMATION  
APPLICANT: Lobel, Leslie

```
; APPLICANT: Lustbader, Joyce
; TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF
; TITLE OF INVENTION: GONADOTROPIN RECEPTOR
; FILE REFERENCE: 0575/62259/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/804,626
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-804-626-8

Query Match      89.6%; Score 3149.5; DB 10; Length 695;
Best Local Similarity 88.9%; Pred. No. 5.1e-254;
Matches 603; Conservative 33; Mismatches 39; Indels 3; Gaps 2;

QY 1 CHHWLCHCSNRVFLCQDSKVTEPTDLPNNAELRVLTGLRVIPKGSFAGFDLEKIEI 60
DB 18 CHHCHCHCSNRVFLCQDSKVTEPTDLPNNAELRVLTGLRVIPKGSFAGFDLEKIEI 77
QY 61 SONDVLEIADVFSLPKLHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 120
DB 78 SONDVLEIADVFSLPKLHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 137
QY 121 VHKIQLQVLLDIQDNIHIVARNFSGLSFESVILWLSKNGIEEIHNCFAFNGTOLDE 180
DB 138 VHKIQLQVLLDIQDNIHIVARNFSGLSFESVILWLSKNGIEEIHNCFAFNGTOLDE 197
QY 181 LNSDNNLEELPNDVFGASGVILDISRTKLVHSLPNHGLENLKLRARSTYRLKLPN 240
DB 198 VNSDNNLEELPNDVFGASGVILDISRTKLVHSLPNHGLENLKLRARSTYRLKLPN 257
QY 241 LDFEVLMEASLYPSHCCAFANLKRQISELHPICNKSILRQDIDDMTOIGDORVSLDD 300
DB 258 LKLVALMEASLYPSHCCAFANLKRQISELHPICNKSILRQEVDMYMTQARGQSSLAED 317
QY 301 -EPSYKSGSDMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLIWFISILAI 359
DB 318 NESSYRGFDMYTFEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLIWFISILAI 377
QY 360 TGNTVLVLTTSQYKLVTPREFLMCNLAFADLCIGIYLLIASVDIHTKSOYHNYAIDWQ 419
DB 378 TGMIVLVLTTSQYKLVTPREFLMCNLAFADLCIGIYLLIASVDIHTKSOYHNYAIDWQ 437
QY 420 TGACDAAGFTTFVASELSVYTLTAITLERWHTITHAMOLECKVOLRHAASVMVLGWTFA 479
DB 438 TGACDAAGFTTFVASELSVYTLTAITLERWHTITHAMOLECKVOLRHAASVMVLGWTFA 497
QY 480 FAALFPFGISSYMKVSIKLPMDIDSPLSQLYMALLVNLVAFVVICGCIYTHIYTVR 539
DB 498 FAALFPFGISSYMKVSIKLPMDIDSPLSQLYMALLVNLVAFVVICGCIYTHIYTVR 557
QY 540 NPTIVSSSDTKIAKRMATLIETDFLCMAPISFFAISASLKVPLITVSKAKILLVFPYI 599
DB 558 NPTIVSSSDTKIAKRMATLIETDFLCMAPISFFAISASLKVPLITVSKAKILLVFPYI 617
QY 600 NSCANPFLYAIETKNFRDRDFILLSKFCGYEMQAQIYRTETSSATHNPHARKSHCSSAPR 659
DB 618 NSCANPFLYAIETKNFRDRDFILLSKFCGYEMQAQIYRTETSSATHNPHARKSHCSSAPR 677
QY 660 VT--NSYVLPVPLNHSSQN 675
DB 678 VTSGSTYILVPLSLHAQN 695

RESULT 6
US-09-965-536A-13
; Sequence 13, Application US/09965536A
; Publication No. US20030027323A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
```

```
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D. R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV5,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
; FILE REFERENCE: D0041NP
; CURRENT APPLICATION NUMBER: US/09/965,36A
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,781
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/306,605
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/310,436
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Equus asinus
US-09-965-536A-13

Query Match      85.6%; Score 3010.5; DB 9; Length 687;
Best Local Similarity 86.0%; Pred. No. 1.9e-242;
Matches 582; Conservative 38; Mismatches 48; Indels 9; Gaps 3;

QY 1 CHHWLCHCSNRVFLCQDSKVTEPTDLPNNAELRVLTGLRVIPKGSFAGFDLEKIEI 60
DB 18 CHHCHCHCSNRVFLCQDSKVTEPTDLPNNAELRVLTGLRVIPKGSFAGFDLEKIEI 77
QY 61 SONDVLEIADVFSLPKLHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 120
DB 78 SONDVLEIADVFSLPKLHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 137
QY 121 VHKIQLQVLLDIQDNIHIVARNFSGLSFESVILWLSKNGIEEIHNCFAFNGTOLDE 180
DB 138 VHKIQLQVLLDIQDNIHIVARNFSGLSFESVILWLSKNGIEEIHNCFAFNGTOLDE 197
QY 181 LNSDNNLEELPNDVFGASGVILDISRTKLVHSLPNHGLENLKLRARSTYRLKLPN 240
DB 198 LNSDNNLEELPNDVFGASGVILDISRTKLVHSLPNHGLENLKLRARSTYRLKLPN 257
QY 241 LDFEVLMEASLYPSHCCAFANLKRQISELHPICNKSILRQDIDDMTOIGDORVSLDD 300
DB 258 LKLVALMEASLYPSHCCAFANLKRQISELHPICNKSILRQEVDMYMTQARGQSSLAED 316
QY 301 -EPSYKSGSDMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLIWFISILAI 360
DB 317 DES-----HWSEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLIWFISILAI 370
QY 361 GNTTVLVLTTSQYKLVTPREFLMCNLAFADLCIGIYLLIASVDIHTKSOYHNYAIDWQ 420
DB 371 GNTTVLVLTTSQYKLVTPREFLMCNLAFADLCIGIYLLIASVDIHTKSOYHNYAIDWQ 430
QY 421 GAGCDAAGFTTFVASELSVYTLTAITLERWHTITHAMOLECKVOLRHAASVMVLGWTFA 480
DB 431 GAGCDAAGFTTFVASELSVYTLTAITLERWHTITHAMOLECKVOLRHAASVMVLGWTFA 490
QY 481 AAALFPFGISSYMKVSIKLPMDIDSPLSQLYMALLVNLVAFVVICGCIYTHIYTVR 540
DB 491 GVGLLPFGISTYMKVSIKLPMDIDSPLSQLYMALLVNLVAFVVICGCIYTHIYTVR 550
QY 541 PTVSSSSDTKIAKRMATLIETDFLCMAPISFFAISASLKVPLITVSKAKILLVFPYI 600
DB 551 PTVSSSSDTKIAKRMATLIETDFLCMAPISFFAISASLKVPLITVSKAKILLVFPYI 610
QY 601 SCANPFLYAIETKNFRDRDFILLSKFCGYEMQAQIYRTETSSATHNPHARKSHCSSAPR 660
DB 611 SCANPFLYAIETKNFRDRDFILLSKFCGYEMQAQIYRTETSSATHNPHARKSHCSSAPR 670
QY 661 TN--SYVLVPLNHSSQN 675
```



## RESULT 9

US-09-877-804-8  
; Sequence 8, Application US/09877804  
; Patent No. US20020061557A1  
; GENERAL INFORMATION:  
; APPLICANT: Nikolics, Karoly  
; APPLICANT: McFarland, Keith C.  
; APPLICANT: Segalo, Deborah L.  
; APPLICANT: Seeburg, Peter H.  
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules  
; FILE REFERENCE: P0576PIC2  
; CURRENT APPLICATION NUMBER: US/09/877,804  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: US 08/207,814  
; PRIOR FILING DATE: 1994-03-07  
; PRIOR APPLICATION NUMBER: US 07/781,153  
; PRIOR FILING DATE: 1991-10-31  
; PRIOR APPLICATION NUMBER: US 07/347,683  
; PRIOR FILING DATE: 1989-05-05  
; NUMBER OF SEQ ID NOS: 22  
; SEQ ID NO 8  
; LENGTH: 348  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: deduced sequence  
US-09-877-804-8

Query Match 52.1%; Score 1832; DB 10; Length 348;  
Best Local Similarity 100.0%; Pred. No. 1.2e-144;  
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CHHWLCHSNRVFLQDSKVTEIPTDLPRNAIELRVLTGLKRVIPKGSFAGFDLEKTEI	60
DB	1	CHHWLCHSNRVFLQDSKVTEIPTDLPRNAIELRVLTGLKRVIPKGSFAGFDLEKTEI	60
QY	61	SONDVELEADVFNPLKHLRIEIKANNLLYINPEAFONLPSRLYLLISNTGKHLPA	120
DB	61	SONDVELEADVFNPLKHLRIEIKANNLLYINPEAFONLPSRLYLLISNTGKHLPA	120
QY	121	VHKIOSLQKVLDDIQDNIHIVARNFMSGLSFESVILWLSKNGIEEHNCAFNQTQD	180
DB	121	VHKIOSLQKVLDDIQDNIHIVARNFMSGLSFESVILWLSKNGIEEHNCAFNQTQD	180
QY	181	LNLSDNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLPN	240
DB	181	LNLSDNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLPN	240
QY	241	LDFKFTLMEASLTPSHCCAFANLAKQISELHPICNKSILRODIDMTQIGDQVSLIDD	300
DB	241	LDFKFTLMEASLTPSHCCAFANLAKQISELHPICNKSILRODIDMTQIGDQVSLIDD	300
QY	301	EPSYKSGSDMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNLR	348
DB	301	EPSYKSGSDMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNLR	348

## RESULT 10

US-09-877-804-3  
; Sequence 3, Application US/09877804  
; Patent No. US20020061557A1  
; GENERAL INFORMATION:  
; APPLICANT: Nikolics, Karoly  
; APPLICANT: McFarland, Keith C.  
; APPLICANT: Segalo, Deborah L.  
; APPLICANT: Seeburg, Peter H.  
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules  
; FILE REFERENCE: P0576PIC2  
; CURRENT APPLICATION NUMBER: US/09/877,804  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: US 08/207,814  
; PRIOR FILING DATE: 1994-03-07  
; PRIOR APPLICATION NUMBER: US 07/781,153

; PRIOR FILING DATE: 1991-10-31  
; PRIOR APPLICATION NUMBER: US 07/347,683  
; PRIOR FILING DATE: 1989-05-05  
; NUMBER OF SEQ ID NOS: 22  
; SEQ ID NO 3  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: deduced sequence  
US-09-877-804-3

Query Match 51.1%; Score 1797; DB 10; Length 674;  
Best Local Similarity 56.5%; Pred. No. 2.6e-141;  
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

QY	28	PRNAIELRVLTGL--RVIPKGSFAGFDLEKIEISONDVLEIVADYFVSNLPLKHLRI	85
DB	25	PRAGL-ARLSLYLPVKVIPSQAFGLNEVVKIEISQSDSLERIEANAFDNLNLSLI	83
QY	86	EKANLLYINPEAFONLPSRLYLLISNTGKHLPAVHKIQSLQ-KVLDDIQDNIHIVA	144
DB	84	QNTKNLLYIEGAFNLPRKLYSLCINTGIRLPDVTKISSSEFNFILLEICDNLHTTP	143
QY	145	RNSFMGLSFESVILWLSKNGIEEHNCAFNQDDELNLSDNNLEELPNDVFOGASGPV	204
DB	144	GNAFOGMNNEVTLKLYNGFEEVQSHAFNGTTLISLELKENIYLEKMHSGAFQATGPS	203
QY	205	ILDISRTKVHSLPNHGLENLKLRARSTYRLKLPNLDKLVTLMEASLTPSHCCAFANL	264
DB	204	ILDISRTKQALPSHGLESIOTPLIALSSYSLKLPSEKFTSLVATLTPSHCCAFANL	263
QY	265	KRQISELHPICNKSILRODIDMTQIGDQVSLIDDEPSYG---KGSOMMYNEFDYDLN	321
DB	264	PKK-----EQNFSEFSEFENFSKQCESTVRKADNETLYSAIFEENELSGWDYD	315
QY	322	EVDVTCSPKPDAPNCPEDIMGYNLRILVLPISILATGNTVTLVLTQYKLTVPFR	381
DB	316	PKT-LQCAPEPDAFPNCPEDIMGYAFRLVILINILINILAFGNLTVFLVLTQYKLTVP	374
QY	382	LMCNLAFADLCIGIYLLIASVDIHTKSOYHNVAIDMTQAGCDAAGFTVFASELSV	441
DB	375	LMCNLSFADFMCGLYLLIASVDSQTKOYVNHADMTQSGCGAAGFTVFASELSV	434
QY	442	LTAITLERWHITTHAMQLECKVQLRHAASVVLGWTFAFAAALFPIFGISSYMKYSICLP	501
DB	435	LTVITLERWHITTYAVQLDQKLRHRAIPIMLGGWLFSTLIATMPLVGLISNTYMKYSICLP	494
QY	502	MDIDSPLSOLYVMAVLLVNLVAFVVICGCTHYIYLTVRNPTIVSSSTQTKIAKRMATLIF	561
DB	495	MDVESTLSQVYLSILNLNVAVVVICACIYIRIYFAVQNPETAPNKTQIAKRMATLIF	554
QY	562	TDFLCMAPISEFAISASLKVPLITYSKAKILLVLEYPINSCANPELYAFTKFNFRDPI	621
DB	555	TDFTCMAPISEFAISAFKVPLITYVNSKILLVLPVNSCANPELYAFTKFNFRDPI	614
QY	622	LLSKFGCYEMAQIYRTTSSATHNFHARKSHCSS	656
DB	615	LLSREGCKRRAEALYRRK-----EFSAYTSNCKN	643

## RESULT 11

US-09-877-804-2  
; Sequence 2, Application US/09877804  
; Patent No. US20020061557A1  
; GENERAL INFORMATION:  
; APPLICANT: Nikolics, Karoly  
; APPLICANT: McFarland, Keith C.  
; APPLICANT: Segalo, Deborah L.  
; APPLICANT: Seeburg, Peter H.  
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules  
; FILE REFERENCE: P0576PIC2  
; CURRENT APPLICATION NUMBER: US/09/877,804

```

1  APPLICANT: HAWKEN, D. B.
2  TITLE OF INVENTION: A NOVEL HUMAN C-PROTEIN COUPLED RECEPTOR, HGRBMY5,
3  AND ITS USES
4  TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
5  FILE REFERENCE: DQOALNP
6  CURRENT APPLICATION NUMBER: US/09/965,536A
7  CURRENT FILING DATE: 2001-09-26
8  PRIOR APPLICATION NUMBER: 60/235,713
9  PRIOR FILING DATE: 2000-09-27
10 PRIOR APPLICATION NUMBER: 60/261,781
11 PRIOR FILING DATE: 2001-01-16
12 PRIOR APPLICATION NUMBER: 60/306,605
13 PRIOR FILING DATE: 2001-07-19
14 PRIOR APPLICATION NUMBER: 60/310,436
15 PRIOR APPLICATION NUMBER: 60/310,436
16 NUMBER OF CLAIMS: 61
17 NUMBER OF SEQ. IDS NOS: 61
18 SOFTWARE: PatentIn Ver. 2.1
19 SEQ. ID NO 15
20 LENGTH: 676
21 TYPE: PRT
22 ORGANISM: Callithrix jacchus
23 US-09-965-536A-15

```

[illegible][illegible]



```
; Sequence 6, Application US/09804626
; Patent No. US20020128190A1
; GENERAL INFORMATION:
; APPLICANT: Lustbader, Joyce
; TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF
; FILE REFERENCE: CONADOTROPIN RECEPTOR
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-804-626-6

Query Match      50.5%   Score 1776; DB 10; Length 699;
Best Local Similarity 55.4%   Pred. No. 1.5e-139;
Matches 349; Conservative 108; Mismatches 147; Indels 26; Gaps 6;

QY 38 LTKL-----RVTPKPSFAGDLEKIEISQNDVLEIADVFNLPKHEIRIEKANN 90
Db 51 LTRLSLAYLPVKVTPSQAFRLNEVIRKIEISQIDSLERIEANAPDNLNLSEILQNTKN 110
QY 91 LLYINPEAFONLPSRLYLLISNTGKIKHLPVHKI-QSLQKVLDDIODNINIHIVARNSPM 149
Db 111 LRYEPGAFNLPLKALYSICNTGIRKFPDVTVPFSSSENFIEICDNLHTTIPGNAFQ 170
QY 150 GLSFESVILMSKNGIEEIHNCAPNGTQDLDELNLSDNNLELPNDVFOGASGVILDIS 209
Db 171 GMMNESVTLYKNGFEVQSHAFNGTTLTSLLEKENVHLEKMHNGAFRATGPKTLDIS 230
QY 210 RTVHSLPNGLNLEKLLKRLARSTYRLKLLPNLDFVTLMEASLTYPSSHCCAFANLKRQIS 269
Db 231 STKLOALPSGLSIEQRIALITSSYSLKPLSPRETFVNLEATLTPSHCCAFANL----- 285
QY 270 ELHPICKNSILRODIDMTQIGDQVSLIDDEPSYGR--GSDMYNEFDYDLCNEVDV 326
Db 286 ---PTKQNFSSHISENFQCESTVRKVNKNTLYSSMLAESELSGWDYEGFCLPKTP- 341
QY 327 TCSKPDAPNCPEDIMGYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPFLMCNL 386
Db 342 RCAPEPDAPNCPEDIMGYDFLRVLILNLILAILNGNTVLFVLTTSYKLTVPFLMCNL 401
QY 387 AFADLCIGIYLLIASVDIHTKSOYHNAIDMTQAGCDAAGFTVPFASLSVYTLTAT 446
Db 402 SFADFGLYLLIASVDSQTKGYHNAIDMTQAGCDAAGFTVPFASLSVYTLTAT 461
QY 447 LERWHTTTHAMQLECKVOLRAHSAVMVGLWTFEFAAALFPFGISSTYKYSICLPMDDIS 506
Db 462 LERWHTTTHAIHLDQKRLRHAILMLGGWLFSSLIAMFLVGVNSNFKVSCICPMDDVET 521
QY 507 PLSQLYMALVNLVAFVVCICGYTHIYLTNRPTIVSSSDTKAKRMATLIFTDFLC 566
Db 522 TLSQVYTLTILNLVFAFFIACYIKIYFAVRNPMLMATNKDTKIAKMAILIFTDFTC 581
QY 567 MAPISFPAISAKVPLITVSKAKILLVLYPPINSCANPFLYALFTKFRDRDFILLSKF 626
Db 582 MAPISFPAISAAKVPPLITVNSKVLVLYPPINSCANPFLYALFTKFRDRDFILLSKF 641
QY 627 GCYEMOQAIYRTETSSATHNPHARKSHCSS 656
Db 642 GCCKERRAELYRK-----DFSAYTSNCKN 665

RESULT 14
US-10-045-624B-2
; Sequence 2, Application US/10045624B
; Publication No. US20030009778A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.

; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING THYROID
; TITLE OF INVENTION: STIMULATING HORMONE RECEPTOR (TSH-R) GENE DISRUPTIONS
; FILE REFERENCE: R-666
; CURRENT APPLICATION NUMBER: US/10/045.624B
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 10/045.624
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-045-624B-2

Query Match      46.6%   Score 1638.5; DB 9; Length 764;
Best Local Similarity 49.2%   Pred. No. 4.9e-128;
Matches 337; Conservative 105; Mismatches 184; Indels 59; Gaps 10;

QY 6 CHCNRVFLCDSKVT-----EIPDLPRAIEIRFVTLKRVIPKSGFAGDLEKTEI 60
Db 29 CECHQE-----DDEFVCTCKELHRIPS-LPPSTQTLKLIETHLKTIPSLAFSSLPNISRYL 83
QY 61 SONDVLEIADVFNLPKHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKIKHLP 120
Db 84 SIDATLQRLPHEPSYNSLKMTHIEIRNTRSLTYIDPDALTLPKLFGLIFNTGLRFPD 143
QY 121 VHKIQSLQ-KVLLDIQDNINIHIVARNSPMGLSPESVILMSKNGIEEIHNCAPNGTQD 179
Db 144 LTKIYSTDIFILEITDNPYMTSVPEAFQGLCNETLTKLYNNGFTSVQGHANGTKLD 203
QY 180 ELNLSODNNLEELPNDVFOGA-SGPVILDISRTKVSHPNHLNGLNKLKRLARSTYRLK 238
Db 204 AVYLNKKYLTATIDNDAFGVYSGPTLLDVSSTVATLPSKGLSHLAKELIAKDTWTLLKL 263
QY 239 PNLDKFVTLMEASLTYPSSHCCAFANLKRQISELHPI-CNKSILR----- 281
Db 264 PLSLSFLHLTRADLUSYSHCCAFANQKIRGILESMLCNESIRNLKORKSVNLRGPY 323
QY 282 ----QDIDDMTQIGDQVSLIDDEPS-----YKGSOM-----MY 312
Db 324 QEVEEDPGD-NSVGKQNSKQFQSPSNHYVVFEEQEDVVGQELKNPQETLQAF 382
QY 313 NEDYDLCNEVDVTCSPKPDAPNCPEDIMGYNILRVLIWFISILAITGNTTVLVLTTS 372
Db 383 SHYDYTCVGDNEQDVCTPKSDEFNCPEDIMGYRFLVWVFWVSLALLGNIFVLLILTS 442
QY 373 QYKLTVPFLMCNLAFADLCIGIYLLIASVDIHTKSOYHNAIDMTQAGCDAAGFTV 432
Db 443 HYKLTVPFLMCNLAFADFCGVYLLIASVDLTHSEYHNAIDMTQAGCDAAGFTV 502
QY 433 FASELSVYTLTATITLERWHTTTHAMQLECKVOLRAHSAVMVGLWTFEFAAALFPFGISS 492
Db 503 FASELSVYTLTITLERWHTTTHAMQLECKVOLRAHSAVMVGLWTFEFAAALFPFGISS 562
QY 493 YMKVSIKCLPMDDISPLSQLYMALVNLVAFVVCICGYTHIYLTNRPTIVSSSDTKI 552
Db 563 YAKVSIKCLPMDDITDPLALAYIVLVLLNVAFVVCICGYTHIYLTNRPTIVSSSDTKI 622
QY 553 AKRMATLIFTDFLCMAPISFPAISAKILLVLYPPINSCANPFLYALFT 612
Db 623 AKRMATLIFTDFLCMAPISFPAISAKILLVLYPPINSCANPFLYALFT 682
QY 613 KNFRDRDFILLSKFGCYEMOQAIYR 637
Db 683 KAFORDVFIILLSKFGICKRQAOAYQ 707

RESULT 15
US-09-804-626-4
; Sequence 4, Application US/09804626
; Patent No. US20020128190A1
; GENERAL INFORMATION:
```

APPLICANT: Lohel, Leslie  
APPLICANT: Luthader, Joyce  
TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF  
FILE REFERENCE: 0575/62259/JPM/SHS  
CURRENT APPLICATION NUMBER: US/09/804,626  
CURRENT FILING DATE: 2001-03-09  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 4  
LENGTH: 516  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-09-804-626-4

Query Match 42.8%; Score 1505.5; DB 10; Length 516;  
Best Local Similarity 85.5%; Pred No 3.5e-17;  
Matches 289; Conservative 22; Mismatches 26; Indels 1; Gaps 1;

Oy 11 RVFLQDSKVTETPTDLPRNAIELRFLVTLKRVIPKSGFAGFGDLEKTEISONDVLEIE 70  
Db 168 RVFLQDSKVTETPTDLPRNAIELRFLVTLKRVIPKSGFAGFGDLEKTEISONDVLEIE 227  
Oy 71 ADVFENLPKLHEIRIEKANNLLYINPEAFONLPRLYLLISNTGKHLPAVHKIQSLQKV 130  
Db 228 ADVFENLPKLHEIRIEKANNLLYINPEAFONLPRLYLLISNTGKHLPAVHKIQSLQKV 287  
Oy 131 LLDIQNINIHIVARNFVGLSPFESVILWLSKNGIEETHNCAFNCTOLDDELNLSNNLE 190  
Db 288 LLDIQNINIHIVARNFVGLSPFESVILWLSKNGIEETHNCAFNCTOLDDELNLSNNLE 347  
Oy 191 ELNDVFGAGSGPVLDISRTKNSLPHNGLENLKLKLRSTYBLKLPNLDKFTYLMXA 250  
Db 348 ELNDVFGAGSGPVLDISRTKNSLPHNGLENLKLKLRSTYBLKLPNLDKFTYLMXA 407  
Oy 251 SLTYPSHCCAFANLKRQISELHPICNKSILRQEVDMYMTQARGORSSLAEDNESSYRGFD 309  
Db 408 SLTYPSHCCAFANLKRQISELHPICNKSILRQEVDMYMTQARGORSSLAEDNESSYRGFD 467  
Oy 310 MMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNIL 347  
Db 468 MMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNIL 505

Search completed: June 16, 2003, 13:52:48  
Job time : 166.911 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2003, 13:26:01 ; Search time 26.1704 Seconds  
(without alignments)  
2479.543 Million cell updates/sec

Title: US-09-877-804-7

Perfect score: 3516  
Sequence: 1 CHMKCHCNRRVFLQDSKV.....SAPRVTNYSVLVPLNHSQSN 675

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR73:..

1: PIR1:..

2: PIR2:..

3: PIR3:..

4: PIR4:..

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	3516	100.0	692	2	A34548	folliotropin recept
2	3164.5	90.0	695	1	ORHUFT	folliotropin recept
3	3160.3	88.9	695	1	JN0898	folliotropin recept
4	3140.3	88.3	695	1	JN3686	follicle stimulat
5	3140.3	88.3	695	1	JN3686	follicle stimulat
6	3140.3	88.3	695	1	JN3686	follicle stimulat
7	3070.5	87.3	694	2	JC2337	folliotropin recept
8	2475	70.4	696	2	JC4301	folliotropin recept
9	1807	51.4	696	2	A41344	lutropin-choriogon
10	1799	51.2	700	2	A42395	lutropin receptor
11	1797	51.1	700	2	I77463	lutropin-choriogon
12	1797	51.1	700	2	A49744	lutropin-choriogon
13	1776	50.5	699	1	ORHUFT	thyrotropin recept
14	1655	47.1	764	2	A40077	thyrotropin recept
15	1648.5	46.7	764	1	ORHUFT	thyrotropin recept
16	1628	46.3	764	2	JC5643	thyroid stimulat
17	1628	46.3	764	2	JC7390	thyroid stimulat
18	1628	46.3	764	2	JC7386	thyroid stimulat
19	1594	45.3	814	2	JC7386	thyroid stimulat
20	1594	45.3	814	2	JC7386	thyroid stimulat
21	861.5	24.3	925	2	J20123	hypothetical
22	805.5	22.9	889	2	J20123	hypothetical
23	628.5	17.9	907	2	J20123	hypothetical
24	628	17.9	907	2	J20123	hypothetical
25	587	16.7	329	2	JG0176	G protein-coupled
26	587	16.7	329	2	B41344	lutropin-choriogon
27	587	16.7	331	2	D41344	lutropin-choriogon
28	578	16.4	342	2	I77461	lutropin-choriogon
29	521.5	14.8	1115	2	S40741	G protein-coupled

#### ALIGNMENTS

##### RESULT 1

A34548  
folliotropin receptor precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 13-Aug-1999  
C:Accession: A34548; A41729  
R:Sprengel, R.; Braun, T.; Nikolic, K.; Segaloff, D.L.; Seeburg, P.H.  
Mol. Endocrinol. 4, 525-530, 1990  
A>Title: The testicular receptor for follicle stimulating hormone: structure and func  
A:Reference number: A34548; MUID:91125358; PMID:2126341  
A:Accession: A34548  
A:Molecule type: mRNA  
A:Residues: 1-692 <SP>  
A:Cross-references: GB:J02842; NID:9204183; PID:AAA1175.1; PID:9204184  
M:Hecker, L.L.; Gilly, J.; Griswold, M.D.  
Mol. Endocrinol. 6, 97-100, 1992  
A>Title: Structural organization of the follicle-stimulating hormone receptor gene.  
A:Reference number: A41729; MUID:92149579; PMID:1738373  
A:Accession: A41729  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-692 <HEC>  
A:Cross-references: GB:S81198; NID:9245344; PID:AA821415.1; PID:9245345  
A>Note: sequence inconsistent with the nucleotide translation  
R:Davis, D.; Liu, X.; Segaloff, D.L.  
Mol. Endocrinol. 9, 159-170, 1995  
A>Title: Identification of the sites of N-linked glycosylation on the follicle-stimul  
A:Reference number: A57562; MUID:95295729; PMID:7776966  
C:Keywords: annotation; glycosylation sites  
A:Description: receptor that mediates the biochemical effects of follitropin  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repoa  
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone r  
F.1-15/Domain: signal sequence #status predicted <SIG>  
F.16-692/Product: follitropin receptor #status predicted <MAT>  
F.16-366/Domain: extracellular hormone binding #status predicted <EHB>  
F.71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F.71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F.96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F.121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F.146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F.172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F.367-389/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F.389-421/Domain: transmembrane #status predicted <TM>  
F.434-465/Domain: transmembrane #status predicted <TM>  
F.486-508/Domain: transmembrane #status predicted <TM>  
F.529-550/Domain: transmembrane #status predicted <TM>  
F.574-597/Domain: transmembrane #status predicted <TM>  
F.609-630/Domain: transmembrane #status predicted <TM>  
F.131.199.293/Binding site: carbohydrate (Asn) #status predicted

lutropin receptor  
lutropinizing hormone  
thyrotropin recept  
thyrotropin recept  
neurotrophin Y/pep  
angiotensin II rec  
MEGF5 protein - ra  
allatostatin recep  
somatostatin recep  
somatostatin recep  
somatostatin recep  
dopamine D1 recept  
somatostatin recep

30 402.5 11.4 173 2 151269  
31 381.5 10.9 431 2 157089  
32 381.5 10.9 431 2 157089  
33 297 8.4 252 1 JG1319  
34 297 8.4 252 1 JG1319  
35 227 6.5 381 2 JN0694  
36 222 6.3 362 2 JN0694  
37 222 6.3 362 2 JN0694  
38 221.5 6.3 423 2 JG7677  
39 217.5 6.2 369 2 B41795  
40 216 6.1 1531 2 T42218  
41 215.5 6.1 369 2 JG2083  
42 207.5 5.9 359 2 I51372  
43 207.5 5.9 369 2 D41795  
44 206.5 5.9 363 2 I50475  
45 206.5 5.9 369 2 A45291

F:554/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
F:595/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 100.0%; Score 3516; DB 2; Length 692;  
Best Local Similarity 100.0%; Pred. No. 9.3e-237;  
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHWLCHSNNRVFCQDSKVTPTDLPRAIAELRVLTLLRVIPKPSFAGFGDLEKIEI 60  
Db 18 CHHWLCHSNNRVFCQDSKVTPTDLPRAIAELRVLTLLRVIPKPSFAGFGDLEKIEI 77  
Qy 61 SONDVLEIVADVSNLPKLEIRKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 120  
Db 78 SONDVLEIVADVSNLPKLEIRKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 137  
Qy 121 VHKIOTLOKVLDDIQDNNINHIARNFSGLSFESVILWLSKNGIEIHNCAFNGLTOLDE 180  
Db 138 VHKIOTLOKVLDDIQDNNINHIARNFSGLSFESVILWLSKNGIEIHNCAFNGLTOLDE 197  
Qy 181 LNLSDNNLELPNDVFGQSGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLLPN 240  
Db 198 LNLSDNNLELPNDVFGQSGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLLPN 257  
Qy 241 LDKFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQIDDDMTQIGDQVSLIDD 300  
Db 258 LDKFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQIDDDMTQIGDQVSLIDD 317  
Qy 301 EPSYKGSDDMYNEFDYDLNCEVVDVTCSPKPAFNCEDIMGNYILRVLIWFISILAIT 360  
Db 318 EPSYKGSDDMYNEFDYDLNCEVVDVTCSPKPAFNCEDIMGNYILRVLIWFISILAIT 377  
Qy 361 GNTTVLVLTTSQYKLVTPRELMLNLAFLADLCIGIYLLIASVDIHTKSOVHNAIDWQT 420  
Db 378 GNTTVLVLTTSQYKLVTPRELMLNLAFLADLCIGIYLLIASVDIHTKSOVHNAIDWQT 437  
Qy 421 GAGCDAAGFTVFASLSVYTLTATILRHWHITTHAMOLECKVOLRAHASVYVLGWTFAF 480  
Db 438 GAGCDAAGFTVFASLSVYTLTATILRHWHITTHAMOLECKVOLRAHASVYVLGWTFAF 497  
Qy 481 AAALFPPIFGISYKWKVSCILPMDIDSPLSQLYVALLVNLVLAFLVFCGCTHYLYLVNRN 540  
Db 498 AAALFPPIFGISYKWKVSCILPMDIDSPLSQLYVALLVNLVLAFLVFCGCTHYLYLVNRN 557  
Qy 541 PTIVSSSDTTRIAKRMATLIPTDFLCMAPIISFAISASLKVPLITVSKAKILLVLYFPIN 600  
Db 558 PTIVSSSDTTRIAKRMATLIPTDFLCMAPIISFAISASLKVPLITVSKAKILLVLYFPIN 617  
Qy 601 SCANPFLYAIPTKFRDRDFILLSKFGCYENQAOIYRTETSSATHNFHARKSHCSSAPRV 660  
Db 618 SCANPFLYAIPTKFRDRDFILLSKFGCYENQAOIYRTETSSATHNFHARKSHCSSAPRV 677  
Qy 661 TNSYLVPLNHSN 675  
Db 678 TNSYLVPLNHSN 692

## RESULT 2

ORHUFT

N:Altitropin receptor precursor - human

N:Altitropin receptor precursor long splice form; follitropin receptor precursor

N:Altitropin receptor precursor long splice form; follitropin receptor precursor

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence revision 06-Sep-1996 #text change 22-Jun-1999

C:Accession: 157661; 156448; PC1147; S30560; 157672; JN0122

R:Gromoll, J.; Dankbar, B.; Gudermann, T.

Mol. Cell. Endocrinol. 102, 93-102, 1994

A:Title: Characterization of the 5' flanking region of the human follicle-stimulating hormone

A:Reference number: 157661; MUID:95011044; PMID:7926278

A:Accession: 157661

A:Status: translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-51 &lt;GRO&gt;

A:Cross-references: GB:S73199; NID:9685036; PIDN:AAB32071.1; PID:9685037

R:Gromoll, J.; Ried, T.; Holtgreve-Grez, H.; Nieschlag, E.; Gudermann, T.  
J. Mol. Endocrinol. 12, 265-271, 1994  
A:Title: Localization of the human FSH receptor to chromosome 2 p21 using a genomic F  
A:Reference number: 156448; MUID:95000244; PMID:7916967

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 286-695 &lt;GR&gt;

A:Cross-references: GB:S73526; NID:9688069; PIDN:AAB32225.1; PID:9688070

R:Gromoll, J.; Gudermann, T.; Nieschlag, E.

Biochem. Biophys. Res. Commun. 188, 1077-1083, 1992

A:Title: Molecular cloning of a truncated isoform of the human follicle stimulating h

A:Reference number: PC1147; MUID:93075197; PMID:1359889

A:Accession: PC1147

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-223,286-294,'P',296-342 &lt;GR3&gt;

A:Cross-references: EMBL:X68044; NID:g31473; PIDN:CAA48179.1; PID:g31474

A:Experimental source: Testis

R:Gromoll, J.

Submitted to the EMBL Data Library, August 1992

A:Reference number: S30560

A:Accession: S30560

A:Molecule type: mRNA

A:Residues: 1-12,'R',14-223,286-294,'P',296-342 &lt;GR4&gt;

A:Cross-references: EMBL:X68044; NID:g31473; PIDN:CAA48179.1; PID:g31474

R:Kelton, C.A.; Cheng, S.V.; Nugent, N.P.; Schweichardt, R.L.; Rosenthal, J.L.; Over

Mol. Cell. Endocrinol. 89, 141-151, 1992

A:Title: The cloning of the human follicle stimulating hormone receptor and its expe

A:Reference number: 157672; MUID:93246012; PMID:1301382

A:Accession: 157672

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-679, N, 681-695 &lt;REL&gt;

A:Cross-references: GB:S59900; NID:g300072; PIDN:AAB26480.1; PID:g300073

R:Minglish, T.; Nakamura, K.; Takakura, Y.; Ibuki, Y.; Igarashi, M.

Biochem. Biophys. Res. Commun. 175, 1125-1130, 1991

A:Title: Cloning and sequencing of human FSH receptor cDNA.

A:Reference number: JN0122; MUID:91222171; PMID:1709010

A:Accession: JN0122

A:Molecule type: mRNA

A:Residues: 1-111,'T',113-136,'AV',199-306,'A',308-695 &lt;MIN&gt;

A:Cross-references: EMBL:M65085; NID:g182770; PIDN:AAA52477.1; PID:g182771

C:Genetics:

A:Gene: GDB:FSHR

A:Cross-references: GDB:127510; OMIM:136435

A:Map position: 2p21-2p16

A:Introns: 223/3

A:Note: the exact position of the intron cannot be determined from the experimental c

C:Function:

A:Description: receptor that mediates the biochemical effects of follitropin

C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repee

C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone

F:1-695/Product: follitropin receptor precursor, long splice form #status predicted

F:1-223,286-695/Product: follitropin receptor precursor, short splice form #status pr

F:1-15/Domin: signal sequence #status predicted &lt;SIG&gt;

F:16-695/Domin: follitropin receptor #status predicted &lt;MAT&gt;

F:16-366/Domin: extracellular hormone binding #status predicted &lt;EHR&gt;

F:56-70/Domin: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR1&gt;

F:71-95/Domin: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR2&gt;

F:96-120/Domin: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR3&gt;

F:121-145/Domin: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR4&gt;

F:146-169/Domin: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR5&gt;

F:172-193/Domin: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR6&gt;

F:194-218/Domin: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR7&gt;

F:367-387/Domin: transmembrane #status predicted &lt;TM1&gt;

F:398-421/Domin: transmembrane #status predicted &lt;TM2&gt;

F:444-465/Domin: transmembrane #status predicted &lt;TM3&gt;

F:486-508/Domin: transmembrane #status predicted &lt;TM4&gt;

F:529-550/Domin: transmembrane #status predicted &lt;TM5&gt;

F:574-597/Domin: transmembrane #status predicted &lt;TM6&gt;

F:609-630/Domin: transmembrane #status predicted &lt;TM7&gt;

F:191,199,293,318/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:555/Binding site: phosphate (Thr) (covalent) (by protein kinase C) status predicted  
F:556/Binding site: phosphate (Ser) (covalent) (by protein kinase C) status predicted

Query Match 90.0%; Score 3160.5; DB 1; Length 695;  
Best Local Similarity 89.4%; Pred. No. 2,7e-212;  
Matches 606; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

OY 1 CHHMLCHSNNRVFLQDSKVTEIPDLPNNAIELRVLTLPKSGFAGFGDLEKIEI 60  
DB 18 CHHMLCHSNNRVFLQDSKVTEIPDLPNNAIELRVLTLPKSGFAGFGDLEKIEI 77  
OY 61 SONDLVLEADVFNKLPKHEIRIEKANNLLYINPEAFONPLSRLLYSNTGKILHPA 120  
DB 78 SONDLVLEADVFNKLPKHEIRIEKANNLLYINPEAFONPLSRLLYSNTGKILHPA 137  
OY 121 VHKIOSLOKVLIDODNINHTVARSFNGLSSESVILMLSKNGIEIHNCAFNQTOLDE 180  
DB 138 VHKIHSQKVLIDODNINHTVARSFNGLSSESVILMLSKNGIEIHNCAFNQTOLDE 197  
OY 181 LNLSDNNLEELPNDVFGASGVILDISRTKVSHPNGLNKLKLRARSTYBLKLPN 240  
DB 198 LNLSDNNLEELPNDVFGASGVILDISRTKVSHPNGLNKLKLRARSTYBLKLPN 257  
OY 241 LDKFVTLMEASLTYPSCCAFANKRQISELHPICNKSILRODIDMTQIGDQVSLIDD 300  
DB 258 LDKFVTLMEASLTYPSCCAFANKRQISELHPICNKSILRODIDMTQIGDQVSLIDD 317  
OY 301 -EPYKSGSDMTNEFDYDLCHNEVDVTCSPKDPNCPEDINGYNILRVLIWIFSI 359  
DB 318 NESSTGDFMTTAFDYLCHNEVDVTCSPKDPNCPEDINGYNILRVLIWIFSI 377  
OY 360 TGNITVVLVTTSOYKLVTPRELKLNAPADLCIGYLLIASVDIHTKSOYHVAIDMQ 419  
DB 378 TGNITVVLVTTSOYKLVTPRELKLNAPADLCIGYLLIASVDIHTKSOYHVAIDMQ 437  
OY 420 TGACDCAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVYVLCWTF 479  
DB 438 TGACDCAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVYVLCWTF 497  
OY 480 FAALPPIFGISSTKVSICLPMIDPSLSQLYMALLVNLVLAEPVWICGCTHYLTVR 539  
DB 498 FAALPPIFGISSTKVSICLPMIDPSLSQLYMALLVNLVLAEPVWICGCTHYLTVR 557  
OY 540 NPTIVSSSDTKIAKRNATLIFTDFLCHMAPISFFAISASUKVPLITVSKAKILLVLPYI 599  
DB 558 NPTIVSSSDTKIAKRNATLIFTDFLCHMAPISFFAISASUKVPLITVSKAKILLVLPYI 617  
OY 600 NSCANPFLYALPTKRNPRDFPILLSKGCYEMQAOIYRTETSSATHNPHARKSCSSAPR 659  
DB 618 NSCANPFLYALPTKRNPRDFPILLSKGCYEMQAOIYRTETSSATHNPHARKSCSSAPR 677  
OY 660 VT--NSTVLVPLNHSQN 675  
DB 678 VTGSGSYILVPLSLAQN 695

RESULT 3

JN0898  
Follicle stimulating hormone precursor - crab-eating macaque  
A:Alternate names: follicle stimulating hormone receptor (FSHR)  
C:Date: 10-Sep-1999  
C:Accession: JN0898; 876457  
R:Gromoll, J.; Donker, B.; Sharma, R.S.; Hieschlag, E.  
Biochem. Biophys. Res. Commun. 196, 1056-1072, 1993  
A:Title: Molecular cloning of the testicular follicle stimulating hormone receptor of th  
A:Reference number: JN0898; MUID:94071854; PMID:7504463  
A:Accession: JN0898  
A:Molecule type: mRNA  
A:Residues: 1-695 <GRO>  
A:Cross-references: EMBL:X7454; MID:g396801; PIDN:CAA52463.1; PID:g396802  
A:Note: the authors translated the codon AGT for residue 488 as Arg  
C:Function:

A:Description: receptor that mediates the biochemical effects of follicle stimulating hormone  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
F:555/Binding site: phosphate (Thr) (covalent) (by protein kinase C) status predicted  
F:556/Binding site: phosphate (Ser) (covalent) (by protein kinase C) status predicted  
F:557/Binding site: phosphate (Thr) (covalent) (by protein kinase C) status predicted  
F:558/Binding site: phosphate (Ser) (covalent) (by protein kinase C) status predicted

Query Match 89.9%; Score 3160.5; DB 1; Length 695;  
Best Local Similarity 89.4%; Pred. No. 5.1e-212;  
Matches 606; Conservative 30; Mismatches 39; Indels 3; Gaps 2;

OY 1 CHHMLCHSNNRVFLQDSKVTEIPDLPNNAIELRVLTLPKSGFAGFGDLEKIEI 60  
DB 18 CHHMLCHSNNRVFLQDSKVTEIPDLPNNAIELRVLTLPKSGFAGFGDLEKIEI 77  
OY 61 SONDLVLEADVFNKLPKHEIRIEKANNLLYINPEAFONPLSRLLYSNTGKILHPA 120  
DB 78 SONDLVLEADVFNKLPKHEIRIEKANNLLYINPEAFONPLSRLLYSNTGKILHPA 137  
OY 121 VHKIOSLOKVLIDODNINHTVARSFNGLSSESVILMLSKNGIEIHNCAFNQTOLDE 180  
DB 138 VHKIHSQKVLIDODNINHTVARSFNGLSSESVILMLSKNGIEIHNCAFNQTOLDE 197  
OY 181 LNLSDNNLEELPNDVFGASGVILDISRTKVSHPNGLNKLKLRARSTYBLKLPN 240  
DB 198 LNLSDNNLEELPNDVFGASGVILDISRTKVSHPNGLNKLKLRARSTYBLKLPN 257  
OY 241 LDKFVTLMEASLTYPSCCAFANKRQISELHPICNKSILRODIDMTQIGDQVSLIDD 300  
DB 258 LDKFVTLMEASLTYPSCCAFANKRQISELHPICNKSILRODIDMTQIGDQVSLIDD 317  
OY 301 -EPYKSGSDMTNEFDYDLCHNEVDVTCSPKDPNCPEDINGYNILRVLIWIFSI 359  
DB 318 NESSTGDFMTTAFDYLCHNEVDVTCSPKDPNCPEDINGYNILRVLIWIFSI 377  
OY 360 TGNITVVLVTTSOYKLVTPRELKLNAPADLCIGYLLIASVDIHTKSOYHVAIDMQ 419  
DB 378 TGNITVVLVTTSOYKLVTPRELKLNAPADLCIGYLLIASVDIHTKSOYHVAIDMQ 437  
OY 420 TGACDCAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVYVLCWTF 479  
DB 438 TGACDCAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVYVLCWTF 497  
OY 480 FAALPPIFGISSTKVSICLPMIDPSLSQLYMALLVNLVLAEPVWICGCTHYLTVR 539  
DB 498 FAALPPIFGISSTKVSICLPMIDPSLSQLYMALLVNLVLAEPVWICGCTHYLTVR 557  
OY 540 NPTIVSSSDTKIAKRNATLIFTDFLCHMAPISFFAISASUKVPLITVSKAKILLVLPYI 599  
DB 558 NPTIVSSSDTKIAKRNATLIFTDFLCHMAPISFFAISASUKVPLITVSKAKILLVLPYI 617  
OY 600 NSCANPFLYALPTKRNPRDFPILLSKGCYEMQAOIYRTETSSATHNPHARKSCSSAPR 659  
DB 618 NSCANPFLYALPTKRNPRDFPILLSKGCYEMQAOIYRTETSSATHNPHARKSCSSAPR 677  
OY 660 VT--NSTVLVPLNHSQN 675  
DB 678 VTGSGSYILVPLSLAQN 695

## RESULT 4

follicle stimulating hormone receptor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 15-Oct-1996 #sequence\_revision 15-Oct-1996 #text\_change 21-Jan-2000  
C:Accession: I45896  
R:House, A.; Lambert, A.; Saumande, J.; Silversides, D.W.; Lussier, J.G.  
Mol. Reprod. Dev. 39, 127-135, 1994  
A:Title: Structure of the bovine follicle-stimulating hormone receptor complementary DNA  
A:Reference number: I45896; MUID:95127199; PMID:7826612  
A:Accession: I45896  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-695 <HOU>  
A:Cross-references: GB:L22319; NID:g404671; PIDN:AAAC37324.1; PID:g404672  
C:Gene: FSHR  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
  
Query Match 89.5%; Score 3145.5; DB 2; Length 695;  
Best Local Similarity 87.9%; Pred. No. 5.6e-211;  
Matches 596; Conservative 45; Mismatches 34; Indels 3; Gaps 2;  
  
Qy 1 CHHWLCHSNRVFLCQDSKVTEIPTDLPRNAIEFLVTLKLVIPKSGFAGFGLKIEI 60  
Db 18 CHHRLCHCSNGVFLCQDSKVTEIPTDLPRDAVELFVTLKLVIPKSGFAGFGLKIEI 77  
  
Qy 61 SONDVLEIADVFSNLPKLEIRKANNLLYNPEAFONLPSRLYLLISNTGKHLPA 120  
Db 78 SONDVLEIVANVFSNLPKLEIRKANNLLYIDPDAFQNLPLRLYLLISNTGKHLPA 137  
  
Qy 121 VHKTQSLQKVLDDIQDNINIHIVARNFPMGLSFESVILWLSKNGIEETHNCAFNQTOLDE 180  
Db 138 VHKTQSLQKVLDDIQDNINIHIVARNFPMGLSFESVILWLSKNGIEETHNCAFNQTOLDE 197  
  
Qy 181 LNLSDNNLELPNDVFGAGSPVILDSRTKVSHPNHLNGLNKKLRARSTYRLKLPN 240  
Db 198 LNLSDNSNLELPNDVFGAGSPVILDSRTKVSHPNHLNGLNKKLRARSTYRLKLPN 257  
  
Qy 241 LDKFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQDIDDMTQIGDQVSLI-D 299  
Db 258 LEKFTVTLMEASLTYPSCCAFANRRQTSDLHPICNKSILRQEVDDMTQARGQVSLAI 317  
  
Qy 300 DEPSYKSGDMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLWIFISILAI 359  
Db 318 DEPSYKSGDMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLWIFISILAI 377  
  
Qy 360 TGNITVVLVLTTSQKLTVPFLMCLNLAFAADLCIGIYLLIASVDVHTKSOYHNYAIDWQ 419  
Db 378 TGNITVVLVLTTSQKLTVPFLMCLNLAFAADLCIGIYLLIASVDVHTKSOYHNYAIDWQ 437  
  
Qy 420 TGACDGAAGPFTVFASLSVYTLTAITLERWHTITHAMOLECKVQLRHAASVVLWGTFEA 479  
Db 438 TGACDGAAGPFTVFASLSVYTLTAITLERWHTITHAMOLECKVQLRHAASVVLWGTFEA 497  
  
Qy 480 FAALFPFTFGISSYMKVSIKLPMDIDSPLSQLYNALVLNLAFAVVICGCTHYLTVR 539  
Db 498 FAVALFPFTFGISSYMKVSIKLPMDIDSPLSQLYNALVLNLAFAVVICGCTHYLTVR 557  
  
Qy 540 NPTIVSSSDTKIAKRMATLFTDFLCNAPISFAISASLKVPLITVSKAKILLVFPYI 599  
Db 558 NPTIVSSSDTKIAKRMATLFTDFLCNAPISFAISASLKVPLITVSKAKILLVFPYI 617  
  
Qy 600 NSCANPFLYALFTNFRDRDFILLSKFCYEQMQAIVRTSTSSATHNPHARKSHCSAPR 659  
Db 618 NSCANPFLYALFTNFRDRDFILLSKFCYEQMQAIVRTSTSSATHNPHARKSHCSAPR 677  
  
Qy 660 VTN--SYVLVPLNHSN 675  
Db 678 VTNGSNYTLPLRLAKN 695

## RESULT 5

follicle stimulating hormone receptor - sheep  
N:Alternate names: follicle stimulating hormone receptor  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C:Accession: JCI1493; I47080  
R:Khan, H.; Yarney, T.A.; Sairam, M.R.  
Biochem. Biophys. Res. Commun. 190, 888-894, 1993  
A:Title: Cloning of alternatively spliced mRNA transcripts coding for variants of ovine  
A:Reference number: JCI1493; MUID:93176195; PMID:8439338  
A:Accession: JCI1493  
A:Molecule type: mRNA  
A:Residues: 1-695 <KHA>  
A:Experimental source: testis  
R:Yarney, T.A.; Sairam, M.R.; Khan, H.; Ravindranath, N.; Payne, S.; Seidah, N.G.  
Mol. Cell. Endocrinol. 93, 219-226, 1993  
A:Title: Molecular cloning and expression of the ovine testicular follicle stimulating  
A:Reference number: I47080; MUID:93351750; PMID:8394255  
A:Accession: I47080  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-695 <YAR>  
A:Cross-references: GB:L07302; NID:g165884; PIDN:AAA31525.1; PID:g165885  
C:Gene: FSH-R  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
F:191/199/Binding site: carbohydrate (Asn) (covalent) #status predicted  
  
Query Match 89.3%; Score 3140.5; DB 2; Length 695;  
Best Local Similarity 87.5%; Pred. No. 1.2e-210;  
Matches 593; Conservative 47; Mismatches 35; Indels 3; Gaps 2;  
  
Qy 1 CHHWLCHSNRVFLCQDSKVTEIPTDLPRNAIEFLVTLKLVIPKSGFAGFGLKIEI 60  
Db 18 CHHRLCHCSNGVFLCQDSKVTEIPTDLPRDAVELFVTLKLVIPKSGFAGFGLKIEI 77  
  
Qy 61 SONDVLEIADVFSNLPKLEIRKANNLLYNPEAFONLPSRLYLLISNTGKHLPA 120  
Db 78 SONDVLEIVANVFSNLPKLEIRKANNLLYIDPDAFQNLPLRLYLLISNTGKHLPA 137  
  
Qy 121 VHKTQSLQKVLDDIQDNINIHIVARNFPMGLSFESVILWLSKNGIEETHNCAFNQTOLDE 180  
Db 138 VHKTQSLQKVLDDIQDNINIHIVARNFPMGLSFESVILWLSKNGIEETHNCAFNQTOLDE 197  
  
Qy 181 LNLSDNNLELPNDVFGAGSPVILDSRTKVSHPNHLNGLNKKLRARSTYRLKLPN 240  
Db 198 LNLSDNSNLELPNDVFGAGSPVILDSRTKVSHPNHLNGLNKKLRARSTYRLKLPN 257  
  
Qy 241 LDKFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQDIDDMTQIGDQVSLI-D 299  
Db 258 LEKFTVTLMEASLTYPSCCAFANRRQTSDLHPICNKSILRQEVDDMTQARGQVSLAI 317  
  
Qy 300 DEPSYKSGDMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLWIFISILAI 359  
Db 318 DEPSYKSGDMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLWIFISILAI 377  
  
Qy 360 TGNITVVLVLTTSQKLTVPFLMCLNLAFAADLCIGIYLLIASVDVHTKSOYHNYAIDWQ 419  
Db 378 TGNITVVLVLTTSQKLTVPFLMCLNLAFAADLCIGIYLLIASVDVHTKSOYHNYAIDWQ 437  
  
Qy 420 TGACDGAAGPFTVFASLSVYTLTAITLERWHTITHAMOLECKVQLRHAASVVLWGTFEA 479  
Db 438 TGACDGAAGPFTVFASLSVYTLTAITLERWHTITHAMOLECKVQLRHAASVVLWGTFEA 497  
  
Qy 480 FAALFPFTFGISSYMKVSIKLPMDIDSPLSQLYNALVLNLAFAVVICGCTHYLTVR 539  
Db 498 FAVALFPFTFGISSYMKVSIKLPMDIDSPLSQLYNALVLNLAFAVVICGCTHYLTVR 557

317 DESSYPKGFDWYSEFEYDCLNEVDVYTCSPKDFANPCEDINGVOLLVILNFIISLAI 376

360 TGNITVVLVLTLSQYKLTVPRLNCLNAPADLCIGIYLLLIASVDITHTSQYHNAYDAQ 419

377 TCGNIVLVILITLSQYKLTVPRLNCLNAPADLCIGIYLLLIASVDITHTSQYHNAYDAQ 436

420 TGACDAAAGFEFTVFASLSVYLTATLTERHHTITHAMOLECKVQLRHAASVYVLGTFEA 479

437 TGACDAAAGFEFTVFASLSVYLTATLTERHHTITHAMOLECKVQLRHAASVYVLGTFEA 496

480 FAALPPIFGISYKHYKVCILPMDISPLSGLYVWALLLVNLVLPVWVGGCYTHIYLTVR 539

497 FNALVLPPIFGISYKHYKVCILPMDISPLSGLYVWALLLVNLVLPVWVGGCYTHIYLTVR 556

540 NPTIVSSSTQSLAKRNWALIFTDFCLNAPISFAISAKLVPLTVSKAILLVLPYI 599

557 NPNVSSSTQSLAKRNWALIFTDFCLNAPISFAISAKLVPLTVSKAILLVLPYI 616

600 NSCANPFLYIAITKFNRRDFFILLSKFCGYEMQAQIYRTTSSATHNFIARKSCSAPR 659

617 NSCANPFLYIAITKFNRRDFFILLSKFCGYEMQAQIYRTTSSATHNFIARKSCSAPR 676

660 VTN--SYVLPLNHSSQN 675

677 VINGANCTVLPISHLAQN 694

RESULT 7

3CJ4301

folliculin receptor - pig

N:Alternate names: follicle-stimulating hormone receptor

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 16-Nov-1995 #sequence\_revision 08-Feb-1996 #tax\_change 21-Jan-2000

C:Accession: JC4301

R:Remy, J.-J.; Labhii-Mansals, V.; Verlie, M.; Bozon, V.; Couture, L.; Pajot, E.; Grebe Gene 163, 257-261, 1995

A:Title: The porcine follitropin receptor: cDNA cloning, functional expression and characterisation

A:Reference number: JC4301; MUID:96011644; PMID:7590277

A:Accession: JC4301

A:Molecule type: mRNA

A:Residues: 1-654 <R6>

A:Experimental references: L31965

A:Experimental references: L31965

C:Comment: This receptor belongs to the family of the G-protein coupled receptors. It is involved in the regulation of oogenesis in female.

C:Genetics:

A:Gene: fshr

A:Map position: 3 q2.2-q2.3

A:Map family: glycoprotein hormone receptor: leucine-rich alpha-2-glycoprotein repeat

C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

F:1-365/Domain: follicle-stimulating hormone binding status predicted <R6>

F:76-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <R6>

F:398-430/Domain: transmembrane status predicted <TM>

F:430-464/Domain: transmembrane status predicted <TM>

F:463-464/Domain: transmembrane status predicted <TM>

F:485-507/Domain: transmembrane status predicted <TM>

F:528-549/Domain: transmembrane status predicted <TM>

F:573-596/Domain: transmembrane status predicted <TM>

F:608-629/Domain: transmembrane status predicted <TM>

Query Match 87.3% Score 3070.5; DB 2; Length 694;

Best Local Similarity 86.1%; Pred. No. 9.2e-206;

Matches 584; Conservative 40; Mismatches 51; Indels 3; Gaps 2;

1 CHWUHCNRRVFLCQSKVTEITDLPNAIELRFLVTLKRLPKGSPAGFGDLKEIKI 60

17 CHHRCVLEIYADVNSPLKRIEIKANLLIINPEAFQNLPSLTLSNGIKHPLA 120

77 SONDLVLEIANVFSNPLKRIEIKANLLIYDPAQNPLNRLYLTLSNGIKHPLA 136

121 VHKIOSLQKVLDDIDNNIHLIVARNSPMGLSEFVSLWLSKNGITEIHNCAFNQTDLR 160

Db 137 VHKIQSLQKVLDDIQDNIHITVERNSFMGLSPESMILWLSKNGIRHNCFAFGTQDLE 196  
Qy 181 LNLSDNNLELNDVDFQAGSGPVILDSRTKVSLSLPHNGLNKKLRARSTYRLKLLPN 240  
Db 197 LNLSDNNLELNDVDFQAGSGPVILDSRTKVSLSLPHNGLNKKLRARSTYRLKLLPN 256  
Qy 241 LDKFVTLMEASLTYPSPHCCAFANLKRQISLHLPICNKSILRQDIDDDTQICDQSVSLDD 300  
Db 257 LEKFTVTLMEASLTYPSPHCCAFANLKRQISLHLPICNKSILRQDIDDDTQICDQSVSLDD 316  
Qy 301 -EPYSGKSDMYNEFDYDLCNEVVDVTCSPKDAFNPCEIDMGYNILRVLWIFISILAI 359  
Db 317 GESSLAKEFDFTMYSEFNVDLCNEVVDVTCSPKDAFNPCEIDMGYNILRVLWIFISILAI 376  
Qy 360 TGNITVTLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLIASVDIHTKSOYHNYAIDWQ 419  
Db 377 TGNITVTLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLIASVDIHTKSOYHNYAIDWQ 436  
Qy 420 TGAGCDAAGFTVPFASLSVYTLTAITLERWHTITHAMOLECKVOLRAHAAVNVLGWTF 479  
Db 437 TGAGCDAAGFTVPFASLSVYTLTAITLERWHTITHAMOLECKVOLRAHAAVNVLGWTF 496  
Qy 480 FTAALPFIPIGSSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCIYHLYTVR 539  
Db 497 FTAALPFIPIGSSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCIYHLYTVR 556  
Qy 540 NPTIVSSSDTKIAKRMATLIFTDFLCMAPISEFAISASLKVPILTVSKAKILLVLPYI 599  
Db 557 NPTIVSSSDTKIAKRMATLIFTDFLCMAPISEFAISASLKVPILTVSKAKILLVLPYI 616  
Qy 600 NSCANPLYAIFTKNFRDRFVILLKFGCYEMOQAQIYRTETSSATHNFHARKSHCSAPR 659  
Db 617 NSCANPLYAIFTKNFRDRFVILLKFGCYEMOQAQIYRTETSSATHNFHARKSHCSAPR 676  
Qy 660 VTN--SYLVPLNHSN 675  
Db 677 ITNSSSYTLPLSLAQN 694

## RESULT 8

JC7361  
folliculin receptor precursor - newt  
N;Alternate names: follicle-stimulating hormone receptor  
C;Species: Cynops pyrrhogaster (newt)  
C;Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 31-Dec-2000  
C;Accession: JC7361  
R;Nakayama, Y.; Tamamoto, T.; Oba, Y.; Nagahama, Y.; Abe, S.  
Biochem. Biophys. Res. Commun. 275, 121-128, 2000  
A;Title: Molecular cloning, functional characterization, and gene expression of a folliculin receptor precursor from the newt, *Cynops pyrrhogaster*  
A;Contents: Testis  
A;Accession: JC7361  
A;Molecule type: mRNA  
A;Residues: 1-696 <NAK>  
A;Cross-references: DDBJ:AB005587  
C;Comment: This protein, containing seven transmembrane domains and a large glycosylated in and thyroid stimulating hormone. This receptor has a common signal transduction pathway in and thyroid stimulating hormone.  
C;Genetics:  
A;Gene: fsh-r  
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
C;Keywords: disulfide bond; glycolysis; glycoprotein; hormone receptor; testis; transmembrane  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-696/Product: follicle-stimulating hormone receptor #status predicted <MAT>  
F;18-359/Domain: extracellular #status predicted <EXT>  
F;370-389/Domain: transmembrane #status predicted <TM1>  
F;402-424/Domain: transmembrane #status predicted <TM2>  
F;447-468/Domain: transmembrane #status predicted <TM3>  
F;489-511/Domain: transmembrane #status predicted <TM4>  
F;532-553/Domain: transmembrane #status predicted <TM5>  
F;577-600/Domain: transmembrane #status predicted <TM6>  
F;612-633/Domain: transmembrane #status predicted <TM7>  
F;46,190,198,267,292/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;445-520/Disulfide bonds: #status predicted

Query Match 70.4% Score 2475; DB 2: Length 696;  
Best Local Similarity 71.1% Pred. No. 2.5e-164;  
Matches 482; Conservative 81; Mismatches 107; Indels 8; Gaps 5;

Qy 1 CHHWLCHSNNRVFLCQDSKVTETDLPNNAIEFLVTLKRVIPKSGFAGGDLKIEI 60  
Db 18 CHP-VCRLARVETCOESHVVOIPRNPRIINRSTELRVLTVPKAAFGFEDVENIEI 76  
Qy 61 SONDVLVIEADVFENLPLKHEIRKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 120  
Db 77 SONDVLVIEADVFENLPLKHEIRKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 136  
Qy 121 VHKIQSLQKVLDDIQDNIHITVERNSFMGLSPESMILWLSKNGIRHNCFAFGTQDLE 180  
Db 137 VSKIRSPHSLVDVQDNIHITVERNSFMGLSPESMILWLSKNGIRHNCFAFGTQDLE 196  
Qy 181 LNLSDNNLELNDVDFQAGSGPVILDSRTKVSLSLPHNGLNKKLRARSTYRLKLLPN 240  
Db 197 LNLSDNNLELNDVDFQAGSGPVILDSRTKVSLSLPHNGLNKKLRARSTYRLKLLPN 256  
Qy 241 LDKFVTLMEASLTYPSPHCCAFANLKRQISLHLPICNKSILRQDIDDDTQICDQSVSLDD 299  
Db 257 LEKFTVTLMEASLTYPSPHCCAFANLKRQISLHLPICNKSILRQDIDDDTQICDQSVSLDD 316  
Qy 300 DEPSYSGKSDMYNEFDYDLCNEVVDVTCSPKDAFNPCEIDMGYNILRVLWIFIS 355  
Db 317 YLSYSGSYSLVENGDEFNDYILCNEVVDVTCSPKDAFNPCEIDMGYNILRVLWIFIS 376  
Qy 356 ILAITGNTVTLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLIASVDIHTKSOYHNYA 415  
Db 377 ILAITGNTVTLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLIASVDIHTKSOYHNYA 436  
Qy 416 IDMQTAGCDAAGFTVPFASLSVYTLTAITLERWHTITHAMOLECKVOLRAHAAVNVLG 475  
Db 437 IDMQTAGCDAAGFTVPFASLSVYTLTAITLERWHTITHAMOLECKVOLRAHAAVNVLG 496  
Qy 476 WTEFAAALPFIPIGSSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCIYH 535  
Db 497 WTEFAAALPFIPIGSSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCIYH 556  
Qy 536 LTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISEFAISASLKVPILTVSKAKILLVL 595  
Db 557 LTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISEFAISASLKVPILTVSKAKILLVL 616  
Qy 596 FYPIINSCANPLYAIFTKNFRDRFVILLKFGCYEMOQAQIYRTETSSATHNFHARKSHCS 655  
Db 617 FYPIINSCANPLYAIFTKNFRDRFVILLKFGCYEMOQAQIYRTETSSATHNFHARKSHCS 676  
Qy 656 SAPR--VTNSYVLVPLNH 671  
Db 677 PAPKYSAASTHTLVPLNH 694

## RESULT 9

A41344  
lutropin-choriogonadotropin receptor precursor (splice form A) - pig  
N;Alternate names: lutinizing hormone-choriogonadotropin receptor  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 21-Jan-2000  
C;Accession: A41344  
R;Loosfelt, H.; Misrahi, M.; Atger, M.; Salesse, R.; Vu Hai-Luu Thi, M.T.; Jolivet, A.  
Science 245, 525-528, 1989  
A;Title: Cloning and sequencing of porcine LH-RG receptor cDNA: variants lacking tra  
A;Reference number: A41344; MUID:89332517; PMID:2502844  
A;Accession: A41344  
A;Molecule type: mRNA  
A;Residues: 1-696 <LOO>  
A;Cross-references: GB:M29525; NID:g164528; PIDN:AAA31062.1; PID:g164529  
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repea  
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; membrane  
F;1-27/Domain: signal sequence #status predicted <SIG>



F:28-696/Product: lutropin-choriogonadotropic hormone receptor #status predicted <MAT>  
F:99-123/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 51.44; Score 1807; DB 2; Length 696;  
Best Local Similarity 57.64; Pred No. 7 4e-118; Indels 26; Gaps 8;  
Matches 361; Conservative 98; Mismatches 142;

QY 28 PNAIETLRVLTILK--RVIPKGSFAGDLEKIEISQNDVLEIVAEVFNPLKLEIRI 85  
DB 47 PRAGLS-RLSUTLTPKVPISQAFNGLEWVKEISQSDSLERIANAFONLLNLSBLLI 105  
QY 86 EXANLLINPEAFONLPSRLYSILNTSGIKHLPVAKHTQSLQ-KVLLDITQONINIHVA 144  
DB 106 QNTRNLYTEPGAPTLPRKLYSLICNTGRTLPDVSKEISSEFNLEICDNLHTTVP 165  
QY 145 RNSPGLSSEVILMLSKNGIEBHNCAPNGTOLDNLSDNNLEELPNDVFGASGPV 204  
DB 166 ANAFQGNHSEITLAKNGFEVSHAFNGTTLISLEKNIHAKHNDAPFRGSPS 225  
QY 205 ILDISRTKVSHPHGLNKLKLRARSTYRLKLPNDKFNVLWEASITYPHCCAFANL 264  
DB 226 ILDISSTKLQALPSGLSITQTLATSSYSLKLPSSREKFTSLNLTATYPHCCAFANL 285  
QY 265 --KRO-----ISELPTCNKSLRQDIDDMTOIGDQVSLIDDEPSYSGKSDMMYNEPD 316  
DB 286 PTKBNFSFISFKNFSKOCSTARRNNETL-----YSAFAE-----SELSDDWDYD 332  
QY 317 YDLCNEVDVTCSPKDPNCPEDINGNTRILRVLNFISILAITGNTVTLVLTYSOKL 376  
DB 333 YGCSPT-LQCAEPDAPNCPEDINGDPLRVILMLINILAIINGNTVTLVLTYSOKL 391  
QY 377 TVPRLNCLAPADLCIGYLLIASVDIHTSKYHNAYIDMOTGAGCDAGFFVFASE 436  
DB 392 TVPRLNCLSPADPCGILILLIASVDIHTSKYHNAYIDMOTGAGCDAGFFVFASE 451  
QY 437 LSVTLTALTRHHTTHAMOLECKVOLHRAASVWVLCWTFAPAAALPFGISYKVC 496  
DB 452 LSVTLTALTRHHTTHAMOLECKVOLHRAASVWVLCWTFAPAAALPFGISYKVC 511  
QY 497 SICLPMDISQVLSQVALLVNLVAFVVCYTHYLVTRNPTIVSSSDTKIAKRM 556  
DB 512 SICLPMDVETLSQVILTLILNVAFVVCYTHYLVTRNPTIVSSSDTKIAKRM 571  
QY 557 ATLIFTDCLMAISFSAISLAKVPLTVSKAKILLVLPVINSKANPFLYAIPTKNER 616  
DB 572 AVLIPTDCLMAISFSAISLAKVPLTVSKAKILLVLPVINSKANPFLYAIPTKNER 631  
QY 617 RDFTLLSEKCYEMAOIYRTETSA 643  
DB 632 RDFTLLSEKCYEMAOIYRTETSA 658

RESULT 10

A42395

lutropin receptor - mouse

N:Alternate names: lutelizing hormone-choriogonadotropin receptor

C:Species: Mus musculus (house mouse)

C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 13-Aug-1999

C:Accession: A42395

R:Gudermaun, T.; Birnbaumer, M.; Birnbaumer, L.

A:Title: Evidence for dual coupling of the murine lutelizing hormone receptor to adeny-

late cyclase and phospholipase C.

A:Reference number: A42395; PMID:92165799; PMID:1311310

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-700 <GUD>

A:Cross-references: GB:M81310; GB:M81318; NID:g198811; PIDN:AAA9432.1; PID:g198812

A:Note: sequence extracted from NCBI backbone (NCBI:M84064, NCBI:P84066)

C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat

C:Keywords: G protein-coupled receptor; transmembrane protein

F:54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

F:78-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
F:129-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
F:180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
F:202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 51.24; Score 1799; DB 2; Length 700;  
Best Local Similarity 55.14; Pred No. 2 7e-117; Indels 34; Gaps 9;

Matches 362; Conservative 108; Mismatches 153;

QY 28 PNAIETLRVLTILK--RVIPKGSFAGDLEKIEISQNDVLEIVAEVFNPLKLEIRI 85  
DB 51 PRAGL-ARLSUTLTPKVPISQAFNGLEWVKEISQSDSLERIANAFONLLNLSBLLI 109  
QY 86 EXANLLINPEAFONLPSRLYSILNTSGIKHLPVAKHTQSLQ-KVLLDITQONINIHVA 144  
DB 110 QNTRNLYTEPGAPTLPRKLYSLICNTGRTLPDVSKEISSEFNLEICDNLHTTVP 169  
QY 145 RNSPGLSSEVILMLSKNGIEBHNCAPNGTOLDNLSDNNLEELPNDVFGASGPV 204  
DB 170 QNTRNLYTEPGAPTLPRKLYSLICNTGRTLPDVSKEISSEFNLEICDNLHTTVP 229  
QY 205 ILDISRTKVSHPHGLNKLKLRARSTYRLKLPNDKFNVLWEASITYPHCCAFANL 264  
DB 230 ILDISSTKLQALPSGLSITQTLATSSYSLKLPSSREKFTSLNLTATYPHCCAFANL 289  
QY 265 KROISELHPICNKSILRQDIDDMTOIGDQVSLIDDEPSYSGKSDMMYNEPDYDLCN 321  
DB 290 PKK-----EQNFSFISFKNFSKOCSTARRNNETLYSAIFEENELSGMDYDDECS 341  
QY 322 EYVDVTCSPKDPNCPEDINGNTRILRVLNFISILAITGNTVTLVLTYSOKLTPRPF 381  
DB 342 PKT-LQCTPEPDAPNCPEDINGDPLRVILMLINILAIINGNTVTLVLTYSOKLTPRPF 400  
QY 382 LKCNLAPADLCIGYLLIASVDIHTSKYHNAYIDMOTGAGCDAGFFVFASELSVYT 441  
DB 401 LKCNLAPADPCGILILLIASVDIHTSKYHNAYIDMOTGAGCDAGFFVFASELSVYT 460  
QY 442 LTAITLERNHTTHAMOLECKVOLHRAASVWVLCWTFAPAAALPFGISYKVC 501  
DB 461 LTVITLERNHTTHAMOLECKVOLHRAASVWVLCWTFAPAAALPFGISYKVC 520  
QY 502 MOISPLSOLVYVALLVNLVAFVVCYTHYLVTRNPTIVSSSDTKIAKRMATLIP 561  
DB 521 MOISPLSOLVYVALLVNLVAFVVCYTHYLVTRNPTIVSSSDTKIAKRMATLIP 580  
QY 562 TPTCLMAISFSAISLAKVPLTVSKAKILLVLPVINSKANPFLYAIPTKNERDFFI 621  
DB 581 TPTCLMAISFSAISLAKVPLTVSKAKILLVLPVINSKANPFLYAIPTKNERDFFI 640  
QY 622 LLSKFCYEMAOIYRTETSA-----FHNFAHKS-----HCS--SAPRV 660  
DB 641 LLSKFCYEMAOIYRTETSA-----FHNFAHKS-----HCS--SAPRV 697

RESULT 11

I77463

lutelizing hormone/chorionic gonadotropin receptor - rat

C:Species: Rattus sp. (rat)

C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jan-2000

C:Accession: I77463

R:Aatsinki, J.T.; Pietila, E.M.; Lakkakorpi, J.T.; Rajaniemi, H.J.

A:Title: Expression of the LH/CG receptor gene in rat ovarian tissue is regulated by

gonadotropin-releasing hormone.

A:Reference number: I57668; PMID:92347604; PMID:1353463

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-700 <RES>

A:Cross-references: GB:S40803; NID:g252163; PIDN:AAB22680.1; PID:g252164

C:Genetics:

A:Introns: 58/2; 82/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2

C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 51.18; Score 1797; DB 2; Length 700;  
Best Local Similarity 56.5%; Pred. No. 3.7e-117;  
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

Qy 28 PRNAIELRVLTKL--RVIPKGSFAGFDLKEIISQNDVLEIEADVFSLPKLHEIRI 85  
Db 51 PRAGL-ARLSITLPLVKVPSQAPRGLNEVVKIEISQSDSLERIEANAFDNLNLSLLI 109

Qy 86 EKANNLLYINPEAFONLPSRLYLISNTGKHLPAVHKIOSLQ-KVLLDIDQDNIHIVA 144  
Db 110 QNTKRLLYIEGAFNLPRKLSICNTGIRTPDVTKISSSEFNFILEICDNLHITIP 169

Qy 145 RNSFGLSFESVILWLSKNGIEETHNCAFNGTQDELNLSNNLBELPNDVFOGASGPV 204  
Db 170 GNAFOGMNNEVTLKLYGNGFEVQSHAFNGTTLSLELKENIYLEKMHSGAFQATGPS 229

Qy 205 ILDISRTKVLSPNHGLENLKLRRARSTYRLKLPNLDKFTVLMESALTYPSHCCAFANL 264  
Db 230 ILDISSTKLQALPHSGLESIQTLALSSYSLKTLPSKEFTSLVATLTPSHCCAFANL 289

Qy 265 KRQISELHPICNKLQDIDDMTQIGDQVSLIDDEPSYG---KGSDDMYNEFDYDLCN 321  
Db 290 PKK-----EQNFSFISFENFSKQCESTVRKADNETLYSAIFEENELSGWDYDYGFS 341

Qy 322 EVDVTCSPKPDANPCEDINGYILNRLVLIWFIISALITGNTVVLVLTTSQYKLTVPFR 381  
Db 342 PKT-LOCAPEDAFNPCEDINGYAFRLVLIWLIILAFGLNLTLVFLVLTTSRYKLTVPFR 400

Qy 382 LMCNLAFADICIGIYLLIASVDIHTKSOYHNYADMTGAGCDAAAGFTVFASLSVYT 441  
Db 401 LMCNLSPADFCMGLYLLIASVDSOTKGYIHNADMTGSGCGAAGFTVFASLSVYT 460

Qy 442 LTATLERTHTTTHAMOLECKVQLRHAASVMVLGNTFAFAALPFIPIGSISSYKVSICLP 501  
Db 461 LTVITLERWHITITAVDQKRLRLHRAIPMLGGNLFSTLIATWPLVGISNMYKVSICLP 520

Qy 502 MDIOSPLSOLVYMLLVNLVAFVVICGYYTHIYLVNPTIVSSSDTKAKRMATLIF 561  
Db 521 MDVESTLSQVLTSLILNNVAFVVICACYIRIYFAVQNPBELTAPNKNKTKAKRMATLIF 580

Qy 562 TDFLCMAIPSFASISAKLPLITVSKAKILLVLPINSCANPLFYAIFTKNFRDFFI 621  
Db 581 TDFTCMAIPSFASIAAFKVLITVTSKILLVLPINSCANPLFYAIFTKAQRDPL 640

Qy 622 ILSKFGCYEMQAQIYRTTSSATHNFARKSHCS 656  
Db 641 LLSRFGCKRRAELYRRK-----EFSATSNCKN 669

## RESULT 12

A49744

lutropin-choriogonadotropin receptor precursor - rat

N:Alternate names: luteinizing hormone-choriogonadotropin receptor

C:Species: Rattus norvegicus (Norway rat)

C:Date: 03-May-1994 #sequence\_revision 13-Sep-1998 #text\_change 13-Aug-1999

C:Accession: A49744; A40545; A41343; A61453; A32460

R:KOO, Y.B.; JI, I.; Slaughter, R.G.; JI, T.H.

Endocrinology 128, 2297-2308, 1991

A:Title: Structure of the luteinizing hormone receptor gene and multiple exons of the co

A:Reference number: A49744; MUID:91209270; PMID:2019252

A:Accession: A49744

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-700 &lt;KOO&gt;

A:Cross-references: GB:M68917

A:Note: authors translated the codon CAA for residue 307 as Glu, AAC for residue 355 as

R:Tsai-Morris, C.H.; Buczeko, E.; Wang, W.; Xie, X.Z.; Dufau, M.L.

J. Biol. Chem. 266, 11355-11359, 1991

A:Title: Structural organization of the rat luteinizing hormone (LH) receptor gene.

A:Reference number: A40545; MUID:91250455; PMID:2040640

A:Accession: A40545  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-320 <TSA>  
A:Cross-references: GB:M63918; GB:M63919; GB:M63920; GB:M63921; GB:M63922; GB:M63923;  
R:McFarland, K.C.; Sprengel, R.; Phillips, H.S.; Koehler, M.; Roseblitt, N.; Nikolic  
Science 245, 494-499, 1989  
A:Title: Lutropin-choriogonadotropin receptor: an unusual member of the G protein-cou  
A:Reference number: A41343; MUID:89332512; PMID:2502842

A:Accession: A41343

A:Molecule type: mRNA

A:Residues: 1-700 &lt;MCF&gt;

A:Cross-references: GB:M26199; NID:g205178; PIDN:AAA41528.1; PID:g205179

R:Dufau, M.L.; Minegishi, T.; Buczeko, E.S.; Delgado, C.J.; Zhang, R.

J. Steroid Biochem. 33, 715-720, 1989

A:Title: Characterization and structure of ovarian and testicular LH/hCG receptors.

A:Reference number: A61453; MUID:90097014; PMID:2601325

A:Accession: A61453

A:Status: preliminary

A:Molecule type: protein

A:Residues: 27-33, 'X', 35-37, 'X', 39, 'X', 41-44 &lt;DUF&gt;

R:Roche, P.C.; Ryan, R.J.

J. Biol. Chem. 264, 4636-4641, 1989

A:Title: Purification, characterization, and amino-terminal sequence of rat ovarian

A:Reference number: A32460; MUID:89174723; PMID:2925659

A:Accession: A32460

A:Molecule type: protein

A:Residues: 27-32, 'LX', 35-37 &lt;ROC&gt;

C:Genetics:

C:Introns: 58/2; 82/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2

C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat

C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone

F:54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR1&gt;

F:78-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR2&gt;

F:103-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR3&gt;

F:128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR4&gt;

F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR5&gt;

F:180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR6&gt;

F:202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR7&gt;

F:368-389/Domain: transmembrane #status predicted &lt;TM1&gt;

F:400-422/Domain: transmembrane #status predicted &lt;TM2&gt;

F:444-466/Domain: transmembrane #status predicted &lt;TM3&gt;

F:489-511/Domain: transmembrane #status predicted &lt;TM4&gt;

F:530-551/Domain: transmembrane #status predicted &lt;TM5&gt;

F:575-598/Domain: transmembrane #status predicted &lt;TM6&gt;

F:610-631/Domain: transmembrane #status predicted &lt;TM7&gt;

F:103, 178, 199, 295, 303, 317/Binding site: carboxylate (Asn) (covalent) #status predict

F:647, 648/Binding site: palmitate (Cys) (covalent) #status predicted

F:681/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict

Query Match 51.18; Score 1797; DB 2; Length 700;

Best Local Similarity 56.5%; Pred. No. 3.7e-117;

Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

Qy 28 PRNAIELRVLTKL--RVIPKGSFAGFDLKEIISQNDVLEIEADVFSLPKLHEIRI 85  
Db 51 PRAGL-ARLSITLPLVKVPSQAPRGLNEVVKIEISQSDSLERIEANAFDNLNLSLLI 109

Qy 86 EKANNLLYINPEAFONLPSRLYLISNTGKHLPAVHKIOSLQ-KVLLDIDQDNIHIVA 144  
Db 110 QNTKRLLYIEGAFNLPRKLSICNTGIRTPDVTKISSSEFNFILEICDNLHITIP 169

Qy 145 RNSFGLSFESVILWLSKNGIEETHNCAFNGTQDELNLSNNLBELPNDVFOGASGPV 204  
Db 170 GNAFOGMNNEVTLKLYGNGFEVQSHAFNGTTLSLELKENIYLEKMHSGAFQATGPS 229

Qy 205 ILDISRTKVLSPNHGLENLKLRRARSTYRLKLPNLDKFTVLMESALTYPSHCCAFANL 264  
Db 230 ILDISSTKLQALPHSGLESIQTLALSSYSLKTLPSKEFTSLVATLTPSHCCAFANL 289

Qy 265 KRQISELHPICNKLQDIDDMTQIGDQVSLIDDEPSYG---KGSDDMYNEFDYDLCN 321  
Db 290 PKK-----EQNFSFISFENFSKQCESTVRKADNETLYSAIFEENELSGWDYDYGFS 341

Oy 322 EYDVTCSKPAQNPCEIDMGYNILRVILNFIISLITAGTNTVTLVLTSTQYKLVDP 381  
Db 342 PKT-LQCAPDPAFNPCEIDMGYNILRVILNFIISLITAGTNTVTLVLTSTQYKLVDP 400  
Oy 382 LKCNLAFADLCIGIYLLLTASVDSVHTKSOYHNATIDMOTGACDAGCFFTFVASELSVYT 441  
Db 401 LKCNLAFADLCIGIYLLLTASVDSVHTKSOYHNATIDMOTGACDAGCFFTFVASELSVYT 460  
Oy 442 LTAITLPHMTTHAMOLECKVLRHAAVNVGLMTFAFAALPPIFGISSYKVSICLP 501  
Db 461 LTAITLPHMTTHAMOLECKVLRHAAVNVGLMTFAFAALPPIFGISSYKVSICLP 520  
Oy 502 WDIDSELSQYLYVLLVAFVVCIGCTHYTHLVNPTVSSSDTKAKMATIIP 561  
Db 521 WDIDSELSQYLYVLLVAFVVCIGCTHYTHLVNPTVSSSDTKAKMATIIP 580  
Oy 562 TDFLCNAPISFAISLAKVPLTVSKAKILLVLPVNSCANPELVAFITKAPRDEFI 621  
Db 581 TDFLCNAPISFAISLAKVPLTVSKAKILLVLPVNSCANPELVAFITKAPRDEFI 640  
Oy 622 LSKFPCYEMOAIYRTTSATNTHPARKSHSS 656  
Db 641 LSKFPCYEMOAIYRTTSATNTHPARKSHSS 669  
RESULT 13  
CHUUT  
Lutropin-choriogonadotropin receptor precursor - human  
M:Complete: Lutropin-choriogonadotropin receptor precursor long splice form; lutropin-choriogonadotropin receptor precursor  
N:Complete: Lutropin-choriogonadotropin receptor precursor long splice form; lutropin-choriogonadotropin receptor precursor  
C:Species: Homo sapiens  
C:Date: 22-Jun-1993  
R:Accession: A36243; B36243; A33728; B36120  
R:Minigene: T.; Nakamura, K.; Takakura, Y.; Miyamoto, K.; Hasegawa, Y.; Ibuki, Y.; Igara  
Biochem. Biophys. Res. Commun. 172, 1049-1054, 1990  
A:Title: Cloning and sequencing of human LH/hCG receptor cDNA.  
A:Reference number: A36243; MUID:91058534; PMID:2244890  
A:Accession: A36243  
A:Molecule type: mRNA  
A:Residues: 1-699 <MT>  
A:Cross-references: GB:663108; NID:9187135; PID:AAA59515.1; PID:9187136  
A:Experimental source: ovary  
A:Accession: B36243  
A:Residue type: mRNA  
R:Jita, X.C.; Oikawa, M.; Bo, M.; Tanaka, T.; NY, T.; Boime, I.; Hsueh, A.J.W.  
Mol. Endocrinol. 5, 759-768, 1991  
A:Title: Expression of human luteinizing hormone (LH) receptor: interaction with LH and  
A:Reference number: A33728; MUID:92017881; PMID:1922095  
A:Accession: A33728  
A:Molecule type: mRNA  
A:Residues: 1-123, 'R', 125-311, 'N', 313-699 <JTA>  
A:Cross-references: GB:857793  
A:Experimental source: ovary granulosa and luteal cells; thyroid  
A:Note: 312-Ser was also found; the authors translated the codon UAC for residue 546 as  
A:Note: mRNA from the thyroid is incompletely processed compared with that from the ova  
R:Fraser, A.L.; Robbins, L.S.; Stork, P.J.; Sprengel, R.; Segaloff, D.L.; Cone, R.D.  
Mol. Endocrinol. 4, 1284-1276, 1990  
A:Title: Isolation of cDNA and LH/hCG receptor cDNAs from human thyroid: regulation by tis  
A:Reference number: A36120; MUID:91159582; PMID:2295030  
A:Accession: B36120  
A:Molecule type: mRNA  
A:Status: not compared with conceptual translation  
A:Residues: 1-6, 'P', 8-18, 'A', 20-26, 'R', 29-43, 'A', 45, 'A', 47, 'RPS', 52-67, 'S', 69-123, 'R', 12  
A:Cross-references: GB:M73746; NID:9903745; PID:AAA70231.1; PID:9903746  
A:Experimental source: thyroid  
R:Zhu, H.; Wang, H.; Ascoli, M.  
Mol. Endocrinol. 9, 141-150, 1995  
A:Title: The lutropin/choriogonadotropin receptor is palmitoylated at intracellular cyst  
A:Reference number: A37564; MUID:9595727; PMID:7776964  
A:Contents: Annotation; mutation analysis of palmitate binding sites  
C:Genetics:

A:Gene: GDB:LUHGR  
A:Cross-references: GDB:125260; OMIM:152790  
A:Map position: 2p21-2p21  
A:Note: The exact position of the intron cannot be determined from the experimental d  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone; repeat  
F:1-699/Product: lutropin-choriogonadotropin receptor precursor; long splice form Fat  
F:1-226,290-699/Product: lutropin-choriogonadotropin receptor precursor, short splice  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-644/Product: lutropin-choriogonadotropin receptor #status predicted <MAT>  
F:23-363/Domain: extracellular hormone binding #status predicted <EBB>  
F:30-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:39-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:99-125/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:124-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:173-173/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:178-232/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:364-385/Domain: transmembrane #status predicted <TM>  
F:396-418/Domain: transmembrane #status predicted <TM2>  
F:441-462/Domain: transmembrane #status predicted <TM3>  
F:483-505/Domain: transmembrane #status predicted <TM4>  
F:526-547/Domain: transmembrane #status predicted <TM5>  
F:571-594/Domain: transmembrane #status predicted <TM6>  
F:606-627/Domain: transmembrane #status predicted <TM7>  
F:645-699/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F:99-174,195,231,299,313/Binding site: carbohydrate (Asn) (covalent) #status predict  
F:561,677/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pred  
F:643-644/Binding site: palmitate (Cys) (covalent) #status experimental  
F:670/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predict  
Query Match 50.5% Score 1776; DB 1; Length 699:  
Best Local Similarity 55.4%; Pred. No. 1,1e-115;  
Matches 349; Conservative 107; Mismatches 148; Indels 26; Gaps 6;  
Oy 38 LTKL-----RVTPKSGFAGDLEKIEISQNDVLETVADVPSNPLKLEIRKANN 90  
Db 51 LTRLSLAVLVVVPVPSQAFGLNEVIEKIEISQDSISLERIEANAFONLLMLSEILQNTKN 110  
Oy 91 LVYINPEAFONPLSLVLLISNTGINKHLPVHKI-OSLQKVLDDIOININHIHVARNSFM 149  
Db 111 LVRIEPAFTNPLGLKYLTCINTGIRKFPDVTKVFSSSENFILICDNLHITIPGNAFQ 170  
Oy 150 GLSPFVILMSKNGIEEIHNCAPNCTQDNLNLDNNLEELPNDFVQAGSPVILDIS 209  
Db 171 GHNESVTLKLYNGFEVSHAFNFTLTSLEKENVHLEKHNGAFRGATGPTLDIS 230  
Oy 210 RTKVSILNIGLEKLLKARSTYTRKLLPNLQKFTPLMEASLTYPSCCAFAFLKROIS 269  
Db 231 STKLQALPSVGLSEIQRLNLYSSLSKLPSTRETFWLLLETLITFSCCAFNLC----- 285  
Oy 270 ELHPICNKSILRQDIDDMOTIGDORVSLIDDEPSYK---GSDMKNYEPDYLCNEVDV 326  
Db 286 ---PTKEQNFHSISENFSKCESTVRKVSNTKLYSSMLAESELSGMDYEGFLPKTP- 341  
Oy 327 TCSKPDPAFNPCEIDMGYNILRVILNFIISLITAGTNTVTLVLTSTQYKLVDPFLMCLN 386  
Db 342 RCAPEDPAFNPCEIDMGYNILRVILNFIISLITAGTNTVTLVLTSTQYKLVDPFLMCLN 401  
Oy 387 AFADLCIGIYLLLTASVDSVHTKSOYHNATIDMOTGACDAGCFFTFVASELSVYTITAIT 446  
Db 402 SFADPCGLYLLLTASVDSVHTKSOYHNATIDMOTGACDAGCFFTFVASELSVYTITAIT 461  
Oy 447 LERHWTTHAMOLECKVLRHAAVNVGLMTFAFAALPPIFGISSYKVSICLPMDIDS 506  
Db 462 LERHWTTHAMOLECKVLRHAAVNVGLMTFAFAALPPIFGISSYKVSICLPMDIVET 521  
Oy 507 PLSQYVALLVNVAFVVCIGCTHYTHLVNPTVSSSDTKAKMATIIPDTFLC 566  
Db 522 TLSQYVALLVNVAFVVCIGCTHYTHLVNPTVSSSDTKAKMATIIPDTFLC 581  
Oy 567 MAPISFAISLAKVPLTVSKAKILLVLPVNSCANPELVAFITKAPRDEFI 626



A:Reference number: S38280; MUID:94019814; PMID:8413627  
A:Accession: S38280  
A:Molecule type: DNA  
A:Residues: 615-642 <PAR>  
A:Experimental source: Thyroid adenomas  
A:Note: mutations to Cys-619 or to Ile-623 in hyperfunctioning thyroid adenomas cause co  
C:Comment: See PIR:JC1319 for a splice form of thyrotropin receptor which lacks the seve  
C:Genetics:  
A:Gene: GDB:TSHR  
A:Cross-references: GDB:125313; OMIM:275200  
A:Map position: 14q31-14q31  
A:Introns: 231/2  
A:Note: the list of introns is incomplete; the eighth of eight introns is shown  
C:Function:  
A:Description: receptor that mediates the biochemical effects of thyrotropin  
C:Description: Glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat h  
C:Description: signal transducing G protein-coupled receptor; glycoprotein; hormone rece  
F:1-21/Domain: signal transducing G protein-coupled receptor  
F:22-76/Product: thyrotropin receptor predicted <LRR1>  
F:53-76/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:152-176/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:201-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:419-440/Domain: transmembrane #status predicted <TM1>  
F:451-473/Domain: transmembrane #status predicted <TM2>  
F:496-517/Domain: transmembrane #status predicted <TM3>  
F:538-560/Domain: transmembrane #status predicted <TM4>  
F:580-602/Domain: transmembrane #status predicted <TM5>  
F:603-627/Domain: transmembrane #status predicted <TM6>  
F:628-652/Domain: transmembrane #status predicted <TM7>  
F:777-99,113,177,198,302/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.78; Score 1642.5; DB 1: Length 764;  
Best Local Similarity 49.28; Pred. No. 2, 3e-106;  
Matches 336; Conservative 110; Mismatches 182; Indels 55; Gaps 11;

Oy	6	CHCSN----	RVELQDSKVEIPEIDLPNMLELRLVLTKLRLPKGSPAGDLEKIEIS	61
Db	20	CECHQEDFRV-TCKD--	IORIPS-LPPSTOTLKLIETHLRIPSHAPSNLPNIRIVS	84
Oy	62	QNDVLEIVADVFNLPKLEIRTEKANNLYINPEAFORLPSRLYLLISMTGIRKLPAY	121	
Db	85	IDVTLOQLSHSFYNLKSVTHIEIRTNLTIIDPOLAKELPLKFLGIFNTGLKMFPL	144	
Oy	122	HKIOSIQ-KVLLDIQDNIHIVARNSPGLSPESVILMLSKNGIEEIHNCAPNGTQDLE	180	
Db	145	TVNVTSDIPIFLIEDRPTWTSIPVWNGCIGMETLKLKLYNNGFTSVGCTAFNGTKLDA	204	
Oy	181	LMLSDNNHLELNDPVGGA-SGPVLDISRTVUSLPHNGLENLKLBASTYRLKLP	239	
Db	205	VLLNKNKLVTDKDAFGVSGPSLDSVTSYALPSPKGLHLELIARNTWTLKLP	264	
Oy	240	NLQKFTVLMESALYTPSHCCAFANLKRQISELHPY-----RODIDDMT-----	288	
Db	265	LSLSFLHLTRADLSTPSHCCAFNKKIRKINGLESIMCNESHQSLRQKSVNALSPLHQ	324	
Oy	289	-----QIGDQVRSLID-----DEPSYKGSDM-----WYNE	314	
Db	325	EYENIGDSIVGTEKSKFODTHNHHYVFEDEDEIIGFGQELANPOETLQAFOSH	384	
Oy	315	FYDGLCNEDVDTCPKPDAPNCPEDIMGYNILRVLIWFIISLAICTNTTVLVVLTQY	374	
Db	385	YDTTICGSDEDAVCPKSDPDEPNCEIDIMGFRLRVWVPSLLALLGNFVLLILTSY	444	
Oy	375	KLVTPPRLKCNLPADLCIGYLLALLASVDIKTSQYHNYAIDHQTGACGACAGETVFA	434	
Db	445	KLAVPRLKCNLPADPCNGMTLLLIASVDLTTHSETYHNAIDMQTCPCGTAGPTVFA	504	
Oy	435	SELSVYTLTITLERNYITAFMRIDRKIRLRHACAIWVGWCCFLALLPLVGISSYA	564	

Db	505	SELSVYTLTITLERNYITAFMRIDRKIRLRHACAIWVGWCCFLALLPLVGISSYA	564
Oy	495	KVSICLPMDIDSPISQLYYNALLVNLVLAFFVIGCCYTHIYTVRNPTIVSSSDTKIAK	554
Db	565	KVSICLPMDIDSPISQLYYNALLVNLVLAFFVIGCCYTHIYTVRNPTIVSSSDTKIAK	624
Oy	555	RMATLIPTDFLCHAPISFPAISLASLAVPLITVSKAKILLVLPYDINSCANPFLYALPTKN	614
Db	625	RMAVLPTDFLCHAPISFPAISLASLAVPLITVSKAKILLVLPYDINSCANPFLYALPTKA	684
Oy	615	FRDFFILLSKFGCYVENQAQIYR	637
Db	685	FORDVFIILSKFGCKCKROAQYR	707

Search completed: June 16, 2003, 13:37:01  
Job time : 28.1704 secs



SMART: SM00013; LRRNT: 1.  
 DR PROSITE: PS00237; G-PROTEIN RECP\_FL1; 1.  
 DR PROSITE: PS50262; G-PROTEIN RECP\_FL2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Phosphorylation; Repeat; Leucine-rich repeat.  
 FT SIGNAL 1 17  
 FT CHAIN 18 692  
 FT DOMAIN 18 365  
 FT TRANSMEM 366 386  
 FT DOMAIN 387 397  
 FT TRANSMEM 398 420  
 FT DOMAIN 421 442  
 FT TRANSMEM 443 464  
 FT DOMAIN 465 484  
 FT TRANSMEM 485 507  
 FT DOMAIN 508 527  
 FT TRANSMEM 528 548  
 FT DOMAIN 550 572  
 FT TRANSMEM 573 596  
 FT DOMAIN 597 607  
 FT TRANSMEM 608 629  
 FT DOMAIN 630 692  
 FT REPEAT 44 68  
 FT REPEAT 69 93  
 FT REPEAT 119 143  
 FT REPEAT 170 192  
 FT REPEAT 193 216  
 FT REPEAT 218 240  
 FT REPEAT 441 516  
 FT DISULFID 441 516  
 FT CARBOHYD 191 191  
 FT CARBOHYD 199 199  
 FT CARBOHYD 293 293  
 SQ SEQUENCE 692 AA; 77681 MW; 267EA78C7CFD8EC6 CRC64;

Query Match 100.0%; Score 3516; DB 1; Length 692;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-219;  
 Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CHHWLCHS NRVLQDQSKVTETPTDLPRAIELRFLVTKLRVLPKGSFAGFGDLEKIEI 60  
 DB 18 CHHWLCHS NRVLQDQSKVTETPTDLPRAIELRFLVTKLRVLPKGSFAGFGDLEKIEI 77  
 OY 61 SONDVLEIADVFSLPKLHEIRIEKANNLLYNPEAFONLPSRLYLLSNTGKHLPA 120  
 DB 78 SONDVLEIADVFSLPKLHEIRIEKANNLLYNPEAFONLPSRLYLLSNTGKHLPA 137  
 OY 121 VHKIQSLQKVLDDIQDNNINIHIVARNFSGLSFESVILWLSKNGIEIHNCAFNGLTOLDE 180  
 DB 138 VHKIQSLQKVLDDIQDNNINIHIVARNFSGLSFESVILWLSKNGIEIHNCAFNGLTOLDE 197  
 OY 181 LNLSDNNLEELNDVFPQAGSGVILDSRTKVLHSLPNHGLENLKLRARSTYRLKLPN 240  
 DB 198 LNLSDNNLEELNDVFPQAGSGVILDSRTKVLHSLPNHGLENLKLRARSTYRLKLPN 257  
 OY 241 LDKFVTLEASLTVPSCCAFANLKRQISELHPICNKSILRODIDMTQIGDQVSLIDD 300  
 DB 258 LDKFVTLEASLTVPSCCAFANLKRQISELHPICNKSILRODIDMTQIGDQVSLIDD 317  
 OY 301 EPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPAFNPCEDIMGYNILRVILWFISILAIT 360  
 DB 318 EPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPAFNPCEDIMGYNILRVILWFISILAIT 377  
 OY 361 GNTTVLVLTTSQYKLVPRFLMCLNLAFLADICIGYLLLIASVDIHKYSQVHNVAIDWQT 420  
 DB 378 GNTTVLVLTTSQYKLVPRFLMCLNLAFLADICIGYLLLIASVDIHKYSQVHNVAIDWQT 437  
 OY 421 GAGCDAAGFFTVFASLSVYTLTATLIERWHITTHAMOLECKVQLRHAASVWVLGWTFAF 480  
 DB 438 GAGCDAAGFFTVFASLSVYTLTATLIERWHITTHAMOLECKVQLRHAASVWVLGWTFAF 497  
 OY 481 AAALFPFIFGSIYMKVSIICLPMDIDSPLSQLYVALLVNLVAFVWICGCTHYLYTVRN 540  
 DB 498 AAALFPFIFGSIYMKVSIICLPMDIDSPLSQLYVALLVNLVAFVWICGCTHYLYTVRN 557

## RESULT 2

FSHR\_MOUSE STANDARD; PRT; 692 AA.  
 AC P35378; Q9QW8; Q9D4C2;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).  
 DE FSHR.  
 GN FSHR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 OX [1]  
 RN [1]  
 RP STRAIN=129/Sv; TISSUE=Testis;  
 RC Tena-Sempere M., Manna P.R., Huhtaniemi I.T.;  
 RA "Molecular cloning of the mouse follicle stimulating hormone receptor complementary deoxyribonucleic acid: functional expression of alternatively spliced variants and receptor inactivation by a C56GT transition in exon 7 of the coding sequence."  
 RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzava K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE OF 1-51 FROM N.A.  
 RX MEDLINE=93093308; PubMed=1459341;  
 RA Huhtaniemi I.T., Eskola V., Pakarinen P., Matikainen T., Sprengel R.;  
 RA "The murine luteinizing hormone and follicle-stimulating hormone receptor genes: transcription initiation sites, putative promoter sequences and promoter activity."  
 RT Mol. Cell. Endocrinol. 88:55-66(1992).  
 RL -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.

Db	138	PHKTSIQKLVLLDDIOMNIHIIHIIARNSPGLSPESVYLWLNKNGIQEIHCAFNGTQDLE	139
Oy	181	LNLSDDNNWLEELPNVDFOGASGPVILDISRTKVIHSLPHNGLNKLKURARSTYELKKLPN	240
Db	198	LNLSDDNNWLEELPNVDFOGASGPVILDISRTKVIHSLPHNGLNKLKURARSTYELKKLPN	257
Oy	241	LQKFTVLPAESLTPSHCCAPANLKQISELHPICHKISILRODIDMTQIGDQRPSELDD	300
Db	258	LQKFTVLPAESLTPSHCCAFANRRQTSLEHPIGHNKISIRODIDMTQIGDQRPSELVDD	317
Oy	301	EPSTYKSGSDMHYNEDFDLCNEVNDVTCSPKPAFNPCEDIMGYNILRVLWFWISLTAIT	360
Db	318	EPSTYKSGSDMLYSEFDYDLNCFEVDVTCSPKPAFNPCEDIMGYNILRVLWFWISLTAIT	377
Oy	361	GNTTVLVLTTSQYKLVTPRFUMLCNLAFADLCIGIYLLLIASVDHTKSOYHNHTADMOT	420
Db	378	GNTTVLVLTTSQYKLVTPRFUMLCNLAFADLCIGIYLLLIASVDHTKSOYHNHTADMOT	437
Oy	421	GAGCDAAGPFTVFASLSVYTLAITLERMHTITHAMOLECKVOLRWASVWLWGTAF	480
Db	438	GAGCDAAGPFTVFASLSVYTLAITLERMHTITHAMOLECKVOLCHHAASVWLWGTAF	497
Oy	481	AAALFPIFGISSMYKVSICLUPMDISDPSQLYVNALVNLVAFVTCGCTHYIYLYVRN	540
Db	498	AAALFPIFGISSMYKVSICLUPMDISDPSQLYVNALVNLVAFVTCGCTHYIYLYVRN	557
Oy	541	PTVSSSSDTRKARKMATLFTDFLCHMAISFPAISAKLVPIYTSKAKILLVLYFPIN	600
Db	558	PTVSSSDTRKARKMATLFTDFLCHMAIPYFAISAKLVPIYTSKAKILLVLYFPIN	617
Oy	601	SCANPELVAFITFNFRDPTPLLSKFCCEYQAOIYKTFSSNTSHARKSHCCSAPRV	660
Db	618	SCANPELVAFITFNFRDPTPLVLSKFCCEYQAOIYKTFSSNTSHARKSHCCSAPRV	677
Oy	661	TSNSVYLVLPHNSQON 675	
Db	678	TSNSVYLVLPHNSVQN 692	

RESULT 3

FSHR\_HUMAN

ID	FSHR_HUMAN	STANDARD; PRG: 695 AA.
DC	P23945; 1992 (Rel. 21, Created)	
DT	01-JUN-1994 (Rel. 20, Sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).	
GN	FSHR.	
GN	On Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_Taxid:9606;	
RN	[1]	
RC	SEQUENCE FROM N.A.	
RC	MDLINE-91222171; PubMed-1709010;	
RC	MDLINE-91222171; PubMed-1709010;	
RT	Mineshish T., Nakamura K., Takakura Y., Ibuki Y., Igarashi M.;	
RT	"Cloning and sequencing of human FSH receptor cDNA";	
RL	Biochem. Biophys. Res. Commun. 175:1125-1130(1991).	
RL	[2]	
RC	SEQUENCE FROM N.A.	
RC	TISSUE-Testis;	
RC	MDLINE-93346012; PubMed-1301382;	
RC	Kailon C.A., Cheng S.V., Nugent N.P., Schweickhardt R.L.,	
RA	Rosenthal J.C., Overton S.A., Wands G.D., Kuzaja J.B., Luchette C.A.,	
RA	Shappel S.C.,	
RT	"The expression of the human follicle stimulating hormone receptor and	
RT	its expression in COS-7 CHO cells";	
RL	Mol. Cell. Endocrinol. 89:141-151(1992).	
RL	[3]	
RC	SEQUENCE FROM N.A.	

-!- SUBCELLULAR LOCATION: Integral membrane protein.  
 -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 PS1/SH/TSH SUBFAMILY  
 -!- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).

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EMBL: AF095642; AAC67559.1; .  
 EMBL: AK016635; BAB3035.1; .  
 EMBL: S49632; AAB24401.1; .  
 EMBL: M87570; AAA37641.1; .  
 MGD: MGI:95583; Fehr.  
 InterPro: IPR000376; GPCR\_Rhodopsn.  
 InterPro: IPR001611; LRR.  
 InterPro: IPR000372; LRR\_Nterm.  
 Pfam: PF00001; 7tm.1.1.  
 Pfam: PF00560; LRR.3.  
 Pfam: PF01462; LRRM.1.  
 Pfam: PF01463; LRRM.2.  
 SMART: SM00037; GPCRHDOPSN.  
 PROSITE: PS00217; LRR\_NTER\_PROTEIN\_RECEP\_F1\_1.  
 PROSITE: PS00262; G-PROTEIN\_RECEP\_F1\_2.  
 G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat.

SIGNAL		POTENTIAL	
CHAIN	1 692	FOLLICLE STIMULATING HORMONE RECEPTOR.	
DONAIN	18 365	EXTRACELLULAR (POTENTIAL).	
TRANSHEM	366 386	1 (POTENTIAL).	
DONAIN	387 397	CYTOPLASMIC (POTENTIAL).	
TRANSHEM	398 420	2 (POTENTIAL).	
DONAIN	421 442	EXTRACELLULAR (POTENTIAL).	
TRANSHEM	443 464	3 (POTENTIAL).	
DONAIN	465 484	CYTOPLASMIC (POTENTIAL).	
TRANSHEM	485 505	4 (POTENTIAL).	
DONAIN	506 527	EXTRACELLULAR (POTENTIAL).	
TRANSHEM	528 549	5 (POTENTIAL).	
DONAIN	550 572	CYTOPLASMIC (POTENTIAL).	
TRANSHEM	573 596	6 (POTENTIAL).	
DONAIN	597 607	EXTRACELLULAR (POTENTIAL).	
TRANSHEM	608 629	7 (POTENTIAL).	
DONAIN	630 692	CYTOPLASMIC (POTENTIAL).	
REPEAT	44 68	LRR 1.	
REPEAT	69 93	LRR 2.	
REPEAT	119 143	LRR 3.	
REPEAT	144 170	LRR 4.	
REPEAT	190 216	LRR 5.	
REPEAT	218 242	LRR 6.	
REPEAT	441 516	BY SIMILARITY	
CARBOHYD	191 191	N-LINKED (GLCNAC. ) (POTENTIAL).	
CARBOHYD	199 199	N-LINKED (GLCNAC. ) (POTENTIAL).	
CARBOHYD	293 293	N-LINKED (GLCNAC. ) (POTENTIAL).	
CONFLICT	436 436	O > K (IN REF. 2).	
SEQUENCE	692 AA;	77769 MW; 4857229180563444 CRC64;	

Query Match 95.2%; Score 3346; DB 1; Length 692;  
 Best local similarity 94.2%; Pred. No. 5,7e-208;  
 Matches 636; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

1 CHRWLCNSRVPLQCDQSKVTEIPDLPNNALIELRVTLKLVYKPGSGFQDLKEI 60  
 18 CHRWLCNSRVPLQCDQSKVTEIPDLPNNALIELRVTLKLVYKPGSGFQDLKEI 77  
 61 SONDVLEIADVFNPLKPLHEIRTEKANNLLYNPEAFQNLPSRLYLLISNTGKILPA 120  
 78 SONDVLEIADVFNPLKPLHEIRTEKANNLLYNPEAFQNLPSRLYLLISNTGKILPA 137  
 121 VHKIQSLQKVLIDQDNTNIHIVANSPFGLSPFESVILWLSKNGIETZHNCFNQTOLDE 180



RA Tilly L.T., Aihara T., Nishimori K., Jai X.-C., Billig H.,  
 RA Kowalski K.I., Perles E.A., Hsueh A.J.;  
 RL Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-342 FROM N.A.  
 RC TISSUE-Testis;  
 RX MEDLINE-93075197; PubMed-1359889;  
 RA Gromoll J., Gudermann T., Nieschlag E.;  
 RT "Molecular cloning of a truncated isoform of the human follicle  
 RT stimulating hormone receptor";  
 RL Biochem. Biophys. Res. Commun. 188:1077-1083(1992).  
 RN [5]  
 RP SEQUENCE OF 1-51 FROM N.A.  
 RX MEDLINE-95011044; PubMed-7926278;  
 RA Gromoll J., Dankbar B., Gudermann T.;  
 RT "Characterization of the 5' flanking region of the human follicle-  
 RT stimulating hormone receptor gene";  
 RL Mol. Cell. Endocrinol. 102:93-102(1994).  
 RN [6]  
 RP 3D-STRUCTURE MODELING OF 49-228.  
 RX MEDLINE-96363672; PubMed-8747461;  
 RA Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H.,  
 RA Hendrickson W.A., el Tayar N.;  
 RT "Structural predictions for the ligand-binding region of glycoprotein  
 RT hormone receptors and the nature of hormone-receptor interactions";  
 RL Structure 3:1341-1353(1995).  
 CC 1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY  
 CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
 CC ADENYLATE CYCLASE.  
 CC 1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC 1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC 1- TISSUE SPECIFICITY: SERTOLI CELLS AND OVARIAN GRANULOSA CELLS.  
 CC 1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC FSH/LSH/TSH SUBFAMILY.  
 CC 1- SIMILARITY: CONTAINS 5 LEUCINE-RICH REPEATS (LRR).  
 CC -----  
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 CC -----  
 DR EMBL; M65085; AAA52477.1;  
 DR EMBL; S59900; AAB26480.1;  
 DR EMBL; M55489; AAA52478.1;  
 DR EMBL; X68044; CAA48179.1;  
 DR EMBL; S73199; AAB32071.1;  
 DR PIR; JN0122; JN0122.  
 DR PDB; 1XUN; 15-MAY-97.  
 DR Genew; HGNC:3969; FSHR.  
 DR MIM; 136435.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR Pfam; PF00560; LRR; 3.  
 DR Pfam; PF01482; LRRNT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1;  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing;  
 KW 3D-structure.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.  
 FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 367 387 1 (POTENTIAL).  
 FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 399 421 2 (POTENTIAL).  
 FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	444	465	3 (POTENTIAL).
FT	DOMAIN	466	485	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	486	508	4 (POTENTIAL).
FT	DOMAIN	509	528	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	529	550	5 (POTENTIAL).
FT	DOMAIN	551	573	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	574	597	6 (POTENTIAL).
FT	DOMAIN	598	608	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	609	630	7 (POTENTIAL).
FT	DOMAIN	631	695	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	69	93	LRR 1.
FT	REPEAT	119	143	LRR 2.
FT	REPEAT	170	192	LRR 3.
FT	REPEAT	193	216	LRR 4.
FT	REPEAT	218	240	LRR 5.
FT	DISULFID	442	517	BY SIMILARITY.
FT	CARBOHYD	191	191	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	199	199	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	318	318	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPPLIC	224	285	MISSING (IN SHORT ISOFORM).
FT	VARSPPLIC	342	695	MISSING (IN SHORT ISOFORM).
FT	CONFLICT	13	13	S -> R (IN REF. 4).
FT	CONFLICT	112	112	N -> T (IN REF. 1).
FT	CONFLICT	197	198	EL -> AV (IN REF. 1).
FT	CONFLICT	295	295	S -> P (IN REF. 4).
FT	CONFLICT	307	307	T -> A (IN REF. 1).
FT	CONFLICT	680	680	N -> S (IN REF. 1).
SQ	SEQUENCE	695 AA; 78294 MW; 723B8E71F76D2CD5 CRC64;		

Query Match 90.1%; Score 3169.5; DB 1; Length 695;  
 Best Local Similarity 89.5%; Pred. No. 1.3e-196;  
 Matches 607; Conservative 31; Mismatches 37; Indels 3; Gaps 2;

QY	1	CHHWLCHSNNRVFLCQDSKVTEIPTDLPRNATELRFVLTKLVRIPKSGPAGDLEKIEI	60
DB	18	CHHRICHGNSRVFLCQESKVTEIPSDLPNATELRFVLTKLVRIPKSGPAGDLEKIEI	77
QY	61	SONDVELEADVFNPKLHEIRIEKANLNYINPEAFONLPSRLYLSINTGKHLPA	120
DB	78	SONDVELEADVFNPKLHEIRIEKANLNYINPEAFONLPSRLYLSINTGKHLPD	137
QY	121	VHKIOSLQKVLIDQDNIHIVARNFGLSFESVILWLSKNGIEIINCAFNPGTOLDE	180
DB	138	VHKIHSLOKVLIDQDNIHIVARNFGLSFESVILWLSKNGIEIINCAFNPGTOLDE	197
QY	181	LNLSDNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKKLPN	240
DB	198	LNLSDNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKKLPN	257
QY	241	LKFVTLMEASLTYPSSHCAFANLKRQISELHPICNKSILRQDIDMTQIGDORVSLDD	300
DB	258	LEKLVALMEASLTYPSSHCAFANWRQISELHPICNKSILRQEVDMYTMOTRGORSLLAE	317
QY	301	-EFSYCKGSDMYNEEDYDLCEVVDVTCSPKDAFNPCEDINGYNLRVLIWFISILAI	359
DB	318	NESSYRGEDMTYTFEDYDLCEVVDVTCSPKDAFNPCEDINGYNLRVLIWFISILAI	377
QY	360	TGNTTVLWLTTSQYKLTVPFLMCMNLAFLADLCIGIYLLLIASVDIHTKSOYHNYAIDWQ	419
DB	378	TGNTTVLWLTTSQYKLTVPFLMCMNLAFLADLCIGIYLLLIASVDIHTKSOYHNYAIDWQ	437
QY	420	TGACDAAAGFTVFASLSVYTLTATLERWHTITHAMQLECKVQLRHAASVAVLGTWFA	479
DB	438	TGACDAAAGFTVFASLSVYTLTATLERWHTITHAMQLECKVQLRHAASVAVLGTWFA	497
QY	480	FAAALPIFGISSYMKVSIKLPMDIDSPLSQVYMLLVNLVAFVVICCYTHIYLTVR	539
DB	498	FAAALPIFGISSYMKVSIKLPMDIDSPLSQVYMLLVNLVAFVVICCYTHIYLTVR	557
QY	540	NPTIVSSSDTKIAKRAMTLIFTDFLCMAPISFAISAKLVPLITYSKAKILLVLPYPI	599
DB	558	NPTIVSSSDTKIAKRAMTLIFTDFLCMAPISFAISAKLVPLITYSKAKILLVLPYPI	617



RESULT 5  
FSHR\_BOVIN STANDARD: PRT; 695 AA.

AC P35376;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).  
DE FSHR.  
GN Bos taurus (Bovine).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Holstein; TISSUE=Ovary, and Testis;  
RC MEDLINE=95127199; PubMed=7826612;  
RX Houde A., Lambert A., Saumande J., Silversides D.W., Lussier J.G.;  
RA "Structure of the bovine follicle-stimulating hormone receptor  
RT complementary DNA and expression in bovine tissues.";  
RL Mol. Reprod. Dev. 39:127-135(1994).  
CC -!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY  
CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
CC ADENYLATE CYCLASE.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC FSH/LSH/TSH SUBFAMILY.  
CC -!- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
CC  
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CC  
DR EMBL; L22319; AAC37324.1; -.  
DR HSSP; P23945; 1XUN.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR Pfam; PF00560; LRR; 4.  
DR Pfam; PF01462; LRRNT; 1.  
DR SMART; SM00013; LRRNT; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECF\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECF\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Phosphorylation; Repeat; Leucine-rich repeat.  
FT SIGNAL 1  
FT CHAIN 17  
FT CHAIN 18  
FT DOMAIN 18  
FT DOMAIN 18  
FT TRANSMEM 367  
FT TRANSMEM 387  
FT TRANSMEM 388  
FT TRANSMEM 399  
FT TRANSMEM 422  
FT TRANSMEM 444  
FT TRANSMEM 466  
FT TRANSMEM 485  
FT TRANSMEM 508  
FT TRANSMEM 509  
FT TRANSMEM 529  
FT TRANSMEM 531  
FT TRANSMEM 551  
FT TRANSMEM 574  
FT TRANSMEM 598  
FT TRANSMEM 609  
FT TRANSMEM 631  
FT REPEAT 44  
FT REPEAT 68  
FT REPEAT 69

FT REPEAT 119 143 LRR 3.  
FT REPEAT 170 192 LRR 4.  
FT REPEAT 193 216 LRR 5.  
FT REPEAT 218 240 LRR 6.  
FT DISULFID 442 517 BY SIMILARITY.  
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 695 AA; 78084 MW; 18F9DFEFC046380D CRC64;  
Query Match 89.5%; Score 3145.5; DB 1; Length 695;  
Best Local Similarity 87.9%; Pred. No. 4.5e-195;  
Matches 596; Conservative 45; Mismatches 34; Indels 3; Gaps 2;  
QY 1 CHHWLCHSNNRVFLCQDSKVTETPTDLPRNAIELRVLTKLRTVPKSPAGFGDLEKIEI 60  
DB 18 CHHRLCHCSNGVFLCQESKVTETPTDPRDAVELRVLTKLRTVPKSPAGFGDLEKIEI 77  
QY 61 SQNDVLEIVADVFENLPKLEIRIEKANNLLYNPEAFQNLPSRLRYLLISNTGKHLPA 120  
DB 78 SQNDVLEIVANVFENLPKLEIRIEKANNLLYIDPDQFQNLPLNRYLLISNTGKHLPA 137  
QY 121 VHKIQSLQKVLDDIQDNINITHIVARNSPFGLSPESVILMSKNGIEIHNCAFNQTLDE 180  
DB 138 VHKIQSLQKVLDDIQDNINITHIVARNSPFGLSPESVILMSKNGIEIHNCAFNQTLDE 197  
QY 181 LNLSDNNLELNDVFGGASGPVILDSRTKVHSLNHNGLNKKLRARSTYRLKLPN 240  
DB 198 LNLSDNNLELNDVFGGASGPVILDSRTKIRISLPSYGLNKKLRANSTYRLKLPN 257  
QY 241 LDKFVTLMEASLTYPSPHCCAFANLKRQISELHPICNKSILRQDIDDDMTQIGDQSVLT-D 299  
DB 258 LDKFVTLMEASLTYPSPHCCAFANRRQTSDLHPICNKSILRQEDVDDMTQAGQSVLAED 317  
QY 300 DEPSYKSGDMMYNEFDYDLCNEVVDVTCSPKPAFNPCEPDIMGNILRVLIWFISILAI 359  
DB 318 DEPSYKSGDMMYNEFDYDLCNEVVDVTCSPKPAFNPCEPDIMGNILRVLIWFISILAI 377  
QY 360 TGNNTVLVLTTSYKLTVPREFLNCNLAFADLCIGIYLLIASVDIHTKSOYHNVAIDMQ 419  
DB 378 TGNLVLVLTTSYKLTVPREFLNCNLAFADLCIGIYLLIASVDVHTKTEHNVAIDMQ 437  
QY 420 TGACGDAAGFTVPFASLSVYTLTAITLERHHTITHAMOLECKVQLRHAASVMVLGWTFA 479  
DB 438 TGACGDAAGFTVPFASLSVYTLTAITLERHHTITHAMOLECKVQLRHAASVMVLGWTFA 497  
QY 480 FFAALPFIPIGSISSYMKVSCICLPMDIDSPLSOLYVALLVNLVAFVVICGCTHYIYLVTR 539  
DB 498 FFAALPFIPIGSISSYMKVSCICLPMDIDSPLSOLYVALLVNLVAFVVICGCTHYIYLVTR 557  
QY 540 NPTIVSSSDTKIAKRWATLITDPLCMAPISFFAISASLKVPLITVSKAKILLVLFYPI 599  
DB 558 NPNITSSSDTKIAKRWAMLIITDPLCMAPISFFAISASLKVPLITVSKAKILLVLFYPI 617  
QY 600 NSCANPELYAIFTNFRDFFILLSKFCGYEQMAQIYRTSSATHNPHARKSHCSSAPR 659  
DB 618 NSCANPELYAIFTNFRDFFILLSKFCGYEQMAQIYRTSSATHNPHARKSHCSSAPR 677  
QY 660 VTN--SYVLVPLNHSSQN 675  
DB 678 VTNGSNYTLPLRLHAKN 695

## RESULT 6

FSHR\_SHEEP

ID FSHR\_SHEEP STANDARD; PRT; 695 AA.  
AC P35379; Q28573; Q28574; Q9TS19;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).  
GN FSHR.

OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 ON NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R1).  
 RC TISSUE=Testis;  
 RX MEDLINE=93351750; PubMed=8394255;  
 RA Yarney T.A., Sairam M.R., Khan H., Ravindranath N., Payne S.,  
 RA Seidah N.G.;  
 RT "Molecular cloning and expression of the ovine testicular follicle  
 RT stimulating hormone receptor";  
 RL Mol. Cell. Endocrinol. 93:219-226(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R2).  
 RC STRAIN=Dorset-Leicester-Suffolk 1; TISSUE=Testis;  
 RX MEDLINE=93176195; PubMed=8439338;  
 RA Khan H., Yarney T.A., Sairam M.R.;  
 RT "Cloning of alternatively spliced mRNA transcripts coding for variants  
 RT of ovine testicular follicle stimulating hormone receptor lacking the G protein  
 RT coupling domains";  
 RL Biochem. Biophys. Res. Commun. 190:888-894(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R3), AND CHARACTERIZATION.  
 RC STRAIN=Dorset-Leicester-Suffolk 1; TISSUE=Testis;  
 RX Yarney T.A., Jiang L., Khan H., MacDonald E.A., Laird D.W.,  
 RA Sairam M.R.;  
 RT "Molecular cloning, structure, and expression of a testicular  
 RT follicle stimulating hormone receptor with selective alteration in the carboxy terminus  
 RT that affects signaling function";  
 RL J. Biol. Reprod. Dev. 48:436-470(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R3), AND CHARACTERIZATION.  
 RC STRAIN=Dorset-Leicester-Suffolk 1; TISSUE=Ovary;  
 RX MEDLINE=20391225; PubMed=10527886;  
 RA Babu P.S., Jiang L., Sairam A.M., Touyz R.M., Sairam M.R.;  
 RT "Structural features and expression of an alternatively spliced growth  
 RT factor type I receptor for follicle stimulating hormone in the developing  
 RT ovary";  
 RL Mol. Cell Biol. Res. Commun. 2:21-27(1999).  
 RN [5]  
 RP SEQUENCE OF 1-51 FROM N.A.  
 RX MEDLINE=98031017; PubMed=9364442;  
 RA Sairam M.R., Subbayan V.S.R.;  
 RT "Cloning and characterization of the human follicle stimulating hormone receptor gene";  
 RL Mol. Reprod. Dev. 48:480-487(1997).  
 CC [1] FUNCTION: Receptor for follicle stimulating hormone. The activity  
 CC of isoform FSH-R1 is mediated by G proteins which activate  
 CC adenylyl cyclase. Isoforms FSH-R2 and FSH-R3 also bind FSH, but  
 CC this does not result in activation of adenylyl cyclase. Isoform  
 CC FSH-R3 may be involved in calcium signaling.  
 CC [2] SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane  
 CC (isoforms FSH-R1 and FSH-R2); Cell surface (isoform FSH-R3).  
 CC [3] ALTERNATIVE PRODUCTS: 4 isoforms; FSH-R1 (shown here), FSH-R2,  
 CC FSH-R3 and FSH-R4; are produced by alternative splicing.  
 CC [4] TISSUE SPECIFICITY: Isoform FSH-R3 is expressed in ovary and  
 CC testis, but not in kidney.  
 CC [5] SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC [6] SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
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DR EMBL: L12766; AAA31523.1;  
 DR EMBL: L12767; AAA31524.1;  
 DR EMBL: L33175; AK006049.1;  
 DR EMBL: L33176; AK006050.1;  
 DR EMBL: AF090438; AAC61749.1;  
 DR PIR: JCI493; JCI493;  
 DR HSP: P23945; IJUN;  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR InterPro: IPR001611; LRR\_Nterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR Pfam: PF00560; LRR; 4.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR SMART: SM00013; LRRNT; 1.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE: PS00262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing.  
 FT SIGNAL  
 FT 1 POLYCLIC STIMULATING HORMONE RECEPTOR.  
 FT 2 POTENTIAL.  
 FT 3 EXTRACELLULAR (POTENTIAL).  
 FT 4 CYTOPLASMIC (POTENTIAL).  
 FT 5 POTENTIAL.  
 FT 6 EXTRACELLULAR (POTENTIAL).  
 FT 7 POTENTIAL.  
 FT 8 CYTOPLASMIC (POTENTIAL).  
 FT 9 POTENTIAL.  
 FT 10 EXTRACELLULAR (POTENTIAL).  
 FT 11 POTENTIAL.  
 FT 12 CYTOPLASMIC (POTENTIAL).  
 FT 13 EXTRACELLULAR (POTENTIAL).  
 FT 14 POTENTIAL.  
 FT 15 BY SIMILARITY.  
 FT 16 N-LINKED (GLYCAC. .) (POTENTIAL).  
 FT 17 N-LINKED (GLYCAC. .) (POTENTIAL).  
 FT 18 N-LINKED (GLYCAC. .) (POTENTIAL).  
 FT 19 LISMTGK -> FKRRNRI (IN ISOFORM FSH-R4).  
 FT 20 MISSING (IN ISOFORM FSH-R4).  
 FT 21 DISNTRISLPSTGLNMLKRMSTYHLKLPSE ->  
 FT 22 LKCHAHLSQSTFYCCQREHISEFOLASKQHPN (IN  
 FT 23 ISOFORM FSH-R3).  
 FT 24 MISSING (IN ISOFORM FSH-R3).  
 FT 25 KGCYEVQVQVRSSTAHNPRNG -> LHCCTVGLI  
 FT 26 CNHPSLPVARGNIFLND (IN ISOFORM FSH-R2).  
 FT 27 MISSING (IN ISOFORM FSH-R2).  
 FT 28 PBF75D89D8C0D4B CRC64;  
 SQ SEQUENCE 695 AA; 78237 MW; PBF75D89D8C0D4B CRC64;  
 Query Match 89.3%; Score 3140.5; DB 1; Length 695;  
 Best Local Similarity 87.5%; Pred. No. 9.4e-195;  
 Matches 593; Conservative 47; Mismatches 35; Indels 3; Gaps 2;  
 OY 1 CHHMLCHSNRVFLQDSKVTETPTDLPNATLRLVTLKRVIPKGSFAGGDEKIEI 60  
 DB 18 CHHRLCHSNRVFLQDSKVTETPTDLPNATLRLVTLKRVIPKGSFAGGDEKIEI 77  
 OY 61 SONDYLEVTEADYFSLPKLHEIRERKANNLLYNPEAFQPLSLYLLISWTGKILPA 120  
 DB 78 SONDYLEVTEADYFSLPKLHEIRERKANNLLYIDPAFQPLSLYLLISWTGKILPA 137  
 OY 121 VHKIOSLOKVLDDTNTNITVANSFGLSPESVILWLSKNGIEETHCAPNCTOLDE 180  
 DB 138 VHKIOSLOKVLDDTNTNITVANSFGLSPESVILWLSKNGIEETHCAPNCTOLDE 197

Qy 181 LNLSDNNLELPNDVFGAGSPVILDSRTKVLHSLPNHGLEKLLKLRARSTYRLKKLPN 240  
D 198 LNLSDNSNLELPNDVFGAGSPVILDSRTKVLHSLPNHGLEKLLKLRARSTYRLKKLPN 257  
Qy 241 LDKFVTLWASLTYPSCCHAFANUKROISELHPICNKSILRQDIDDMTQIGDQORVSLI-D 299  
D 258 LEKFTVTLWASLTYPSCCHAFANRRQTSDLHPICNKSILRQEVDDMTQARGORISLAED 317  
Qy 300 DEPSYGRGSDMYNEFDYDLCLNEVDVTCSPKDPADFNPCEDIMCYNILRLVLIWIFISLAI 359  
D 318 DEPSYGRGSDMYNEFDYDLCLNEVDVTCSPKDPADFNPCEDIMCYNILRLVLIWIFISLAI 377  
Qy 360 TGNITVLTWLTTSYKLTVPFRLMCLNLAFLADLCIGIYLLIASVDIHTKSOYHNYAIDWQ 419  
D 378 TGNITVLTWLTTSYKLTVPFRLMCLNLAFLADLCIGIYLLIASVDIHTKSOYHNYAIDWQ 437  
Qy 420 TGACDAAAGFTVPFASLSVYTLTAITLERWHTITHAMQLECKVQLRHAASVMVLGWTFA 479  
D 438 TGACDAAAGFTVPFASLSVYTLTAITLERWHTITHAMQLECKVQLRHAASVMVLGWTFA 497  
Qy 480 FAALFPIEGISSYMKVSYICLPMDIDPSLYVWALLVNLVAFVVICGYTHIYLTVR 539  
D 498 FAVALFPIEGISSYMKVSYICLPMDIDPSLYVWALLVNLVAFVVICGYTHIYLTVR 557  
Qy 540 NPTIVSSSDTKIAKRMATLIFTDFLCMAPISFAISASLKVPITVSKAKILLVLFYPI 599  
D 558 NPNTIVSSSDTKIAKRMATLIFTDFLCMAPISFAISASLKVPITVSKAKILLVLFYPI 617  
Qy 600 NSCANPELYAIFTNFRDRFILLSKFCYEMQAQIYRTSSATHNFHARKSCSAPR 659  
D 618 NSCANPELYAIFTNFRDRFILLSKFCYEMQAQIYRTSSATHNFHARKSCSAPR 677  
Qy 660 VTN--SYVLVPLNISSON 675  
D 678 VTNGSNYTLPLRLHAKN 695

## RESULT 7

FSHR\_PIG STANDARD: PRT: 695 AA.  
AC P49059; 077514;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).  
GN FSHR.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=96011644; PubMed=7590277;  
RA Remy J.J., Labib-Mansais Y., Yerie M., Bozon V., Couture L.,  
RA Pajot E., Grebert D., Salese R.;  
RT The porcine follitropin receptor: cDNA cloning, functional  
expression and chromosomal localization of the gene.;  
RL Gene 163:257-261(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RA Wang Y.F., Meyer K.B., Schmidt K., Wan S.J., Degen S.J.F.,  
RA la Barbera A.R.;  
RT Porcine follicle-stimulating hormone receptor.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY  
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
CC ADENYLATE CYCLASE.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC FSH/LSH/TSH SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: L31966; AAC86933.1; -  
CC HSP: AF025377; AAC24981.1; -  
CC HSP: P23945; 1XUN.  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR Pfam: PF00560; LRR; 2.  
DR Pfam: PF01462; LRRNT; 1.  
DR SMART: SM00013; LRRNT; 1.  
DR PROSITE: PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
DR PROSITE: PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Phosphorylation; Repeat; Leucine-rich repeat.  
FT SIGNAL 1 17 POTENTIAL  
FT CHAIN 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.  
FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 367 387 1 (POTENTIAL).  
FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 399 421 2 (POTENTIAL).  
FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 444 465 3 (POTENTIAL).  
FT DOMAIN 466 485 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 486 508 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 509 528 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 529 550 5 (POTENTIAL).  
FT DOMAIN 551 573 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 574 597 6 (POTENTIAL).  
FT DOMAIN 598 608 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 609 630 7 (POTENTIAL).  
FT DOMAIN 631 695 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 44 68 LRR 1.  
FT REPEAT 69 93 LRR 2.  
FT REPEAT 119 143 LRR 3.  
FT REPEAT 170 192 LRR 4.  
FT REPEAT 193 216 LRR 5.  
FT REPEAT 218 240 LRR 6.  
FT DISULFID 442 517 BY SIMILARITY.  
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 2 2 S -> A (IN REF. 1).  
FT CONFLICT 13 13 T -> S (IN REF. 1).  
FT CONFLICT 60 60 V -> A (IN REF. 1).  
FT CONFLICT 166 166 V -> M (IN REF. 1).  
FT CONFLICT 215 215 Q -> H (IN REF. 1).  
FT CONFLICT 247 247 K -> R (IN REF. 1).  
FT CONFLICT 257 257 S -> T (IN REF. 1).  
FT CONFLICT 334 334 D -> N (IN REF. 1).  
FT CONFLICT 349 349 E -> K (IN REF. 1).  
FT CONFLICT 352 352 T -> A (IN REF. 1).  
FT CONFLICT 383 383 V -> E (IN REF. 1).  
FT CONFLICT 407 407 A -> T (IN REF. 1).  
FT CONFLICT 421 421 V -> I (IN REF. 1).  
FT CONFLICT 427 427 T -> S (IN REF. 1).  
FT CONFLICT 435 435 D -> N (IN REF. 1).  
FT CONFLICT 483 483 L -> V (IN REF. 1).  
FT CONFLICT 550 550 T -> I (IN REF. 1).  
FT CONFLICT 586 586 A -> V (IN REF. 1).  
FT CONFLICT 607 607 S -> L (IN REF. 1).  
FT CONFLICT 691 691 R -> H (IN REF. 1).  
SQ SEQUENCE 695 AA; 78172 MW; E9EBEDB29C79C450 CRC64;



Db 78 SONDVLEVEANVSNLPKLEIRIEKANNLLYIDHDAFONLPNLOYLLISNTGKHLPA 137  
 Qy 121 VHKSQLOKVLDDIQQNINIHIVARNFMSGLSPESVILWLSKNGIEIHNCAFNQGLDE 180  
 Db 138 VHKSQLOKVLDDIQQNINIHIVARNFMSGLSPESVILWLSKNGIEIHNCAFNQGLDE 197  
 Qy 181 LNLSDNNLEELPNDVFGAGSGPVILDISRTKRVHSLPNHGLNKKLRARSTYRLKLPN 240  
 Db 198 LNLSDNNLEELPNDVFGAGSGPVILDISRTKRVHSLPNHGLNKKLRARSTYRLKLPN 257  
 Qy 241 LKAFVTLMEASLYPSHCCAFANLKROISELHPICNKSILRQDIDDMTOIGDORVSLI-D 299  
 Db 258 LKAFVTLMEASLYPSHCCAFANLKROISELHPICNKSILRQDIDDMTOIGDORVSLI-D 316  
 Qy 300 DEPSYKSGDMYNEFDYDLCEVVDVTCSPKPDFAFNPCEDIMGYNLRVLIWFSILAI 359  
 Db 317 DEPSYKSGDMYNEFDYDLCEVVDVTCSPKPDFAFNPCEDIMGYNLRVLIWFSILAI 376  
 Qy 360 TGNTVTLVLTQYKLTVPFLMCNLAFAADLCIGIYVLLLIASVDIHTKSQYHNYAIDWQ 419  
 Db 377 TGNIIVLVLTQYKLTVPFLMCNLAFAADLCIGIYVLLLIASVDIHTKSQYHNYAIDWQ 436  
 Qy 420 TGACDAGFTVFASLSVYTLTALRWHHTITHAMQLECKVQLRHAASVVLGWTFA 479  
 Db 437 TGACDAGFTVFASLSVYTLTALRWHHTITHAMQLECKVQLRHAASVVLGWTFA 496  
 Qy 480 FAALPFIPIGSIYMYKVSICPLMDIDSPLSQLYVMALLVNLVAFVVCYTHIYLTVR 539  
 Db 497 FAVALPFIPIGSIYMYKVSICPLMDIDSPLSQLYVMALLVNLVAFVVCYTHIYLTVR 556  
 Qy 540 NPTIVSSSDTKAKRATLIFTDFLCMAPISEFAISASLKVPILTVSKAKILLVLFYPI 599  
 Db 557 NPTIVSSSDTKAKRATLIFTDFLCMAPISEFAISASLKVPILTVSKAKILLVLFYPI 616  
 Qy 600 NSCANPLYAIFTNFRDRDFILLSKFCYEMOAOIYRTTSSATHNFHARKSHCSAPR 659  
 Db 617 NSCANPLYAIFTNFRDRDFILLSKFCYEMOAOIYRTTSSATHNFHARKSHCSAPR 676  
 Qy 660 VTN--SYVLPLNHSSON 675  
 Db 677 VINGANCTVPLSLHAQN 694

RESULT 9  
 FSHR\_EQUAS STANDARD: PRT: 687 AA.  
 AC Q95179;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).  
 OS Equus asinus (Donkey).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 CC NCBI\_TaxID=9793;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Testis;  
 RX MEDLINE=97338913; PubMed=9195473;  
 RA Richard F., Martinat N., Remy J.-J., Salesse R., Combarnous Y.;  
 RT "Cloning, sequencing and in vitro functional expression of recombinant donkey follicle-stimulating hormone receptor: a new insight into the binding specificity of gonadotrophin receptors.";  
 RL J. Mol. Endocrinol. 18:193-202(1997).  
 CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. FSH/LSH/TSH SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
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 CC EMBL: U73659; AAB18245.1;  
 DR HSSP: P23945; LXUN.  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR InterPro: IPR001611; LRR\_Nterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR Pfam: PF00360; LRR\_3.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR PRINTS: PR00237; GPCR\_Rhodopsin.  
 DR SMART: SM00013; LRRNT; 1.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEPTOR\_1; 1.  
 DR PROSITE: PS00262; G-PROTEIN\_RECEPTOR\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 687 FOLLICLE STIMULATING HORMONE RECEPTOR.  
 FT DOMAIN 18 358 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 359 379 1 (POTENTIAL).  
 FT DOMAIN 380 390 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 391 413 2 (POTENTIAL).  
 FT DOMAIN 414 435 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 436 457 3 (POTENTIAL).  
 FT DOMAIN 458 477 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 478 500 4 (POTENTIAL).  
 FT DOMAIN 501 520 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 521 542 5 (POTENTIAL).  
 FT DOMAIN 543 565 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 566 589 6 (POTENTIAL).  
 FT DOMAIN 590 600 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 601 622 7 (POTENTIAL).  
 FT DOMAIN 623 687 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 69 93 LRR 1.  
 FT REPEAT 94 100 LRR 2.  
 FT REPEAT 101 107 LRR 3.  
 FT REPEAT 108 114 LRR 4.  
 FT REPEAT 115 121 LRR 5.  
 FT REPEAT 122 128 LRR 6.  
 FT DISULFID 434 509 BY SIMILARITY.  
 FT CARBOHYD 191 191 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 199 199 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 687 AA; FC3AF0B5531DA9A CRC64;  
 Query Match 85.6%; Score 3010.5; DB 1; Length 687;  
 Best Local Similarity 86.0%; Pred. No. 2.1e-186;  
 Matches 582; Conservative 38; Mismatches 48; Indels 9; Gaps 3;  
 Qy 1 CHHWLCHSNRFLCQDSKYTEIPTDLPNRIALRFLVTLKRVIPKSGFAGDLEKIEI 60  
 Db 18 CHHQVCHSNRFLCQDSKYTEIPTDLPNRIALRFLVTLKRVIPKSGFAGDLEKIEI 77  
 Qy 61 SONDVLEVEADVFNLPKLEIRIEKANNLLYINPEAFONLPRLSLRLLISNTGKHLPA 120  
 Db 78 SONDVLEVEADVFNLPKLEIRIEKANNLLYIDHDAFONLPNLOYLLISNTGKHLPA 137  
 Qy 121 VHKSQLOKVLDDIQQNINIHIVARNFMSGLSPESVILWLSKNGIEIHNCAFNQGLDE 180  
 Db 138 VHKSQLOKVLDDIQQNINIHIVARNFMSGLSPESVILWLSKNGIEIHNCAFNQGLDE 197  
 Qy 181 LNLSDNNLEELPNDVFGAGSGPVILDISRTKRVHSLPNHGLNKKLRARSTYRLKLPN 240  
 Db 198 LNLSDNNLEELPNDVFGAGSGPVILDISRTKRVHSLPNHGLNKKLRARSTYRLKLPN 257





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Db 138 VHKVHSFQVLDVQDNHIRTIERNTFMGLSSSEVILRLNKNQIQEIKDHAFNGTCLDE 197
Cc 181 LNLSDNNLEELPNDVFOGASPVLDISRTKVSHPNHLNGLKLRARSTYRLKLPN 240
Cc 198 LNLSDNNLEELPEKVPFOGAGIPVVDLISRTKVSHPNHLNGLKLRARSTYRLKLPN 257
Cc 241 LDKFVTLMEASITPSSHCAFANLKRQISELHPICNKSILRQDDIMDTQIGDQVSLDD 300
Cc 258 VNKFRSLJEANFTYPSHCCATNRKQNTQTEFPYICMSMPAKODLGEQTKRHRSAED 317
Cc 301 EPS-YGKGSMDMYNEFDYDLNEVVVTCSPKPAFNPCECDIMGNILRLVIFWISLAI 359
Cc 318 YISHYGRFGPVNEFDYGLCNEVVVTCSPKPAFNPCECDIMGNILRLVIFWISLAI 377
Cc 360 TGNTVLVLTTSOVKLVPRFLMCLNFAFADLCIGIYLLIASVDIHTKSOVHNAIDWQ 419
Cc 378 TGNTVLVLTTSOVKLVPRFLMCLNFAFADLCIGIYLLIASVDIHTKSOVHNAIDWQ 437
Cc 420 TGAGDAAGFFTFVASELSVYTLTATLIERWHITTHAMQLECKVOLRHAASVMVLGTF 479
Cc 438 TGAGDAAGFFTFVASELSVYTLTATLIERWHITTHAMQLECKVOLRHAASVMVLGTF 497
Cc 480 FAALFPPIGSSYKWSICLPMDDSPSLQVYVALLVNLVAFVTCGCTHYLYLVR 539
Cc 498 FTVALLPFGISSYKWSICLPMDDSPSLQVYVALLVNLVAFVTCGCTHYLYLVR 557
Cc 540 NPTIVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLVPLTVSKAKILLVLEVP 599
Cc 558 NPWVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLVPLTVSKAKILLVLEVP 617
Cc 600 NSCANPFLYAIKTKFRFRDFILLSKFCYEMQAIYRTETSSATHNFHARKSHGSSAPR 659
Cc 618 NSCANPFLYAIKTKFRFRDFILLSKFCYEMQAIYRTETSSATHNFHARKSHGSSAPR 677
Cc 660 VTNSS--YVVLPLNH 671
Cc 678 NSDGTIYSLVPLNH 691

RESULT 11
LSHR_BOVIN STANDARD; PRT; 701 AA.
AC Q28005; P79133;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)
DE (LSH-R) (Luteinizing hormone receptor).
GN LHGR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Holstein; TISSUE-Ovary, and Testis;
RA Lussier J.G., Houde A., Ethier J., Silversides D.W.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 80-701 FROM N.A.
RX MEDLINE=98193601; PubMed=9532424;
RA Mamluk R., Wolfenson D., Meidan R.;
RT "LH receptor mRNA and cytochrome P450 side-chain cleavage expression
in bovine theca and granulosa cells luteinized by LH or forskolin.";
RC Domest. Anim. Endocrinol. 15:103-114(1998).
CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYLATE CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
```

FSH/LSH/TSH SUBFAMILY.  
-!- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
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EMBL: U20504; AAC24012.1; -  
EMBL: U87230; AAC33486.1; -  
HSSP: P22888; ILUT.  
DR InterPro: IPR00276; GPCR\_Rhodpsn.  
DR InterPro: IPR001611; LRR\_Nterm.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR Pfam: PF00560; LRR; 2.  
DR SMART: SM00013; LRRNT; 1.  
DR PROSITE: PS00237; G\_PROTEIN\_RECP\_FL\_1; 1.  
DR PROSITE: PS00262; G\_PROTEIN\_RECP\_FL\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing.  
FT SIGNAL 1 26  
FT CHAIN 27 701  
FT LUTROPIN-CHORIOGONADOTROPIC HORMONE  
FT RECEPTOR.  
FT DOMAIN 27 365  
FT TRANSMEM 366 397  
FT DOMAIN 398 397  
FT TRANSMEM 398 418  
FT DOMAIN 419 441  
FT TRANSMEM 442 464  
FT DOMAIN 465 484  
FT TRANSMEM 485 507  
FT DOMAIN 508 527  
FT TRANSMEM 528 551  
FT DOMAIN 552 572  
FT TRANSMEM 573 596  
FT DOMAIN 597 607  
FT TRANSMEM 608 629  
FT DOMAIN 630 701  
FT REPEAT 50 73  
FT REPEAT 124 149  
FT REPEAT 151 173  
FT REPEAT 174 198  
FT REPEAT 200 222  
FT REPEAT 223 246  
FT DISULFID 441 516  
FT CARBOHYD 101 101  
FT CARBOHYD 176 176  
FT CARBOHYD 197 197  
FT CARBOHYD 293 293  
FT CARBOHYD 301 301  
FT CARBOHYD 315 315  
FT VARSPLIC 229 291  
FT CONFLICT 557 557  
FT CONFLICT 577 577  
FT CONFLICT 589 589  
SQ SEQUENCE 701 AA; 78455 MW; 8CDQEP2F59EDBD7 CRC64;  
Query Match 51.4%; Score 1807.5; DB 1; Length 701;  
Best Local Similarity 56.8%; Pred. No. 5.2e-109;  
Matches 357; Conservative 105; Mismatches 145; Indels 21; Gaps 6;  
OY 35 RFLVTKL--RVIPKGSFAGFDLEKIEISONDVLEIADVFNLPKLHIREKANLL 92  
DB 55 RLSLTLPKIPVPSQAPRGLNEVIKIEISQDSLEKIEANAFNLLNLSEILQNTKLV 114  
OY 93 YINPEAFONPLSLRYLLISNTGKILHPLAVHKIOSLQ-KVLLDIODNINIHVARNSEFGL 151  
DB 115 HIEAGFTNPLRLKYLSCNTGTHKLPDVTKIFSEFNFILEICDNLHITTPRNFAGM 174

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OY 152 SPESVILWLSKNGIEZHNCAFGCTGDELNLSDNNLELPLNDVPOGACRVIDLSRT 211
Db 175 NNEISITLKVNGFEEIQSHAFNNTTJLSLEKLENALEKHNDAFRATGPSILDSST 234
OY 212 KVHSLPHNGLNLEKLRARSTYRKLKPLNDLFTVLMASLTYSFHCACAFANLKRQISEL 271
Db 235 KQALPTYGLSIOITLIATSSYSKAKLPSREFNLLDQATLTYPHSCCAFRLN----- 287
OY 272 HPICKKILRODIDDMTOIGDQVRSUIDDEPSYG---KGSMDMNFDFYDLCHNEVDVTC 328
Db 288 -PTNDNFSSYIFKNSFCESCESTARPNNTLYSAIPAESELSOMDYDGFCLPKT-LOC 345
OY 329 SPKPDANPCEDINGNINLRLVILWFLTSILATGNTVTVLVVTSQVLTVPRLMCLNAP 388
Db 346 APEDNAPCEDINGNINLRLVILWFLTSILATGNTVTVLVVTSQVLTVPRLMCLNAP 405
OY 389 ADLCIGVILLTASVDHSTSOVHYVADQGTGACDAGCEFTVFASELSVYLTATLE 448
Db 406 ADPCNGLYLLLSVADQVTKCOYINHAIDNQTCSCNAGPTTVFASELSVYLTATLE 465
OY 449 RHTITTHAQDLCEVLRHAAVSVLWGLVTFAPAAALPFIPIGSSYKVSICLPMIDISPL 508
Db 466 RHTITTAIQLOOLRLKHAIPKVLGMLSTLAVLPLVGVSNKVSICLPMIDVSTL 525
OY 509 SOLYPMALVLLVAFVYICGCTHYIYVTRPVTIVSSSDTKTKAKMATLFTDFLCA 568
Db 526 SOYVILILNMFVFIICACIKIYFVONPELMATNKTAKKMAVLFTDFTCA 585
OY 569 SIPTFASLAKVPLTVYSKAKILVLVYPINSCANPFLYALFTKFRDFPILLSKFGC 628
Db 586 PISFPAISAFKVLPIVFNKVLVLPVNSCANPFLYALFTKFAOPDFILLSKFGC 645
OY 629 YEMAOIYVETSSATHNFARSHCSS 656
Db 646 CKYRAELYREK-----DFSATLSNCKN 667

RESULT 12
LSHR_PIG STANDARD: PRT: 696 AA.
AC PL1582;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)
GN LUCR (Luteinizing hormone receptor).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RX MEDLINE=4933217; PubMed=250284;
RA Loosfelt H., Mirrehi M., Atger M., Salcesse R., Thi M.T.V.H.-L.,
RA Jolivet A., Guichon-Mantel A., Sar S., Jallat B., Garnier J.,
RA Milgrom E.;
RA Cloning and sequencing of porcine LH-hCG receptor cDNA: variants
RA lacking transmembrane domain.;
RL Science 245:525-528(1989).
CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ARE CYTOPLASMIC ENDOPLASMIC RETICULUM RESIDENT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), B, C AND D; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC FSH/LSH/TSR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 6 LUTEININE-RICH REPEATS (LRR).
CC
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CC entlib.htm#license)
CC -----
CC ENBL: M29525; AAA31062.1; -
DR ENBL: M29526; AAA31063.1; -
DR ENBL: M29527; AAA31064.1; -
DR ENBL: M29528; AAA31065.1; -
DR PIR: A41344; A41344.
DR PIR: B41344; B41344.
DR PIR: C41344; C41344.
DR HSP: P22888; LUUT.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003372; LRR_Nterm.
DR Pfam: PF00400; LRR_1.
DR Pfam: PF00560; LRR_2.
DR SMART: SM00013; LRRNT; 1.
DR PROSITE: PS00237; G-PROTEIN RECP_FL1; 1.
DR PROSITE: PS0262; G-PROTEIN RECP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing.
FT SIGNAL 1 27
FT CHAIN 28 696
FT DOMAIN 28 358
FT TRANSHEM 359 386
FT DOMAIN 387 395
FT TRANSHEM 396 418
FT DOMAIN 419 439
FT TRANSHEM 440 462
FT DOMAIN 463 482
FT TRANSHEM 483 506
FT DOMAIN 506 525
FT TRANSHEM 526 547
FT DOMAIN 548 570
FT TRANSHEM 571 594
FT DOMAIN 595 605
FT TRANSHEM 606 626
FT DOMAIN 627 696
FT REPEAT 48 71
FT REPEAT 122 147
FT REPEAT 149 171
FT REPEAT 172 196
FT REPEAT 198 220
FT REPEAT 221 244
FT REPEAT 245 268
FT CARBOHYD 98 99
FT CARBOHYD 174 174
FT CARBOHYD 195 195
FT CARBOHYD 291 291
FT CARBOHYD 299 299
FT CARBOHYD 313 313
FT VARSPIC 317 329
FT VARSPIC 330 696
FT VARSPIC 317 331
FT VARSPIC 332 696
FT VARSPIC 317 628
SQ SEQUENCE 696 AA; 78092 MW; 593DEFC2F982FE CRC64;
Query Match Best Local Similarity 51.48; Score 1807; DB:1; Length 696;
Matches 361; Conservative 98; Mismatches 142; Indels 26; Gaps 8;
OY 28 PRNATLRFVTLK--RVTPKPSFAGCDLEKTEISQNDVLEADVFNSLPKLHEIRI 85
Db 47 PRAGLS-RSLTLPKIPVPSQFRLGVNVEVLEISQSDLEKTEIANAFONLLNLSILL 105
OY 86 EKANNLLYNPEAFONPLSLRYLLISNTGKHLPAVHKIQSLQ-KVLLDQDNINHIYA 144
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Db 106 ONTKNLVYIEPGFTNLPRKLYSICNTGIRKLPDVKYKIPSSSENFLEICDNLHTTVP 165  
Qy 145 RNSFMGLSPESVILMSKNGIEBHNCAPNGTQDELNLSDNNLEELPNDFVQSGGPV 204  
Db 166 ANAFQGNNSISITKLYGNGFEEIOSHAFNGTTLSLELKENAHLKMKHNDAPRGARPS 225  
Qy 205 ILDISRTKVSHPNGLNKKLRARSTYELKLPNLDKRVTLMEASLYTPSHCCAFANL 264  
Db 226 ILDISSTKQALSYGLESQTLATSSYSKLLPSREKFTNLNLDATLTPSHCCAFANL 285  
Qy 265 --RRQ-----ISELHPICKNSILRODIDDMTOIGDQVRSIDDEPSYGRGKMVNEED 316  
Db 286 PTKRONFSFISIKNFSCQCESTARRPNETL-----YSAIFAE-----SELSWDYD 332  
Qy 317 YDLNEVDVTCSPKPDAPNCPEDINGYNILRVLIWIFISILATGNTVTLVLTTSOYKL 376  
Db 333 YGCSPT--LQCAPEPDAPNCPEDINGYDLRLVLIWILINLAIMGVNTVLFVLTSHYKL 391  
Qy 377 TVPRFLMCLNFAFADLCIGIYLLIASVDIHTKSOYHNYAIDMOTGACDAGGFTTFASE 436  
Db 392 TVPRFLMCLNFAFADFCMGLYLLIASVDQTKGYTHAIDMOTGACDAGGFTTFASE 451  
Qy 437 LSVYTLTATLFRWHITTHAMOLECKVQLRHAASVMVLGWTFAFAAALPFIIGISSVMKV 496  
Db 452 LSVYTLTATLFRWHITTAIQLDKLRHAPIMLGWFLSTLAMLPVGVSSIMKV 511  
Qy 497 SICLPMDIDPLSOLYVMAILLVLAFLVVCYTHIYLVTRNPTIVSSSDTKIAKRM 556  
Db 512 SICLPMDVETLSQVLTILNVAFLIACIKIYFVQNPMLMATNKDTKIAKRM 571  
Qy 557 ATLITFELCMAPISFAISALKVPLITVSKAKILLVLPYNSCANPFLYAIFTKPR 616  
Db 572 AVLITFDTCMAPISFAISALKVPLITVSKAKILLVLPYNSCANPFLYAIFTKPR 631  
Qy 617 RDFILLKPGCYEQMAQIYRTETSSA 643  
Db 632 RDFILLKSGCKQHAELRYRKDFS 658

## RESULT 13

LSHR\_MOUSE STANDARD; PRT; 700 AA.  
ID LSHR\_MOUSE  
AC P30730;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)  
DE (LSH-R) (Luteinizing hormone receptor).  
GN LHCR OR LHR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92165799; PubMed=1311310;  
RA Gudermann T., Birnbaumer M., Birnbaumer L.;  
RT Evidence for dual coupling of the murine luteinizing hormone  
RT receptor to adenylyl cyclase and phosphoinositide breakdown and Ca2+  
RT mobilization. Studies with the cloned murine luteinizing hormone  
RT receptor expressed in L cells.  
RL J. Biol. Chem. 267:4479-4488(1992).  
RN [2]  
RP SEQUENCE OF 1-58 FROM N.A.  
RX MEDLINE=93093308; PubMed=1459341;  
RA Huhtaniemi I.T., Eskola V., Pakarinen P., Matikainen T., Sprengel R.;  
RT The murine luteinizing hormone and follicle-stimulating hormone  
RT receptor genes: transcription initiation sites, putative promoter  
RT sequences and promoter activity.  
RL Mol. Cell. Endocrinol. 88:55-66(1992).  
CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.  
CC -1- THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH

CC CC ACTIVATE ADENYLATE CYCLASE.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC FSH/LSH/TSH SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 4 LEUCINE-RICH REPEATS (LRR).  
CC -----  
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CC -----  
CC EMBL; S49753; AAB24402.1; -  
CC EMBL; M81310; AAA39432.1; -  
CC EMBL; M87571; AAA39433.1; -  
CC PIR; A42395; A42395.  
CC HSP; P22888; ILUT.  
CC MGD; MGI:96783; Lhcgr.  
CC InterPro: IPR000276; GPCR\_Rhodpsn.  
CC InterPro: IPR001611; LRR.  
CC InterPro: IPR000372; LRR\_Nterm.  
CC Pfam; PF00001; 7tm\_1; 1.  
CC Pfam; PF00560; LRR; 1.  
CC SMART; SM00013; LRRT; 1.  
CC PROSITE; PS00237; G\_PROTEIN\_RECP\_FL\_1; 1.  
CC PROSITE; PS0262; G\_PROTEIN\_RECP\_FL\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
CC phosphorylation; Repeat; Leucine-rich repeat.  
FT SIGNAL 1 26  
FT CHAIN 27 700  
FT LUTROPIN-CHORIOGONADOTROPIC HORMONE  
FT RECEPTOR.  
FT DOMAIN 27 362  
FT TRANSMEM 363 390  
FT DOMAIN 391 399  
FT TRANSMEM 400 422  
FT DOMAIN 423 443  
FT TRANSMEM 444 466  
FT DOMAIN 467 486  
FT TRANSMEM 487 509  
FT DOMAIN 510 529  
FT TRANSMEM 530 551  
FT DOMAIN 552 574  
FT TRANSMEM 575 598  
FT DOMAIN 599 609  
FT TRANSMEM 610 631  
FT DOMAIN 632 700  
FT REPEAT 52 75  
FT REPEAT 126 150  
FT REPEAT 176 200  
FT REPEAT 225 248  
FT DISULFID 443 518  
FT CARBOHYD 103 103  
FT CARBOHYD 178 178  
FT CARBOHYD 199 199  
FT CARBOHYD 295 295  
FT CARBOHYD 303 303  
FT CARBOHYD 317 317  
SQ SEQUENCE 700 AA; 78214 MB; 8A6840A011E014 CRC64;  
Query Match 51.2%; Score 1799; DB 1; Length 700;  
Best Local Similarity 55.1%; Pred. No. 1.8e-108;  
Matches 362; Conservative 108; Mismatches 153; Indels 34; Gaps 9;  
Qy 28 PRNAIELRVFLVKL--RVTPKGSFAGDLEKIEISONDVLEIVAEVFNLPKLHEIRI 85  
Db 51 PRAGL-ARLSLTYPVKVIPSQAFLGNEVVKISQSDSLERIEANAFNLNLSELI 109  
Qy 86 EKANNLLYNPEAFONLPSRLYLLISNTGKHLPAVHKIOSLO-KVLLDQDNIHIVA 144  
Db 110 QNTKNLLYEPGAFNLPRLKLSICNTGIRLPDVKYKIPSSSENFLEICDNLHTTVP 169

145 RNSFGLSFEVILWLSKNGIEELHNCAPNGTQDLDELNSDNNHLELNDVDFQAGSPV 204  
170 GNAPOGNNESITLKYNGEVEVQSHAFNGTTLISLEKENYILKXHSCTTGQRTOPS 229  
205 ILDSRTKHSPLNHLKLLKRASTYRLKLNEDKFTVTLMEASLYTSHCCAFANL 264  
230 ILOVSTKIOALPSHGLESTLIATSTSLATLPSREKFTSLVATLTYPSHCCAFANL 289  
265 KRQISELHPICNKSTLRQIDDMTOIGDQVSLIDDEPSVG---KGSOMMYNEFYDLCH 321  
290 PKX-----EQNFSPSIFENFSKQCESTVEANNETLYSAIFENELSGQDYDFCS 341  
322 EYVDVTSKPAQNPCEIDMGYNILRLVWFLWFLTSLAIGTNTVTLVLTSTSKYLVPRF 381  
342 PKT-LOCTPEPQNPCEIDMGYNILRLVWFLWFLTSLAIGTNTVTLVLTSTSKYLVPRF 400  
382 LKCNLAPADICIGITLLIASVDHKSQHYKVAIDMGQAGCCDAGCTTFVASELSVYT 441  
401 LKCNLAPADICIGITLLIASVDHKSQHYKVAIDMGQAGCCDAGCTTFVASELSVYT 460  
442 LTAITLERHHTITHAQGLCKVOLRHAASVYLVGTFEFAAALFPFGLISYKVSICLP 501  
461 LTVITLERHHTITAVLOOLKRLRAIPILMGGMFSTLMATLPLVGVSYKVSICLP 520  
502 MDIDSPLSOLYVALLVWLAFLVFCGCTTHIYITVRNPTIVSSSDTKIAKRNATLIF 561  
521 MDVESTLSQVYITSLILLNAFVFCACIVRYFAYONPELTAPKDKTKIAKRNATLIF 580  
562 TDPLCAPISFTASLSKVLPIVTSKAKILVLPVINSKANPFLYATFKNFRDFFI 621  
581 TDPLCAPISFTASLSKVLPIVTSKAKILVLPVINSKANPFLYATFKNFRDFFI 640  
622 LLSKGCYVQAOIYRTESNA-----THNPARKS-----HCS--GAPRV 660  
641 LLSRGCCKHRAELRKEFSACTPNSKNGFPRESSQNALKSIVHCQPTPRV 697

RESULT 14  
LSHR\_RAT  
ID LSHR\_RAT STANDARD: PRT: 700 AA.  
AC P16235; P70646; 063807; 063808; 063809;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)  
GN (LH/CG-R) (luteinizing hormone receptor).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE-89332512; PubMed-2502842;  
RA McFarland K.C., Sprengel R., Phillips H.S., Koehler M.,  
RA Rosenblatt N., Nikolic K., Segaloff D.L., Seeburg P.H.,  
RT "Lutropin-choriogonadotropic hormone receptor: an unusual member of the G  
RL protein-coupled receptor family";  
RL Science 245:494-499(1989).  
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE-91339166; PubMed-1357483;  
RA Aaltonen J.T., Pieltonen P., Katakorp J.T., Rejmanli H.J.,  
RT "Expression of the LH/CG receptor gene in rat: ovarian tissue is  
RT regulated by an extensive alternative splicing of the primary  
RL transcript";  
RL Mol. Cell. Endocrinol. 84:127-135(1992).  
RN (3)  
RP SEQUENCE FROM N.A.  
RX MEDLINE-91209270; PubMed-2019252;  
RA Foo Y.B., Slaughter R.G., Ji T.H.,  
RT "Structure of the luteinizing hormone receptor gene and multiple

RT exons of the coding sequence";  
RL Endocrinology 128:2297-2308(1991).  
RN (4)  
RX SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RL MEDLINE-91006810; PubMed-1976554;  
RA Bernard M.P., Myers R.V., Moble W.R.,  
RT "Cloning of rat lutropin (LH) receptor analogs lacking the soybean  
RL lectin domain";  
RL Mol. Cell. Endocrinol. 71:R19-R23(1990).  
RN (5)  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE-91126285; PubMed-2281186;  
RA Segaloff D.L., Sprengel R., Nikolic K., Ascoli M.,  
RT "Structure of the lutropin/choriogonadotropin receptor";  
RL Recent Prog. Horm. Res. 46:261-303(1990).  
RN (6)  
RP SEQUENCE OF 295-700 FROM N.A.  
RX MEDLINE-91060531; PubMed-2174034;  
RA "esi-Morris C.H., Guozao E., Meng W., Dufau M.L.; receptor gene defines  
RL a soluble nature of the rat luteinizing hormone receptor gene defines  
RL a soluble nature of the rat luteinizing hormone receptor gene defines  
RL J. Biol. Chem. 265:19385-19388(1990).  
RN (7)  
RP SEQUENCE OF 27-37.  
RX MEDLINE-89174723; PubMed-2925659;  
RA Roche P.C., Ryan R.J.,  
RT "Purification, characterization, and amino-terminal sequence of rat  
RL ovarian receptor for luteinizing hormone/human chorogonadotropin";  
RL J. Biol. Chem. 264:4636-4641(1989).  
RN (8)  
RP MUTAGENESIS:  
RX MEDLINE-91332007; PubMed-1714448;  
RA "Ji T.H.,  
RT "Asp383 in the second transmembrane domain of the lutropin receptor.  
RL J. Biol. Chem. 266:9531-9537(1991).  
RN (9)  
CC "-1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGNADOTROPIC HORMONE.  
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
CC ACTIVATE ADENYLATE CYCLASE.  
CC "-1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC "-1- ALTERNATIVE PRODUCTS: AT LEAST 11 ISOFORMS WHICH DIFFER IN  
CC SUBCELLULAR LOCATION ARE PRODUCED BY ALTERNATIVE SPLICING  
CC OF THE SAME GENE.  
CC "-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC FSH/LSH/TSH SUBFAMILY.  
CC "-1- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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DR	EMBL; S40905;	AAB22681.1;	JOINED.
DR	EMBL; S40907;	AAB22681.1;	JOINED.
DR	EMBL; S40909;	AAB22681.1;	JOINED.
DR	EMBL; S40918;	AAB22681.1;	JOINED.
DR	EMBL; S40920;	AAB22681.1;	JOINED.
DR	EMBL; S40803;	AAB22682.2;	-
DR	EMBL; S40787;	AAB22682.2;	JOINED.
DR	EMBL; S40903;	AAB22682.2;	JOINED.
DR	EMBL; S40907;	AAB22682.2;	JOINED.
DR	EMBL; S40909;	AAB22682.2;	JOINED.
DR	EMBL; S40918;	AAB22682.2;	JOINED.
DR	EMBL; S40920;	AAB22682.2;	JOINED.
DR	EMBL; S40795;	AAB22682.2;	JOINED.
DR	EMBL; S40798;	AAB22682.2;	JOINED.
DR	EMBL; S40803;	AAB22683.1;	-
DR	EMBL; S40787;	AAB22683.1;	JOINED.
DR	EMBL; S40903;	AAB22683.1;	JOINED.
DR	EMBL; S40904;	AAB22683.1;	JOINED.
DR	EMBL; S40905;	AAB22683.1;	JOINED.
DR	EMBL; S40907;	AAB22683.1;	JOINED.
DR	EMBL; S40909;	AAB22683.1;	JOINED.
DR	EMBL; S40918;	AAB22683.1;	JOINED.
DR	EMBL; S40920;	AAB22683.1;	JOINED.
DR	EMBL; S40795;	AAB22683.1;	JOINED.
DR	EMBL; S40798;	AAB22683.1;	JOINED.
DR	EMBL; S40803;	AAB22684.2;	-
DR	EMBL; S40787;	AAB22684.2;	JOINED.
DR	EMBL; S40903;	AAB22684.2;	JOINED.
DR	EMBL; S40904;	AAB22684.2;	JOINED.
DR	EMBL; S40905;	AAB22684.2;	JOINED.
DR	EMBL; S40909;	AAB22684.2;	JOINED.
DR	EMBL; S40918;	AAB22684.2;	JOINED.
DR	EMBL; S40920;	AAB22684.2;	JOINED.
DR	EMBL; S40795;	AAB22684.2;	JOINED.
DR	EMBL; S40798;	AAB22684.2;	JOINED.
DR	EMBL; M68928;	AAA41529.1;	-
DR	EMBL; M68917;	AAA41529.1;	JOINED.
DR	EMBL; M68918;	AAA41529.1;	JOINED.
DR	EMBL; M68919;	AAA41529.1;	JOINED.
DR	EMBL; M68920;	AAA41529.1;	JOINED.
DR	EMBL; M68921;	AAA41529.1;	JOINED.
DR	EMBL; M68922;	AAA41529.1;	JOINED.
DR	EMBL; M68923;	AAA41529.1;	JOINED.
DR	EMBL; M68925;	AAA41529.1;	JOINED.
DR	EMBL; M68926;	AAA41529.1;	JOINED.
DR	EMBL; M68927;	AAA41529.1;	JOINED.
DR	PfR; A32460;	A32460.	
DR	PfR; A41343;	A41343.	
DR	HSP; P22888;	ILUT.	
DR	InterPro: IPR000276;	GPCR_Rhodpsn.	
DR	InterPro: IPR001611;	LRR_Nterm.	
DR	InterPro: IPR000372;	LRR_Nterm.	
DR	Pfam: PF00001;	7tm_1; 1.	
DR	Pfam: PF00360;	LRR; 1.	
DR	SMART; SM00013;	LRNT; 1.	
DR	PROSITE; PS00337;	G.PROTEIN RECP_FL_1; 1.	
DR	PROSITE; PS00362;	G.PROTEIN RECP_FL_2; 1.	
KW	G-protein coupled receptor;	Transmembrane; Signal;	
KW	Phosphorylation;	Repeat; Leucine-rich repeat;	
FT	SIGNAL	1 26	
FT	CHAIN	27 700	LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR.
FT	DOMAIN	27 362	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEN	363 390	1 (POTENTIAL).
FT	DOMAIN	391 399	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEN	400 422	2 (POTENTIAL).
FT	DOMAIN	423 443	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEN	444 466	3 (POTENTIAL).
FT	DOMAIN	467 486	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEN	487 509	4 (POTENTIAL).
FT	DOMAIN	510 529	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEN	530 551	5 (POTENTIAL).
FT	DOMAIN	552 574	CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	575	598	6 (POTENTIAL).
FT	DOMAIN	599	609	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	610	631	7 (POTENTIAL).
FT	DOMAIN	632	700	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	52	75	LRR 1.
FT	REPEAT	126	150	LRR 2.
FT	REPEAT	152	175	LRR 3.
FT	REPEAT	176	200	LRR 4.
FT	REPEAT	202	224	LRR 5.
FT	REPEAT	225	248	LRR 6.
FT	REPEAT	250	271	LRR 7.
FT	DISULFID	443	518	BY SIMILARITY.
FT	CARBOHYD	103	103	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	178	178	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	199	199	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	303	303	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	317	317	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	83	132	MISSING (IN ISOFORM 1950).
FT	VARSPLIC	133	157	MISSING (IN ISOFORM 1759).
Query Match				
Best Local Similarity				
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7				
Qy	28	PRNAIEURFVLTKL--RVIPKSGFAGDGLKIEISQNDVLEIVTEADVESNLPLKLEHRI	85	
Db	51	PRAGL-ARLSITYLPVKVIPSQAFRGNEVVKKIEISQSDSLERIEANAFDNLNUSELLI	109	
Qy	86	EKANLLYINPEAFQNLPSRLLYSINTGIKHPAVHKIQSLQ-KVLLDIOONIHIVA	144	
Db	110	QNTKNLLYIEGAFNLPRLLKYLISICNTGIRTLPDVTKISSSEFNFILEICDNLHTIP	169	
Qy	145	RNSFMGLSPFSVILWLSKNGIEETHNCAFNGTQDELNLSNNNLEELPNDVFGASGV	204	
Db	170	GNAPQGNNEVSVTLLKXGNGFEEVQSHAFNGTTLISLEKENIYLEKMHSGAFQATGPS	229	
Qy	205	ILDISRTKVSPLNPHLENLKLRASTRYRLKLPNDLKFVTLMEASLTYPSSHCCAFANL	264	
Db	230	ILDISSTKLQNALPSHGLESTQTLALSSYSKLTLPSEKFTSLLVATLTYPSHCCAFANL	289	
Qy	265	KRQISELHPICNKSILRQDDMTQIGDQRVSLIDDEPSYG---KGSMDMYNEFDYDLCN	321	
Db	290	PKK-----EQNFSFISPFENFSKQCESTVRKADNETLYSAIPEENELSGWDYDGFCS	341	
Qy	322	EVDVDTCSPPDAFNPCEDEINGYILRLVLIWFISILATGNTTVLVLTTSQYKLTVPFR	381	
Db	342	PKT--LQCAPEPDAFNPCEDEINGYAFRLVLIWLIINLAIFGNLTFLVLTTRYKLTVPFR	400	
Qy	382	LMCNLAFADLCIGTYLLLIASVDTHTKSOYHNVAIDMQTAGCDAAGFTTFVASELSVYT	441	
Db	401	LMCNLSFADFCMGYLLLIASVDSQTKQYHNHAIIDMQTGSCGGAAGFTTFVASELSVYT	460	
Qy	442	LTATTLERWHTITHAMGLECKVQLRHAASVNLGWTFAFAALFPFIGISSYMKVYSICLP	501	
Db	461	LTVTTLERWHTITTVAVOLDQRLRLRHAIPIMLGGMFLSTLIATMPLVGISNMYKYSICLP	520	
Qy	502	MDIDSPLSQLYMALLVNLVLAFFVIGCYTHIYLTVRNPTRIVSSSSTKTAKRMATLIF	561	
Db	521	MDVESTLSQYVILSILNLYVAVFVACACIRIYFAVQNPELTAPNKDTKIAKKNAILIF	580	
Qy	562	TDFLCMAPIFFFAISASLKVPLIVTSKAKILLVLPINSCANPFLYAIFTKFNRRDPFI	621	
Db	581	TDFTCMAPIFFFAISAAFKVPLIIVTNSKILLVLPYVNSCANPFLYAIFTKAPORDLELL	640	
Qy	622	LLSKFGCYEQMAQIYRTTSSATHNFARKSHCSS	656	
Db	641	LLSRFGCKKRAELYYRK-----EFSAYTNSCKN	669	
RESULT 15				
LSHR_HUMAN				
ID	LSHR_HUMAN	STANDARD:	PRT:	699 AA.

AC P22888; 01-AUG-1991 (Rel. 19, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Luteinizing-horogonadotropin hormone receptor precursor (LH/CG-R)  
 DE (LSH-R) (Luteinizing hormone receptor).  
 GN LHCR OR LHRR OR LCGR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1] Sequence from N.A.  
 RN [2] MEDLINE-91075314; PubMed-7244890;  
 RA Mitsuhashi T, Nakamura K., Takakura Y., Miyamoto K., Hasegawa Y.,  
 RA Tsukui Y., Igarashi M.;  
 RA "Cloning and sequencing of human LH/hCG receptor cDNA.";  
 RL Biochem. Biophys. Res. Commun. 172:1049-1054(1990).  
 RN [2]  
 RP Sequence from N.A.  
 RP Tissue=Ovary;  
 RA Jia X.-C., Oikawa M., Bo M., Tanaka T., Ny T., Boine I., Hsueh A.J.W.;  
 RA "Expression of human luteinizing hormone (LH) receptor: interaction  
 RA with LH and chorionic gonadotropin from human but not equine, rat,  
 RA and ovine species.";  
 RL Mol. Endocrinol. 5:759-768(1991).  
 RN [3]  
 RP Sequence from N.A.  
 RP Tissue=Thyroid;  
 RA Frazier A.L., Robbins L.S., Stork P.J., Sprengel R., Segaloff D.L.,  
 RA Cone R.D.;  
 RA "Isolation of TSH and LH/CG receptor cDNAs from human thyroid:  
 RA regulation by tissue specific splicing.";  
 RL Mol. Endocrinol. 4:1264-1276(1990).  
 RN [4]  
 RP 3D-STRUCTURE MODELING OF 51-232.  
 RA Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H.,  
 RA Hendrickson W.A., el Tayar N.;  
 RA "Structural predictions for the ligand-binding region of glycoprotein  
 RA hormone receptors and the nature of hormone-receptor interactions.";  
 RL Structure 3:1341-1353(1995).  
 RN [5]  
 RP VARIANT FMPP GLY-578.  
 RA MEDLINE-94019815; PubMed-7692306;  
 RA Shenter A., Leue L., Kousl S., Merendino J.J. Jr., Minegishi T.,  
 RA Cutler G.B. Jr.;  
 RA "A constitutively activating mutation of the luteinizing hormone  
 RA receptor in familial male precocious puberty.";  
 RL Nature 365:652-654(1993).  
 RN [6]  
 RP VARIANTS FMPP ILE-571 AND GLY-578.  
 RA MEDLINE-94108425; PubMed-8281137;  
 RA Kremer H., Mariman E., Otten B.J., Moll G.W. Jr., Stoeltinga G.B.A.,  
 RA Wit J.M., Jansen M., Drop S.L., Faas B., Ropers H.-H., Brunner H.G.;  
 RA "Co-segregation of missense mutations of the luteinizing hormone  
 RA receptor gene with familial male-limited precocious puberty.";  
 RL Hum. Mol. Genet. 2:1779-1783(1993).  
 RN [7]  
 RP VARIANT FMPP ILE-577.  
 RA MEDLINE-95276728; PubMed-7757065;  
 RA Kousl S., van Dop C., Geffner M.E., Rabi W., Carel J.-C.,  
 RA Chausain J.-L., Mori T., Merendino J.J. Jr., Shenker A.;  
 RA "Characterization of heterogeneous mutations causing constitutive  
 RA activation of the luteinizing hormone receptor in familial male  
 RA precocious puberty.";  
 RL Hum. Mol. Genet. 4:183-188(1995).  
 RN [8]  
 RP VARIANT FMPP VAL-572.  
 RA MEDLINE-95229804; PubMed-7714085;  
 RA  
 RA Yano K., Saji M., Hataka A., Moriya N., Okuno A., Kohn L.D.,  
 RA Cutler G.B. Jr.;  
 RA "Constitutively activating point mutation in the luteinizing  
 RA hormone/choriogonadotropin receptor gene in cases of male-limited  
 RA precocious puberty.";  
 RL J. Clin. Endocrinol. Metab. 80:1162-1168(1995).  
 RN [9]  
 RP VARIANT FMPP VAL-568.  
 RA MEDLINE-9535560; PubMed-7629248;  
 RA Latronico A.C., Anast J., Arnold I.J., Mendonca B.B., Domenice S.,  
 RA Albano M.C., Zachman K., Wajchenberg B.L., Tsigos C.;  
 RA "A novel mutation of the luteinizing hormone receptor gene causing  
 RA male gonadotropin-independent precocious puberty.";  
 RL J. Clin. Endocrinol. Metab. 80:2490-2494(1995).  
 RN [10]  
 RP VARIANT LCH PRO-593.  
 RA MEDLINE-95225561; PubMed-7719243;  
 RA Kousl S., van Dop C., Geffner M.E., Rabi W., Carel J.-C.,  
 RA Chausain J.-L., Mori T., Merendino J.J. Jr., Shenker A.;  
 RA "Characterization of heterogeneous mutations causing constitutive  
 RA activation of the luteinizing hormone receptor in familial male  
 RA precocious puberty.";  
 RL Hum. Mol. Genet. 4:183-188(1995).  
 RN [11]  
 RP VARIANT FMPP ILE-577.  
 RA MEDLINE-96233936; PubMed-8829636;  
 RA Cocco S., Meloni A., Marini M.G., Cao A., Mol P.;  
 RA "A missense (T577I) mutation in the luteinizing hormone receptor gene  
 RA associated with familial male-limited precocious puberty.";  
 RL Hum. Mutat. 7:164-166(1996).  
 RN [12]  
 RP VARIANT FMPP THR-398.  
 RA MEDLINE-9703378; PubMed-8929952;  
 RA Pina B.A., Brown D.J., Smith J., Clayton P.E., Gregory J.M.;  
 RA "A mutation in the luteinizing hormone receptor gene  
 RA familial and sporadic male-limited precocious puberty: genotype does  
 RA not always correlate with phenotype.";  
 RL J. Med. Genet. 33:143-147(1996).  
 RN [13]  
 RP VARIANT LCH TYR-616.  
 RA MEDLINE-96157015; PubMed-8559204;  
 RA Latronico A.C., Anast J., Arnold I.J., Rapaport R., Mendonca B.B.,  
 RA Bloise W., Castro M., Tsigos C., Chrousos G.P.;  
 RA "Brief report: testicular and ovarian resistance to luteinizing  
 RA hormone caused by inactivating mutations of the luteinizing  
 RA hormone-receptor gene.";  
 RL New Engl. J. Med. 334:507-512(1996).  
 RN [14]  
 RP VARIANT LCH ARG-131.  
 RA MEDLINE-97358168; PubMed-9215288;  
 RA Miarashi M., Meduri G., Pissard S.,  
 RA Loosfelt H., Jolivet A., Rapaport R., Milgrom E., Bougneres P.;  
 RA "Comparison of immunocytochemical and molecular features with the  
 RA phenotype in a case of incomplete male pseudohypogonadism  
 RA associated with a mutation of the luteinizing hormone receptor.";  
 RL J. Clin. Endocrinol. Metab. 82:2159-2165(1997).  
 RN [15]  
 RP VARIANTS LEU-GLN-13 INS: SER-284 AND ASN-306.  
 RA Wu S.-M., Jose M., Hallermeier K., Rennert O.M., Chan W.-Y.;  
 RA "Polymorphisms in the coding exons of the human luteinizing hormone  
 RA receptor gene.";  
 RL Hum. Mutat. 11:333-334(1998).  
 RN [16]  
 RP VARIANT FMPP VAL-373.  
 RA MEDLINE-98138569; PubMed-9467560;  
 RA Gromoll J., Patach C.-J., Simoni M., Nordhoff V., Sippell W.G.,  
 RA Nieschlag E., Szekes B.B.;  
 RA "A mutation in the first transmembrane domain of the lutropin receptor  
 RA causes male precocious puberty.";  
 RL J. Clin. Endocrinol. Metab. 83:476-480(1998).  
 RN [17]  
 RP VARIANT LCH LYS-354.  
 RA MEDLINE-98289384; PubMed-9626144;  
 RA







KW Receptor. 688 AA; 77341 MW; 441P0D9E7D01DF18 CRC64;  
SQ SEQUENCE 688 AA; 77341 MW; 441P0D9E7D01DF18 CRC64;  
Query Match 99.0%; Score 3482; DB 11; Length 688;  
Best Local Similarity 99.3%; Pred. No. 5.4e-251;  
Matches 670; Conservative 0; Mismatches 1; Indels 4; Gaps 1;  
QY 1 CHWLCHCSNRVFLCQDSKVTEIPTDLPNAIELRVLTCLRVIPKGSFAGFDLEKIEI 60  
DB 18 CHWLCHCSNRVFLCQDSKVTEIPTDLPNAIELRVLTCLRVIPKGSFAGFDLEKIEI 77  
QY 61 SONDVLEIEADVSNPLKHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 120  
DB 78 SONDVLEIEADVSNPLKHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 137  
QY 121 VHKIOSLOKVLDDIQQNINIHIVARNFSGLSFESVILWLSKNGIEIEHNCAPNGTOLDE 180  
DB 138 VHKIOSLOKVLDDIQQNINIHIVARNFSGLSFESVILWLSKNGIEIEHNCAPNGTOLDE 193  
QY 181 LNLSDNNLEELPNDVFOGASGVPVLDISRTKVHSLPNHGLENLKLRARSTYRLKLPN 240  
DB 194 LNLSDNNLEELPNDVFOGASGVPVLDISRTKVHSLPNHGLENLKLRARSTYRLKLPN 253  
QY 241 LDKFVTLMEASLTYPSCCAFAANLKRQISELHPICNKSILRODDMTQIGDQVSLIDD 300  
DB 254 LDKFVTLMEASLTYPSCCAFAANLKRQISELHPICNKSILRODDMTQIGDQVSLIDD 313  
QY 301 EPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNILRVLIWFTSILAIT 360  
DB 314 EPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNILRVLIWFTSILAIT 373  
QY 361 GNTTVLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLLIASVDHTKSOYHNYAIDWOT 420  
DB 374 GNTTVLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLLIASVDHTKSOYHNYAIDWOT 433  
QY 421 GAGCDAAGFTTFVASELSVYTLTTLERWHITTHAMOLECKVQLRHAASVNLGWTFAF 480  
DB 434 GAGCDAAGFTTFVASELSVYTLTTLERWHITTHAMOLECKVQLRHAASVNLGWTFAF 493  
QY 481 AAALPFIPIGSISSYKMSVCLPMDIDSPLSQVYVMAALLVNLVAFVVICGCTHYIYLVN 540  
DB 494 AAALPFIPIGSISSYKMSVCLPMDIDSPLSQVYVMAALLVNLVAFVVICGCTHYIYLVN 553  
QY 541 PTIVSSSDTKIAKRNATLIPTDFLCMAPISFAISASLKVPITVSKAKILLVLFYPI 600  
DB 554 PTIVSSSDTKIAKRNATLIPTDFLCMAPISFAISASLKVPITVSKAKILLVLFYPI 613  
QY 601 SCANPELYAIFTKNFRDRDFILLSKFCGYEMOQAIYRTTSSATHNFHARKSHCSAPRV 660  
DB 614 SCANPELYAIFTKNFRDRDFILLSKFCGYEMOQAIYRTTSSATHNFHARKSHCSAPRV 673  
QY 661 TNSYVLVPLNHSOON 675  
DB 674 TNSYVLVPLNHSOON 688

RESULT 2  
Q8R428 PRELIMINARY; PRT; 695 AA.  
ID Q8R428  
AC Q8R428  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Follicle stimulating hormone receptor.  
CN FSHR.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-HARTLEY; TISSUE-TESTIS;  
RA Suzuki O.

\*Guinea pig follicle stimulating hormone receptor.\*  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY082514; AAL92577.1; -  
KW Receptor. 695 AA; 77838 MW; 9A3ECF419C45227B CRC64;  
SQ SEQUENCE 695 AA; 77838 MW; 9A3ECF419C45227B CRC64;  
Query Match 87.6%; Score 3080.5; DB 11; Length 695;  
Best Local Similarity 87.2%; Pred. No. 4.4e-221;  
Matches 591; Conservative 37; Mismatches 47; Indels 3; Gaps 2;  
QY 1 CHWLCHCSNRVFLCQDSKVTEIPTDLPNAIELRVLTCLRVIPKGSFAGFDLEKIEI 60  
DB 18 CHWLCHCSNRVFLCQDSKVTEIPTDLPNAIELRVLTCLRVIPKGSFAGFDLEKIEI 77  
QY 61 SONDVLEIEADVSNPLKHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 120  
DB 78 SONDVLEIEADVSNPLKHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 137  
QY 121 VHKIOSLOKVLDDIQQNINIHIVARNFSGLSFESVILWLSKNGIEIEHNCAPNGTOLDE 180  
DB 138 VHKIOSLOKVLDDIQQNINIHIVARNFSGLSFESVILWLSKNGIEIEHNCAPNGTOLDE 197  
QY 181 LNLSDNNLEELPNDVFOGASGVPVLDISRTKVHSLPNHGLENLKLRARSTYRLKLPN 240  
DB 198 LNLSDNNLEELPNDVFOGASGVPVLDISRTKVHSLPNHGLENLKLRARSTYRLKLPN 257  
QY 241 LDKFVTLMEASLTYPSCCAFAANLKRQISELHPICNKSILRODDMTQIGDQVSLIDD 299  
DB 258 LDKFVTLMEASLTYPSCCAFAANLKRQISELHPICNKSILRODDMTQIGDQVSLIDD 317  
QY 300 EPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNILRVLIWFTSILAIT 359  
DB 318 DEFSYSGRGTMYAEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNILRVLIWFTSILAIT 377  
QY 360 GNTTVLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLLIASVDHTKSOYHNYAIDWOT 419  
DB 378 GNTTVLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLLIASVDHTKSOYHNYAIDWOT 437  
QY 420 GAGCDAAGFTTFVASELSVYTLTTLERWHITTHAMOLECKVQLRHAASVNLGWTFA 479  
DB 438 GAGCDAAGFTTFVASELSVYTLTTLERWHITTHAMOLECKVQLRHAASVNLGWTFA 497  
QY 480 AAALPFIPIGSISSYKMSVCLPMDIDSPLSQVYVMAALLVNLVAFVVICGCTHYIYLVN 539  
DB 498 AAALPFIPIGSISSYKMSVCLPMDIDSPLSQVYVMAALLVNLVAFVVICGCTHYIYLVN 557  
QY 540 NPTIVSSSDTKIAKRNATLIPTDFLCMAPISFAISASLKVPITVSKAKILLVLFYPI 599  
DB 558 NPTIVSSSDTKIAKRNATLIPTDFLCMAPISFAISASLKVPITVSKAKILLVLFYPI 617  
QY 600 NSCANPELYAIFTKNFRDRDFILLSKFCGYEMOQAIYRTTSSATHNFHARKSHCSAPRV 659  
DB 618 NSCANPELYAIFTKNFRDRDFILLSKFCGYEMOQAIYRTTSSATHNFHARKSHCSAPRV 677  
QY 660 VTN--SYVLVPLNHSOON 675  
DB 678 VTN--SYVLVPLNHSOON 695

RESULT 3  
Q9DGF5 PRELIMINARY; PRT; 696 AA.  
ID Q9DGF5  
AC Q9DGF5  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Follicle stimulating hormone receptor precursor.  
OS Cynops pyrrhogaster (Japanese common newt).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae; Cynops.  
OX NCBI\_TaxID=8330;  
RN [1]  
RP SEQUENCE FROM N.A.

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RC TISSUE-TESTIS;
RX MEDLINE=20403884; PubMed=10944452;
RA Nakayama Y., Yamamoto T., Oba Y., Nagahama Y., Abe S.-I.;
RT "Molecular cloning, functional characterization, and gene expression
of a follicle-stimulating hormone receptor in the testis of newt
Cyrops pyrrhogaster.";
RL Biochem. Biophys. Res. Commun. 275:121-128(2000).
DR HSP: P23945; 1XUN.
DR EMBL: AB005587; BAB13501.1; -.
DR InterPro: IPR000276; GPCR_Rhodpan.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR Pfam: PF00001; 7cml_1; 1.
DR Pfam: PF00560; LRR; 2.
DR SMART: SM00237; GPCR_Rhodpan.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 696 POTENTIAL.
FT SEQUENCE 696 AA: 78633 MW: 179A6FC800B71E57 CRC64;

Query Match 70.5%; Score 2479; DB 13; Length 696;
Best Local Similarity 71.4%; Pred. No. 2.8e-176;
Matches 484; Conservative 79; Mismatches 107; Indels 8; Gaps 5;

OY 1 CHHLCNHRVFLCDSKVTETDLPRLNATLRLVTLKRVIPKGSFAGCDLEKIEI 60
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 18 CHP-VCCLNHRVFTQESHVQIDIPRINSTRFLRVLTQVTPKAAFGSDFEDVNEI 76
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 61 SQNVLEVTEADVSNPKLHETRIKANKLLYNPAPQMLPRLYLLISNTGKILPA 120
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 77 SQNDVLTATDANVSHLPALRIETRIKANKLLYIDPQNPUSKLLISNTGLQVPA 136
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 121 VHKIOSQVLDQDNIINHIIVARNSPGLSFVTLMSKNGIEIEHNCAP 180
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 137 VSRISFHVLDVDNIINRIHGNKSPAGLSSEITIRLKNKNGIEIEHNCAP 196
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 181 LNLSDNNKLELNDVFOGASGVPLDTSRTKVSHPNGLNKLKRASTYTRKLLPN 240
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 197 LNLSDNQRLEKLPDVOGATGVPLDTSRTKVSHPNGLNKLKRASTYTRKLLPN 256
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 241 LDRPVTLMASLTPSHCCAFANLAKROISELHPICNKSILRQDIDMTQICD-ORVSLID 299
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 257 LERFALTEANLTPSHCCAFANREKSEMPICNKSFGKHSKEDNKLRRPSNED 316
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 300 DEPSYKGSQDNTN-REYD-ICNEVDVYTCSPKPDAPNCPEDINGNLRVLPIS 355
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 317 YLSSTGFSYLVNGDFWYDILCNEVDVYTCSPKPDAPNCPEDINGNLRVLPIS 376
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 356 ILAITGNTVVLVLTTSQYKLTVPRLMCLNAPADLCIGYLLLIASVDIHTKSOYNYA 415
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 377 ILAITGNTVVLVLTTSQYKLTVPRLMCLNAPADLCIGYLLLIASVDIHTKSOYNYA 436
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 416 IDNQTGACDAAGFTVPASLSVYLTATLIERHHTITHAMOLECKVOLRAHSAVYLG 475
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 437 IDNQTGSCAAGFTVPASLSVYLTATLIERHHTITHAMOLDKRVFRHATAIMVG 496
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 476 WTPAALPPIFGISYKYSICLPMQDPSLSQYVALLVNLVAFVVICGYTHY 535
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 497 WTPAALPPIFGISYKYSICLPMQDPSLSQYVALLVNLVAFVVICGYTHY 556
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 536 LTVRNPVYSSSDTKLARNATLPTDPLCHAPISFPAISAKVLPATYSKALVYL 595
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 557 LTVRNPVYSSSDTKLARNATLPTDPLCHAPISFPAISAKVLPATYSKALVYL 616
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 596 PTPINSCANPFLYATPTKFRDPFTLLSKFCCEMAOATYTESSTATHFRHAKS 655
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 617 PTPINSCANPFLYATPTKFRDPFTLLSKFCCEMAOATYTESSTATHFRHAKS 676
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 656 SAPR--VTNNTVYVPLNN 671
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 677 PAKYSAASHTVPLNN 694

RESULT 4
OQOMP8 PRELIMINARY; PRT; 673 AA.
AC OQOMP8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE FSH receptor.
DE FSH RECEPTOR.
OS Podarcis sicula.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Lacertoidea;
OC Lacertidae; Podarcis.
OX NCBI_TaxID=65484;
RN [1] JENSEN FROM N.A.
RC TISSUE=OVARY.
RX MEDLINE=21458565; PubMed=11574163;
RA Borrelli L., De Stasio R., Parfiet E., Filosa S.;
RT "Molecular cloning, sequence and expression of follicle-stimulating
hormone receptor in the lizard Podarcis sicula.";
RL "Gene 275:149-156(2001)".
DR EMBL: AJ292553; CAC82173.1; -.
DR InterPro: IPR000276; GPCR_Rhodpan.
DR InterPro: IPR001611; LRR.
DR Pfam: PF00001; 7cml_1; 1.
DR Pfam: PF00560; LRR; 2.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 673 AA: 76288 MW: 68994C8B5F67B5 CRC64;

Query Match 55.5%; Score 1956; DB 13; Length 673;
Best Local Similarity 55.3%; Pred. No. 2.5e-13;
Matches 407; Conservative 80; Mismatches 149; Indels 48; Gaps 11;

OY 3 HWLHC-CSRNVFLCDSKVTETDLPRLNATLRLVTLKRVIP- 53
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 21 HPTCOPDLNMLNFTCDSKVTQVOTPSQERHG-----TGIFPHQNKHITERAFLGLD 71
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 54 DLEKTEISQNDVLEVTEADVSNPKLHETRIKANKLLYNPAPQMLPRLYLLISNT 113
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 72 EYEKTEISQNDALGTIESNVFSLPKLYETIIEKANKLLYIDRYAPQMLPRLYLLISNT 131
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 114 GIKHLPVAVHKIOSQVLDQDNIINHIIVARNSPGLSFVTLMSKNGIEIEHNCAP 173
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 132 AHTLPVYVQIHSSVAFVLDVDQDNIINHIIVARNSPGLSFVTLMSKNGIEIEHNCAP 191
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 174 NGTOLDLNLSDNNKLELNDVFOGASGVPLDTSRTKVSHPNGLNKLKRASTY 233
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 192 NGTILSDNLSDNKLKLELNEVFOGASGVPLDTSRTKVSHPNGLNKLKRASTY 251
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 234 RLKLPNMLKRVTLMEASLTPSHCCAFANLAKROISELHPICNKSILRQDIDMTQICDQ 293
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 252 NLKVPPLDKPRSLTEANLTPSHCCAFANLAKROISELHPICNKSILRQDIDMTQICDQ 303
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 294 RYSLDDPSYKGSQDNTN-REYD-ICNEVDVYTCSPKPDAPNCPEDINGNLRVYL 350
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 304 -----GTDFDLDDDEHDYQSLCKEVEVICFEPDAPNCPEDINGNLRVYL 350
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 351 IWPISILATGNTVVLVLTTSQYKLTVPRLMCLNAPADLCIGYLLLIASVDIHTKSO 410
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 351 IWPISILATGNTVVLVLTTSQYKLTVPRLMCLNAPADLCIGYLLLIASVDIHTKSO 410
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 411 YHYAIDHQTGACDAAGFTVPASLSVYLTATLIERHHTITHAMOLECKVOLRAHSA 470
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 411 YHYAIDHQTGACDAAGFTVPASLSVYLTATLIERHHTITHAMOLECKVOLRAHSA 470
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 471 VVYLGMTFAFAALPPIFGISYKYSICLPMQDPSLSQYVALLVNLVAFVVICG 530
DB II : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db      470 FHLVGFARFTVAIIPIFOVSYMKVSIKLPMDIETPPCQAIIMFLLVLNITLAFLLISTS 529
Qy      531 YTHIYLVTRNPTIVSSSDTKIAKRMATLIITDFLCMAPISEFFAISLKLPLITVSKAK 590
Db      530 YISIYITVTRNPTIISNSDTKIAKRMATLIITDFLCMAPISEFFAISLKLPLITVSKAK 589
Qy      591 ILLVLFPYINSCAN--PELYAIFTKNFRDFFILLSKFCYEMOAOIYRTETSSATHNPHA 649
Db      590 ILLVLFPYINRAPTVVRH--LHQEPQDFFILLSKFGLCEKQAOIYRTETSSYPTTSHM 647
Qy      650 RKSHCSSAPRVTN--SYVLVPLNH 671
Db      648 KNGCHTPASKASEGPAYALVPLNY 671

RESULT 5
Q16225 PRELIMINARY; PRT; 410 AA.
AC Q16225:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Follicle-stimulating hormone receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95000244; PubMed=7916967;
RA Gromoll J., Ried T., Holtgreve-Grez H., Nieschlag E., Gudermann T.;
RT "Localization of the human FSH receptor to chromosome 2 p21 using a
RT genomic probe comprising exon 10.";
RL J. Mol. Endocrinol. 12:265-271(1994).
DR EMBL; S73526; AAB32225.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPT_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEPT_FL_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 410 AA; 46008 MW; F345E029C16BC792 CRC64;

Query Match 54.18; Score 1901.5; DB 4; Length 410;
Best Local Similarity 89.5%; Pred. No. 1.5e-133;
Matches 367; Conservative 15; Mismatches 25; Indels 3; Gaps 2;

Qy      269 SELHPICNKSILRODIDMTQIGDQVSLIDD--EPSYKSGSDMMYNEFDYDLCEVVDVT 327
Db      1 SELHPICNKSILROEVDMTQRCORSLAEDNESSYRGFDMTYTFEDYDLCEVVDVT 60
Qy      328 CSPKPDAPNCPEDIMGYNLRVLIWIFISILAITGNTTVLVVLTTSQYKLTVPFRLMCLNLA 387
Db      61 CSPKPDAPNCPEDIMGYNLRVLIWIFISILAITGNTTVLVVLTTSQYKLTVPFRLMCLNLA 120
Qy      388 FADLCIGIYLLIASVDHTSKQHNHYAIDWQTGAGCDAAGFFTFVASELSVYTLTATL 447
Db      121 FADLCIGIYLLIASVDHTSKQHNHYAIDWQTGAGCDAAGFFTFVASELSVYTLTATL 180
Qy      448 ERWHTITHAMOLECKVQLRHAASVMVLCWTFAPAAALPFIQISSYMKVSLCPMDIDSP 507
Db      181 ERWHTITHAMOLDCKVQLRHAASVMVLCWTFAPAAALPFIQISSYMKVSLCPMDIDSP 240
Qy      508 LSQIVMALLVNLVAFVVICGYTHIYLTNRNPTIVSSSDTKIAKRMATLIITDFLCM 567
Db      241 LSQIVMALLVNLVAFVVICGYTHIYLTNRNPTIVSSSDTKIAKRMATLIITDFLCM 300
Qy      568 APISFAISASLKLPLITVSKAKILLVLPYINSCANPFLYAIFTKNTFRDFFILLSKFG 627
Db      301 APISFAISASLKLPLITVSKAKILLVLPYINSCANPFLYAIFTKNTFRDFFILLSKFG 360
Qy      628 CYEMOAOIYRTETSSATHNPHARKSHCSSAPRV--NSVVLVPLNHSSQN 675

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Db      361 CYEMOAOIYRTETSTVHTHPRNGHCSSAPRVTSSTGYIILVPLSLHAQN 410

RESULT 6
Q98T84 PRELIMINARY; PRT; 662 AA.
ID Q98T84:
AC Q98T84:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Follicle-stimulating hormone receptor precursor.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Kumar R.S., Ijiri S., Trant J.M.;
RT "Molecular Biology of Channel Catfish Gonadotropin Receptors: 2. cDNA
RT Cloning, Functional Expression, and Seasonal Gene Expression of the
RT Follicle-Stimulating Hormone Receptor.";
RL Biol. Reprod. 0:0-0(2001).
DR EMBL; AF285182; AAK16067.1; -.
DR HSSP; P23945; 1XUN.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR001611; LRR.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF00560; LRR; 4.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPT_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEPT_FL_2; 1.
KW Receptor; Signal.
FT SIGNAL
SQ SEQUENCE 662 AA; 74846 MW; DC19F07A2CADEED CRC64;

Query Match 52.38; Score 1840.5; DB 13; Length 662;
Best Local Similarity 55.3%; Pred. No. 9.7e-129;
Matches 356; Conservative 107; Mismatches 150; Indels 31; Gaps 5;

Qy      5 LCHCSNRVFLCQDSKVTEITDLPNNAIEIURFVLTKLRVLPKGSFAGOLEKTEISQND 64
Db      24 LANGTTRSFCLASKVHMPYHIPKNTTYVEIKLTRIIMLPSPRAMSSLDLKLRLVSENG 83
Qy      65 VLEVEIADVFENLPKLHEIRTEKANNLLYINPEAFONLPURLYLLISNTGKHLPAVHKI 124
Db      84 VLQRIEAYAFANLKLKEITITKSNLVCMDRHTFWGLPKRLYLTISNTGLTLPDFSKV 143
Qy      125 QSLQ-KVLLDQDNNIHIIVARNSEFMGLSPESVI-LMLSKNGIEEIHNCAPNGTOLDEN 182
Db      144 QSAFAEFLDLEDNHNHIEVIPSNAFAGLTSGTITELRTKNGITEVDNRNAGTKIEKF 203
Qy      183 LSDNNNLEELPNDVQFQASGVILDDISRTKVHSLPNHGLENLKLRARSTYLRKLPLND 242
Db      204 LMGNOQLKRIHNYAFLGAEGLVLDISRTAISLSPENMLRLKLLIATSVSLRWLPLE 263
Qy      243 KFTVLMESLTPSHCCAFANLKRQISELHPICKNSILRQDIDDDMTQIGDQVSLIDDEP 302
Db      264 IFTELQANLTPSHCCAFKPKKNNKNNKRLNDSTIR-----NQEP 306
Qy      303 SYGKSDMMYNEFDYDLCEVVDVTCSKPDAPNCPEDIMGYNLRVLIWIFISILAITGN 362
Db      307 -----YFEEHCKDVEVRCYEPEDAFNCPEDIMGTFLRLVLIWIFISVLAVLGN 355
Qy      363 TTVLVLTTSQYKLTVPFRLMCLNLAFCADLCIGIYLLIASVDHTSKQHNHYAIDWQTGA 422
Db      356 FTVLVLVLLSSRTKLVKPKFLMCHLAFADFCMGLYLLIIGSDVLDQTRSHYNYGIMQTV 415
Qy      423 GCDAGGFTVFASELSVYTLTATLTERWHTITHAMOLECKVQLRHAASVMVLCWTFAPAA 482
Db      416 GCGTAGFLTVFASELSVYTLTATLTERWHTITHAMLERQLRLHHACSVMAFGWLFVLA 475

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OY 483 ALPDPICSSNYSKVSICLDPDLSOLYVALLVLYLAFVVICGCTHYHLYTVNPT 542
DB 476 ALTPVIGSSVMTSKSLCPDMDVETASSOAYINLLVLYLAFVTVACVYRILYTVHPA 535
OY 543 IVSSSDTKIARMTALFTDFLCHWAFSPFAISAKVPLITVSKAKILLVLPVNSC 602
DB 536 SVPDADARVAKRMVLYVFTDFLCHAFISFAISALAKOPLITVSHARVLLVLPVNSC 595
OY 603 ANPFLYAFETRRDRPFIILSKPCCYEMQAIYRTETSSATHN 646
DB 596 ANPFLYAFETSKDFVLTSPFCFESRARTVETSS-LHN 638

RESULT 7
QSPS8 QSPS8 PRELIMINARY: PRT: 701 AA.
AC QSPS8
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DE Luteinizing hormone receptor.
OS Bos taurus (Bovine).
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HOLSTEIN; TISSUE-CORPUS LUTEUM;
RA Kawada N., Tanada H., Inaba T., Sawada T.;
RT Molecular cloning of a full-length cDNA encoding bovine luteinizing
RT hormone receptor and its expression in COS cells.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL: AF491303; AM09535.1;
KW Receptor.
SQ SEQUENCE 701 AA: 78455 MW: D70AE862EB265CCF CRC64;
Query Watch 51.3%; Score 1803.5; DB 6; Length 701;
Best Local Similarity 56.7%; Pred. No. 5.9e-126;
Matches 356; Conservative 106; Mismatches 145; Indels 21; Gaps 6;
OY 35 RPYLTKL--RVIPKSPAGFDLEKIEISONDVLEYEADVFNPLKHLRIEKANLL 92
DB 55 RSLTLPYKIPVSOAPGLNEVIEISODSLEKIEANFNLNLSEILQNTKNV 114
OY 93 YINPEAPNLPRLYLLISWTGKILPAPVHKIOSLQ-KVLLDQDNINHIYARNPMGL 151
DB 115 HITAGATNPLPLATLISCTGINKLPVTRIFSPFNFLIEICDMLAITIPRNPOOM 174
OY 152 SPESVILLWLSKNGTEIHNKAPNGTOLDLNLSDNNHLPNDVPOGASGVLLDTSPT 211
DB 175 NNESTILKLYGPEZIOSHAFNGTLLISLKNARLEKMHNDAPRGATGPSILDIST 234
OY 212 KYHSLPHHGLENLKLRARSTYRLKPLNLDKFTVLMKASLTYPSCCANLKRQISEL 271
DB 235 QLOALPTIGLESIGTILATSSYSKLKPSREKFTNLLDATALTPSHCCAFRNL----- 287
OY 272 HPICKNSILRODDMTQIGDORVSLIDDEPSYG---KGSOMNTEFDYDLCEVVDYC 328
DB 288 -PTNDFNPSIFKNSKQCESTARPNNETLYSAFAESELSDYDYGCLPRT-LQC 345
OY 339 SPKDAFNPCEDINGYNILVNLVNLSTLAIATGVTYVLYVTTSQYKLTVPRLCNLAP 388
DB 346 APEPDAPNCEIDINGNLYLVNLVNLINLAIATGVTYVLYVTTSQYKLTVPRLCNLAP 405
OY 389 ADICIGITALLASVDIHTKSOYHNAYIDNQTGACDAGPPTVPASELSVYTLTATLE 448
DB 406 ADPCNGLYLLIASVDAQTKQGYNHAIADNQTGSCSAAGPTVPASELSVYTLTATLE 465
OY 449 RNHTITHAOLCEKVLORHAAVYVLYGTFAAALFPFGISSYKVSICLPMIDISPL 508
DB 466 RNHTITTAIOLDKLRHAIKPVKLGGLHFTLIAVLPLVGVSTKVSICLPMIDVSTL 525
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OY 509 SOLYVALLVLYLAFVVICGCTHYHLYTVNPTIVSSSDTKIARMTALFTDFLCH 568
DB 526 SVPTGILTLILNKNAPILITCTKIKYIFAYQNPALATNKTOKIARMTALFTDFLCH 585
OY 569 PISFPAISAKVPLITVSKAKILLVLPVNSCANPFLYATFNFRDRPFIILSKPCC 628
DB 586 PISFPAISAKVPLITVSKAKILLVLPVNSCANPFLYATFNFRDRPFIILSKPCC 645
OY 629 YEMQAIYRTETSSATHNPHARKSCSS 656
DB 646 CKYRAELYRRK-----DFSAYISCKN 667

RESULT 8
QSPW16 QSPW16 PRELIMINARY: PRT: 662 AA.
AC QSPW16
DT 01-MAR-2000 (T-EMBLrel. 13, Created)
DT 01-MAR-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Follicle-stimulating hormone receptor precursor.
OS Clarias gariepinus (Sharptooth catfish) (African catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Clariidae; Clariis.
OX NCBI_TaxID=13013;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA Bogerd J., Andersson E., Blomenrohr M., Tensen C.P., Granneman J.C.,
RA Schulz R.W., Goos H.J.;
RT Cloning and functional characterization of a testicular follicle-
RT stimulating hormone receptor from the African catfish;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RW EMBL: AJ012647; CAB31907.1;
KW RSP;
DR HSP; P23945; IUN
DR InterPro: IPR000276; GPCR_Rhodopn.
DR InterPro: IPR001611; LRR_
DR Pfam: PF00001; 7tm_1; 1.
DR Pfam: PF00560; LRR; 4.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; Signal.
FT CHAIN 1 22 POTENTIAL.
FT SIGNAL 1 22 FOLLICLE-STIMULATING HORMONE RECEPTOR.
SQ SEQUENCE 662 AA: 74891 MW: 5C849EDDBDID4F5 CRC64;
Query Watch 51.2%; Score 1798.5; DB 13; Length 662;
Best Local Similarity 54.2%; Pred. No. 1.3e-125;
Matches 352; Conservative 109; Mismatches 158; Indels 31; Gaps 5;
OY 9 SNRPVLCDSKVYEIPDLPNRAIELRVLTKLRVLPKSPAGFDLEKIEISONDVLEV 68
DB 28 TTRSFCLAGSKVQHPHPIPIINTVVEIKUTQIIFPYRAMSSLDKLRIMVSENGALOR 87
OY 69 IEADVFNPLKHLRIEKANLLINPEAFONLPSRLYLLISNTGIRKHPAVHKIOSLQ 128
DB 88 IEAVAFANULTILEITITKSNLVSNDRDTPNGLPKRLYLTISNGLTVPDFSKVQSA 147
OY 129 -KVLLDQDNINHIYARNPMGLSPFSVY-LWLSKNGIEIHNKAPNGTOLDLNLSDN 186
DB 148 FEFLDNDNHIEVHISNAFAGLSGTITELRITKNGITEVERNPNFTKMLKPLMGN 207
OY 187 NNLDELNDVFOGASGVLLDTSRTKVSILPHHGLENLKLRARSTYRLKPLNLDKFTV 246
DB 208 QOLKRIHNAFLGAEGLVLDISRTAIISSLPENMLRLKLLIATSVYSLRMLPNELEFAE 267
OY 247 LMEASLTYPSCCANLKRQISELHPICNKLSILRODDMTQIGDORVSLIDDEPSYCK 306
DB 268 LTOANLTPSHCCAFNKKFNKLEKHLNLCNVSTIR-----NOEP----- 306
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Db 564 AKVSIQLPMDTEPLALAYILVLLLVNVAITVSCVYKIIYITVNPQNPQKOTKIA 623
Oy 554 KRMATLITDPLCMAPISFPAISASLKVPLITVSKAKITLLVLPYDINSCANPFLYAIETK 613
Db 624 KMAVLITDPLCMAPISFPAISASLKVPLITVSKAKITLLVLPYDINSCANPFLYAIETK 623
Oy 614 NFRDFFILLSKFGCYENAOIYR-----TETSSATNHFARKSHCSAPRVN 662
Db 684 AFORDVILLSKFGCKROAQAYRCORVSPKSTGTOVKVTONMR-----QSLPNMOD 737
Oy 663 SYVLVPLNR 671
Db 738 DYELLENH 746

RESULT 14
OSPP9 PRELIMINARY; PRT: 764 AA.
AC OSPP9;
DT 01-JUN-2002 (T:EMBLrel. 21, Created)
DT 01-JUN-2002 (T:EMBLrel. 21, Last sequence update)
DE Thyroid stimulating hormone receptor.
GN TSHR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP Igarashi M., Nagata A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL082601; AAL2560.1; -.
KW Receptor.
SQ
SEQUENCE 764 AA; 86647 MW; 188BED1B617E7052 CRC64;
Query Match 47.1%; Score 1657; DB 6; Length 764;
Best Local Similarity 47.2%; Pred. No. 54e-115;
Matches 344; Conservative 113; Mismatches 198; Indels 74; Gaps 13;
Oy 6 CHCSN-----RVFLQDSKVTETDLPRLNATLRLVTLKRVIPKSGFAGCDLEKIETS 61
Db 29 CEHQEDDFRV-TCKD--IHSIP-PLPPTOTLKFIEHLKLTIPSRFSLNLSRIYLS 84
Oy 62 QNDVLEIADVPSNLPKLHEIRIEKANNILYINPEAFONLPSRLYLLISMTGKHLPAV 121
Db 85 IDATLQLESOSPLNSLHMEIRNTRSLTYINPCALKDPLKFLGTFNGTGLVPPOL 144
Oy 122 HKIOSLQK-VLLDIOONTNTHIVARNSPGLSFESVILMSKNGIEEHNKAFNGTOLDE 180
Db 145 TKVYSTDVFFLEITDNPYMTSIPANAFQGLCNETLTKLYNNGFTSIOGHAFNGTKLDA 204
Oy 181 LNLSDNNLELNDVFOGA-SGPVLDISRTKVSHPNGLNKLKRLARSTYRLKLP 239
Db 205 VYLNKKNYLTVDKDAFGVSGPTLDDVSVTSVTLPPKGLSHLKLARNTLTKLP 264
Oy 240 NLDFKVTLMKASLTTPSCCAFNLRKPSLHP-ICNKSILRQ-----DI 284
Db 434 ASLSVYTLITLERNHITTHAMQLECKVQLRHAASVNLGTFAPAAALPIPIGTSY 493

RESULT 15
OSPP9 PRELIMINARY; PRT: 763 AA.
AC OSPP9;
DT 01-JUN-2001 (T:EMBLrel. 17, Created)
DT 01-JUN-2001 (T:EMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (T:EMBLrel. 21, Last annotation update)
DE Thyrotropin receptor.
GN TRHR.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxId=9685;
RN [1]
RP Nguyen L.O., Karamanoglu Arseven O., Gerber H., Stein B.S.;
RL Cloning of the cat thyrotropin receptor and evidence against an
RT autoantibody recognition of feline hyperthyroidism.;
DR EMBL; AF218264; AA00133.1; -.
KW Receptor.
SQ
SEQUENCE FROM N.A.
RA Jameson L.O., Kopp P.;
RL Cloning of the cat thyrotropin receptor and evidence against an
RT autoantibody recognition of feline hyperthyroidism.;
DR EMBL; AF218264; AA00133.1; -.
KW Receptor.
SQ
SEQUENCE 763 AA; 86588 MW; 937P60A140487D60 CRC64;
Query Match 47.1%; Score 1654.5; DB 6; Length 763;
Best Local Similarity 46.9%; Pred. No. 8.3e-115;
Matches 343; Conservative 112; Mismatches 205; Indels 71; Gaps 11;
Oy 6 CHCSN-----RVFLQDSKVTETDLPRLNATLRLVTLKRVIPKSGFAGCDLEKIETS 61
Db 29 CEHQEDDFRV-TCKD--IHSIP-PLPPTOTLKFIEHLKLTIPSRFSLNLSRIYLS 84
Oy 62 QNDVLEIADVPSNLPKLHEIRIEKANNILYINPEAFONLPSRLYLLISMTGKHLPAV 121
Db 85 IDATLQLESOSPLNSLHMEIRNTRSLTYINPCALKDPLKFLGTFNGTGLVPPOL 144
Oy 122 HKIOSLQK-VLLDIOONTNTHIVARNSPGLSFESVILMSKNGIEEHNKAFNGTOLDE 180
Db 145 TKVYSTDVFFLEITDNPYMTSIPANAFQGLCNETLTKLYNNGFTSIOGHAFNGTKLDA 204
Oy 181 LNLSDNNLELNDVFOGA-SGPVLDISRTKVSHPNGLNKLKRLARSTYRLKLP 239
Db 205 VYLNKKNYLTVDKDAFGVSGPTLDDVSVTSVTLPPKGLSHLKLARNTLTKLP 264
Oy 240 NLDFKVTLMKASLTTPSCCAFNLRKPSLHP-ICNKSILRQ-----DI 284
Db 434 ASLSVYTLITLERNHITTHAMQLECKVQLRHAASVNLGTFAPAAALPIPIGTSY 493
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Db      265 LTLSEHLTRADLSYPSHCFAKNOKIKIGLESFMCNDSIRSLRQRKSVNALNGPFDQ 324
QY      285 DDMTOIGBORVSLIDDEPSYKGSMDMY-----NEF 315
Db      325 EYEXYLGDSHAGYKDNNSKFRQDTRSNSHYVFFEEODEILGFCOELKNPOEETIQAFDSHY 384
QY      316 DYDLCEVVDVTCSPKPDAPNCPCEIDIMGYNLRVLIMFISILAITGNTVLVVLTTSOYK 375
Db      385 DYTVCGNEDMCTKSPDEFNCEIDIMGYKFLRIYVWFSLALGNFVLITLITSHYK 444
QY      376 LTVPRFLMCNLAFAADLCIGIYLLLIASVDIHTKSOYHNYAIDMOTGAGCDAAGFTVFAS 435
Db      445 LTVPRFLMCNLAFADEFCMGWYLLIASVDLYTHSEYNNHAIIDMOTGPCNAGFTVFAS 504
QY      436 ELSVYTLTAITLERHHTTHAMOLECKVOLRHAASVYLGWTFAPFAALFPIFGISSYK 495
Db      505 ELSVYTLTAITLERHHTTHAMOLECKVOLRHAASVYLGWTFAPFAALFPIFGISSYK 564
QY      496 VSIQCPMDISPLSQLYVVALLVNLVAFVVICGCTHYLTVRNPYIVSSSDTKIAKR 555
Db      565 VSIQCPMDIETPLALAYITLVLNLVAFIIVCSCYKITYITVRNPQYMTGDKDKIAKR 624
QY      556 MATLIETDFLCMAPISEFAISASLKYPLITVSKAKILVLYFPINSCANPFLYAITFTKNF 615
Db      625 MAVLIETDFMCMAPISFVLSALMKNKPLITVNSKILLVLYFPINSCANPFLYAITFTKTF 684
QY      616 RRDFFILSKFCGCEYMOAOIYR-----TETSATVHNPARKSHSCSAPRVYNSY 664
Db      685 QRDVFFILSKFCIGCKROAOAYRGORVSPKNSGTGICQVOKYTRNMR-----QSLPNMODDY 738
QY      665 VLVPPLNHSSON 675
Db      739 ELLENSHLTPN 749

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